us-10-074-225a-5.rag

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GenCore version 5.1.6
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OM protein - protein search, using sw model

2005, 13:31:29; Search time 140.273 Seconds (without alignments) 408.065 Million cell updates/sec June 15 Run on:

US-10-074-225A-5 966 1 HPHKHHSHEQHPHGHHPHAH.....PSFPLPHHKHPLKPDNQPFP 148 Title: Perfect score: Sequence:

Searched:

seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 2105692 Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_16Dec04:\* .: geneseqp1980s:\*

1: geneseqp1980s:\*
2: geneseqp1990s:\*
4: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result		Query				
No.	Score	Match	Match Length DB	DB	ID	Description
	996	100.0	148	5	ABB79807	Abb79807 Rabbit hi
7	996	100.0	148	Ŋ	ABB79806	Abb79806 Human his
m	996	100.0	148	Φ	ADH10411	Adh10411 Human HPR
4	996	100.0	525	'n	ABB79804	
2	996	100.0		Φ	ADH10409	Adh10409 Human HPR
9	949	98.2		Φ)	ADE76897	
7	949	98.2		Φ	ADL12335	Adl12335 Human ste
α	543	56.2		ഗ	ABB79805	Abb79805 Rabbit hi
σ	543	56.2		æ	ADH10410	Adh10410 Rabbit HP
10	302	31.3		ഹ	ABB07123	Abb07123 HRGP thro
rr T	280.5	29.0		ထ	ADH10412	Adh10412 Rabbit HP
12	254.5	26.3		4	ABG28019	
13	251.5	26.0		4	ABG25331	Novel
14	248.5	25.7		4	ABG27250	Abg27250 Novel hum
15	242.5	25.1		4	ABG19767	Novel
16	242.5	25.1		Φ	ABO60258	Abo60258 Human gen
17	241.5	25.0		~	AAR24393	Segue
18	240	24.8		4	ABG09949	
19	230	23.8		4	ABG25337	7
20	225.5	23.3		4	ABG23595	Abg23595 Novel hum
21	221	22.9		4	AAM18326	9
22	221	22.9		4	ABB37360	Abb37360 Peptide #
23	221	22.9		4	AAM3 0 8 1 4	Aam30814 Peptide #
24	221	22.9	292	4,	ABB32108	Abb32108 Peptide #
25	221	22.9		4	ABB22646	Abb22646 Protein #

4 4 4 4 5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	292 4 AAM70490 292 4 AAM58050 292 4 AAM58050 292 4 AAM52171 292 5 AAG12171 292 5 AAG1293 227 4 AAG12879 82 4 AAG12879 82 4 AAM13580 82 4 AAM25978 82 4 AAM55978 82 4 AAM53343 82 4 AAM53343 82 4 AAM53343 82 4 AAM65721 82 5 AAG36289 304 4 AAG08412 86 5 ADK36683		Abg52171 Human liv Aam05933 Peptide #	Abg40129 Human pep Abg14399 Novel hum	-	Aam13580 Peptide # Abb32509 Peptide #			Abb18015 Protein #	Aam65721 Human bon	Aam53343 Human bra	Abg47362 Human liv	Aam01333 Peptide #	Abg35350 Human pep	Novel	Abg08412 Novel hum	Adk36683 Novel hum
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## ALIGNMENTS

Histidine proline rich glycoprotein; HPGP; rabbit; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator. Rabbit histidine proline rich glycoprotein His/Pro-rich domain. ABB79807 standard; protein; 148 AA (first entry) Oryctolagus cuniculus WO200264621-A2. 22-AUG-2002. 25-NOV-2002 ABB79807; 

14-FEB-2002; 2002WO-US004336

14-FEB-2001; 2001US-0268370P

(ATTE-) ATTENUON LLC.

Mazar AP; Plunkett ML, Donate F, Harris S,

WPI; 2002-666989/71. P-PSDB; ABN84910.

New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.

Claim 1; Page 13; 82pp; English

The present sequence is the protein sequence of the histidine-proline-rich (H/P) domain of rabbit anti-angiogenic histidine proline rich glycoprotein (HPRG, see also ABB79805). Claimed anti-angiogenic polypeptides or peptides comprise: the H/P domain (see ABB79806) of human HPRG; an H/P domain of rabbit HPRG; a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or therapeutically labeled anti-angiogenic polypeptide, peptide

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the diagnostically labeled polypeptide, peptide or peptide multimer; an antibody specific for an epitope of HPRG that is present in the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any of the domain, or an antigen-binding fragment of the antibody; a method for inhibiting cell migration, cell invasion, cell proliferation or angiogenesis, or for inducing apoptosis; a method for treating a subject having a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis; a method of midration, invasion, proliferation, or angiogenesis; a method of cetecting the presence of HPRG or its cleavage product or its peptide in a biological sample; isolated mucleic acids encoding the polypeptide, cetecting the presence of HPRG or its cleavage product or its peptide in a biological sample; isolated mucleic acids encoding the polypeptide, cetransfected cells; a method of providing to a cell, tissue or organ and angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its peptide or peptide multimer; an affinity ligand useful for angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an affinity ligand useful for charageptide, or the peptide multimer; an affinity ligand useful for binding molecule, comprising the comprising or enriching cells (compositions and methods are useful in diagnosing or treating a disease or confition associated with undesired cell migration, invasion, compositions and methods are useful in diagnosing or treating a disease or confitient in the periode confitient and methods are useful in diagnosing or treating a disease or confitients. All produces and methods are useful in inhibiting the growth of primary criticatures. HPRG is especially useful in inhibiting the growth of primary criticatures is a large and methods are useful in inhibiting molecules. The criticopathy, inflaammation, endometricals, arthritis, attended are disease. comprising diseases like Alzheimer's or Parkinson's disease. The antibodies iogenesis and are useful for promoting in pertinent disease states, and in various stically useful HPRG-related composition, stimulators of ang neovascularization stimulators of multimer; a 

Ž Sequence 148

ö 9 PPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV PPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV <u>НРНКНН</u>SHEQH РНGНН РНАНН РНЕНD ТНRQH РНGHH РНGHH РНGHH РНGHH РНGHH РНС Gaps . 0 Length 148; Indels 100.0%; Score 966; DB 5; 100.0%; Pred. No. 5.2e-80; ive 0; Mismatches 0; SFPLPHHKHPLKPDNOPFP 148 vative 121 LPLPEANFP Query Match Best Local Similarity Matches 148; Conser DFQDYGPCD propyceco LPLPEANFP Н 61 61 121 셤 a ઠે à

Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian. Human histidine proline rich glycoprotein His/Pro-rich domain. protein; 148 AA entry) (first ABB79806 standard; WO200264621-A2 Homo sapiens 25-NOV-2002 ABB79806; RESULT 2 ABB79806 

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DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV

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22-AUG-2002

The present sequence is the protein sequence of the histidine-prolinerich (II/P) Gonain of human anti-angiogenic histidine proline rich
cit (II/P) Gonain of human anti-angiogenic histidine proline rich
cycoprotein (HPRG, see also ABF99804). Claimed anti-angiogenic
cylyooprotein (HPRG, see ABB12818); a variant of these that is capable
of inhibiting angiogensels, endothalial cell proliferation or endothalial
tube formation in vitro or in vivo; or a pentapeptide having the generic
sequence given in ABB79808. Also claimed are: chemically synthesised or
recombinantly produced peptide multimers; a diagnostically wintro or in vivo; or a pentapeptide having the generic
sequence given in ABB79808. Also claimed are: chemically synthesised or
recombinantly produced peptide multimers; a diagnostically useful HPRG-related composition, comprising
the domains in a way which inhibits the anti-angiogenic activity of
HPRG or the domain, or an mitigen-binding fragment of the antibody; a
method for inhibiting cell migration, cell invasion, cell proliferation
cc of the domains in a way which inhibits the anti-angiogenic activity of
HPRG or Inhibiting cell migration, or angiogenesis; a method of
subject having a disease or condition associated with undesired cell
engration, invasion, proliferation, or angiogenesis; a method of
ctertung the presence of HPRG or its cleavage product or its peptide
migration, invasion, proliferation, or angiogenesis a method of
ctertung the presence of HPRG or its cleavage product or its peptide
a biological sample; isolated multimer; an expression vector; transfected cells; a method of
ctertung the peptide multimer; an expression vector; transfected cells; a method of
ctertung the peptide multimer; an expression or corpical migration, or angiogenesis, e New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis. DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 
 1
 HPHKHRSHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGHHPHGHHPHGHHPHGHHPHCH
 Gaps diseases like Alzheimer's or Parkinson's disease. The antibodies stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various .; 0 Length 148 Indels Query Match 100.0%; Score 966; DB 5; Best Local Similarity 100.0%; Pred. No. 5.2e-80; Matches 148; Conservative 0; Mismatches 0; Mazar AP Plunkett ML, Claim 1; Page 13; 82pp; English 14-FEB-2002; 2002WO-US004336 2001US-0268370P (ATTE-) ATTENUON LLC Harris S, WPI; 2002-666989/71. P-PSDB; ABN84910. Sequence 148 AA; 14-FEB-2001; immunoassays Donate F, 61 ద ଚ ਨੇ

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The invention relates to an isolated tropomyosin (Tpm)-related
antiangiogenic receptor polypeptide or peptide, which is a is a fragment
of a full-length native Tpm protein expressed on the surface of
endothelial cells, or a variant of the fragment. It has a molecular mass
of about 17 kDa and corresponds in its sequence to, or is a variant of,
an internal fragment of a native Tpm isoform which is a binding site for
antiangiogenic polypeptide agents; The isolated antiangiogenic receptor
polypeptide, peptide or variant has substantially the same biochemical
activity of binding to the antiangiogenic polypeptide agent that
classification to the isolated polypeptide or peptide is human histidine-proline
crich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic
human kininogen (HK), the D5 domain of HK, or a Tpm-binding,
antiangiogenic homologue, variant, domain or fragment of the HK or its D5
domain. The Tpm-related antiangiogenic receptor polypeptide or peptide,
antiangiogenic compositions are useful for inhibiting endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        migration, invasion, proliferation or angiogenesis, for inducing endothelial cell apoptosis, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease or peripheral artery disease. The present sequence represents a human HPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; human.
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121 LPLPEANFPSFPLPHHKHPLKPDNOPFP
                                         SFPLPHHKHPLKPDNQPFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HPRG protein
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                                                                                                                                                                                                                                                                  ADH10411 standard;
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                                                                                                                                                                                                                                                                                                                                         ADH10411;
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y disease. The pro (H/P) rich domain

protein His-Pro Sequence 148 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
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                                                                                               Gaps
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/note= "Proline-rich domain"
350. .497
/note= "Histidine-proline-rich domain, region also
specifically claimed in Claim 1"
                                             ö
               Length 148;
                                            Indels
            Score 966; DB 8;
Pred. No. 5.2e-80;
Mismatches 0;
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100.0%; SC.
100.0%; Pr/
                                                                                                                                                                                                                                                                                                                          ABB79804 standard; protein; 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002; 2002WO-US004336
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                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                             Best Local Similarity 100 Matches 148; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-666989/71.
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                                                                                                                                                                                                                                                                                                                                                          ABB79804;
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               Query Match
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congigating purpoposition, resping the diagnostically labeled polypeptide, peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the H/P demain of specific for an epitope of HPRG that is present in the H/P demain of a way which inhibits the anti-angiogenic activity of HPRG or the domain of a way which inhibits the anti-angiogenic activity of HPRG or the domain.

CC and martigen-binding fragment of the antibody; a method for inhibiting cor an antigen-binding fragment of the antibody; a method of inhibiting diagonesis, a method for treating a subject having a disease or induction associated with undesired claim a subject and in associated with undesired claimistation, invasion, colding apoptosis; a method of etherting the presence of HPRG or proliferation, or angiogenesis; a method of etherting the presence of HPRG or its cleavage product or proliferation, invasion, solated nucleic acids encoding the polypeptide, peptide or peptide multimer; an expression vector; transformed or transferred cells; a method of providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an affinity ligand useful for binding molecule, comprising the polypeptide, peptide or peptide multimer, immobilised to a solid support or cartier; and a method of isolating HPRG-binding molecule, or isolating or cells expressing the binding molecule, or receptor, from a complex mixture. The compositions and methods are useful in diagnosing or treating alsease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis, such as cancer, archritis, peptic ulcers, or fracturers. HPRG is especially useful; in inhibiting the growth of primary tumours or metastases, and manded encared in treating neurodegenesis and are useful for promoting metastion in pertinent disease states, and in various in pertinent disease states, and in various in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 1.9e-79;
; Mismatches 0;
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  angiogenic polypeptide, peptide or
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100.0%;
rvative 0;
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Best Local Similarity
Matches 148; Conser
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angiogenesis; gene
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ADH10409
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The invention relates to an isolated tropomyosin (Tpm)-related
antiangiogenic receptor polypeptide or peptide, which is a is a fragment
cof a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass
cof about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isolated antiangiogenic peotypeptide agents; The isolated antiangiogenic receptor
colypeptide, peptide or variant has substantially the same biochemical
cativity of binding to the antiangiogenic polypeptide agent that
contive Tpm internal fragment. The antiangiogenic polypeptide agent that
contive Tpm internal fragment. The antiangiogenic polypeptide agent that
contive Tpm internal fragment of reagment of binds to the isolated polypeptide or peptide, a Tpm-binding, antiangiogenic
contine to the isolated polypeptide or peptide, a Tpm-binding, antiangiogenic
contine to the isolated polypeptide or peptide, a Tpm-binding,
contine to the DS domain of HK, or a Tpm-binding,
contine The Tpm-related antiangiogenic receptor polypeptide or peptide,
contine Tpm-related antiangiogenic receptor polypeptide or peptide,
contine the Tpm-related antiangiogenic receptor polypeptide or peptide,
contine The Tpm-related antiangiogenic receptor polypeptide or peptide,
contine thy invasion, proliferation or angiogenesis, or conterting
contentalial cell apoptosis, or for treating tumours or cancer, diabetic
contenpathy, neovascular glaucoma, uveitis, endometriosis, arthritis,
contensed angiogenesis is desired, e.g. coronary artery disease or
content despetator of a properiode or peripheral sample, for
coronary arter
                                                                                                                                                                                                                                                                                                                                                                                                                           New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer.
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                                                /note = His-Pro rich domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 LPLPEANFPSFPLPHHKHPLKPDNQPFP 497
/note = pro-rich domain 350. .497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; SEQ ID NO 21; 117pp; English
                                                                                                                                                                                                                                                                                                                                        Juarez J,
                                                                                                                                                                                           17-MAR-2003; 2003WO-US008060.
                                                                                                                                                                                                                                                                                                                                      Donate F,
                                                                                                                                                                                                                                                                                        (ATTE-) ATTENUON LLC
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-090604/09.
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                                                                                                  WO2003077872-A2
                                                                                                                                                                                                                                         15-MAR-2002;
                                                                                                                                              25-SEP-2003
                                                                                                                                                                                                                                                                                                                                        Mccrae K,
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RESULT 6 ADE76897

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Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                             human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                               Human protein expressed in a liver disorder #18.
 Z
protein; 525
                                                                                                                                           30-JUL-2001; 2001US-00919039
                                                                                                                                                           28-JUL-2000; 2000US-0222113P.
                               (first entry)
                                                                                                                                                                                                          WPI; 2004-031227/03
N-PSDB; ADE76896.
standard;
                                                                                                                                                                           (KASE/) KASER M R.
                                                                                                            US2003108871-A1
                                                                                             Homo sapiens
                               29-JAN-2004
                                                                                                                            12-JUN-2003
                                                                                                                                                                                                                                                  disorders
                                                                                                                                                                                           Æ.
               ADE76897;
ADE76897
                                                                                                                                                                                           Кавег
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62; 41pp; English Claim 1; SEQ ID NO The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and between the protein and a molecule or compound. t 0 molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a liver disorder.

Seguence 525 AA;

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                                                               1 НРИКНИЅНЕО́НРИGНИРНАНИРНЕНОТИКО́НРИGНИРНСКИРНСКИРНСКИРНСКИ
                                                                                  350 HPHKHISHEQHPHGHRPHAAHPHEHDTHRQHPHGHHPHGHHPHGHHPHGHHPHGHHPHGHHPHCH
                                                                                                                           DFQDYGPCDPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV
                                                                                                                                            DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPCPFHCRQIGSVYRLPPLRKGEV
                                  Gaps
                                 .;
0
 Length 525;
                                 2; Indels
 Score 949; DB 8;
Pred. No. 6.6e-78;
0; Mismatches 2.
                                                                                                                                                                                       LPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                                                                                                         98.2%;
Query Match
Best Local Similarity 98.6
Matches 146; Conservative
                                                                                                                                                        410
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The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with wilson disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human protein which is differentially expressed in steroid-induced C3A liver cells. Note: The specification but was obtained in electronic format directly from USPTO at sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNAs that are differentially expressed in response to steroid treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 НРНКИНЅНЕОНРНСНИРНАННРНЕНОТНКОНРИСКИРНСКИРНСКИРНСКИРНСК
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   НЕНКЕНІЗНЕОН РИСИНЬРИАНИРИЕНОТИКОНРИСИН РИСИНРИСИН РИСИНРИСИН РИСИНРИСИ
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                                                                                                                                                                           Hepatotropic; Gene therapy; Wilson disease; liver disorder; steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
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                                                                                                                                              Human steroid-induced C3A liver cell protein #11
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                                   525
                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001; 2001US-00976594.
                                                                                                                                                                                                                                                                                                                                                                                    2000US-0240409P
                                   ADL12335 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchbinder JL;
                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                         US6673549-B1.
                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Furness LM,
                                                                                                                                                                                                                                                                                                             06-JAN-2004.
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RESULT 7
ADL12335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
ADH10410
   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein sequence of rabbit histidine proline rich glycoprotein (HPRG), a proteinaceous chelator that can be used to inhibit angiogenesis and treat cancer. Claimed anti-angiogenic polypeptides or peptides comprise: the histidine-proline-rich (H/P) domain (see ABB79806) of human HPRG; an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or therapeutically labeled anti-angiogenic polypeptide, peptide or peptide or peptide multimer; a diagnostically angiogenic polypeptide, peptide or peptide multimer; an antibody specific for an epitope of HPRG that is present in the H/P domain of polypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the H/P domain or any which inhibits the anti-angiogenic activity of HPRG or the domain, or an antigen-binding fragment of the antibody; a method for inhibiting coldition associated with undesired cell migration, invasion, proliferation, or angiogenesis; a method of stimulating or inhibiting angiogenesis in a subject; a method of stimulating or inhibiting angiogenesis in a subject and a sandiogenesis; a method of stimulating or inhibiting angiogenesis in a subject in a biological sample; isolated nucleic acids encoding the polypeptide, peptide or peptide multimer; an expression vector; transformed or transfected cells; a method of expression peptide multimer; and expression vector; transformed or transfected cells; a method of encoding cells; and condition associated with undesired cell migratical cells; and the cells; and cells; and cells; and cells and cells; and cells and cells and cells; and cells and cells and cells and cells; and cells and cells and cells and cells.
                                                                                                                                                                                                                                                                                                 Histidine proline rich glycoprotein; HPRG; rabbit; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ine rich glycoprotein (HPRG) polypeptide, useful for
ting diseases associated with undesired cell migration,
ation, or angiogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
251. .296
/note= "Proline-rich domain"
321. .421
/note= "Histidine-proline-rich domain, region also specifically claimed in Claim 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ting diseases association, or angiogenesis, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mazar AP;
                                                                                                                                                                                                                                                    Rabbit histidine proline rich glycoprotein.
470 LPLPEANFPSFPLPHHKHPLKPDIQPFP 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plunkett ML,
                                                                                                                    Z
                                                                                                                protein; 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-FEB-2002; 2002WO-US004336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2001; 2001US-0268370P
                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ATTE-) ATTENUON LLC.
                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-666989/7:
P-PSDB; ABN84911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New histidine-prol diagnosing or trea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 12-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosing or trea
invasion, prolifer
                                                                                                              ABB79805 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200264621-A2
                                                                                                                                                                                                        25-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Donate F,
                                                                                                                                                             ABB79805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                     RESULT 8
ABB79805
                                                                   RESULT
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providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an affinity ligand useful for binding to, or isolating, an HPRG-binding consecule or cells expressing the binding molecule, comprising the polypeptide, peptide or peptide multimer, immobilised to a solid support or carrier; and a method of isolating HPRG-binding molecule, or isolating or enriching cells expressing HPRG-binding site or receptor, from a complex mixture. The compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's disease, Parkinson's disease and amyotrophic lateral sclerosis. The antibodies are stimulators of angiogenesis and are useful for promoting in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 HGHPPHGPPPHGHPPHGHGFHDHGPCDPPSHKEGPQDLH-QHAMGPPPKHPGKRGPGKGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 РИКНІЗНЕДИРИСИНРИА------НИ-----РИЕНDTИКДИРИСИНРИСИНР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGHHPHGHHPHGHDFQDYGPCDPPPHNQG----HCCHGHGPPPGHLRRRGPGKGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabeticophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPFHCROIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNOPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 543; DB 5; Length 526;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9e-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.968; Mismatches
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/note = pro-rich domain
321. .421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        angiogenesis; gene therapy; rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Juarez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rabbit HPRG protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2003; 2003WO-US008060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADH10410 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ATTE-) ATTENUON LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
tes 98; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003077872-A2
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US2001041670-A1.

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The invention relates to an isolated tropomyosin (Tpm)-related
antianglogenic receptor polypeptide or peptide, which is a is a fragment
of a full-length native Tpm protein expressed on the surface of
endothelial cells, or a variant of the fragment. It has a molecular mass
of about 17 kDa and corresponds in its sequence to, or is a variant of,
an internal fragment of a native Tpm isoform which is a binding site for
antianglogenic polypeptide agents; The isolated antianglogenic receptor
polypeptide, peptide or variant has substantially the same biochemical
activity of binding to the antianglogenic polypeptide agent that
continue Tpm internal fragment. The antianglogenic polypeptide agent that
continue to the isolated polypeptide or peptide is human histidine-proline
continue to the isolated polypeptide or peptide is human histidine-proline
continue to the isolated polypeptide or peptide is antianglogenic
continue kininogen (HRK), the D5 domain of HK, or a Tpm-binding,
antianglogenic homologue, variant, domain or fragment of the HK or its D5
continuedies and compositions are useful for inhibiting endothelial cell
continued invasion, proliferation or anglogenesis, for inducing
continued invasion, proliferation or anglogenesis, for inducing
contobablial cell appoptosis, or for treating tumours or cancer, diabetic
contobablial cell appoptosis, or for treating tumours or cancer, diabetic
contobablial cell appoptosis, or for treating tumours or cancer, diabetic
contobablial actions are useful diseases or conditions in which
contorned angiogenesis is desired, e.g. coronary artery disease or
contract processed angiogenesis is desired, e.g. coronary artery disease or
contorned and processed angiogenesis or conditions in which
                                                                               New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
                                                                                                                                                                                                                                    22; 117pp; English
                             WPI; 2004-090604/09.
                                                                                                                                                                                                                                Claim 6; SEQ ID NO
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рнаниереренаниерернанеренанереректереренанерернанеренанере -----НН------РНЕН ОТНКОН РНСНИР 43 HGHHPHCHHPHCHDFQDYGPCDPPHNQG----HCCHGHGPPPGHLRRRGPGKGP 390 нанррисрриненененоприсрежние сропи-онамсррине скасрска 24; RPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQPFP 148 FPFHWRRIGSVYQLPPLQKGEVLPLPEANFPQLLLRNHTHPLKPEIQPFP 498 Query Match 56.2%; Score 543; DB 8; Length 526; Best Local Similarity 57.6%; Pred. No. 4.9e-41; Matches 98; Conservative 8; Mismatches 40; Indels РНКННЅНЕОНРНGННРНА----Sequence 526 AA 330 66 N 449 පු 셤 ð ઠે ઠે

Gaps

Thrombospondin; TSP-1; histidine-rich glycoprotein; HRGP; cytostatic; cardiovascular; protein therapy; gene therapy; antisense inhibition; ribozyme inhibition; antibody inhibition; angiogenesis; human; cancer; TSP. HRGP thrombospondin (TSP)-binding domain fragment (residues 443-517). protein; 75 AA (first entry) ABB07123 standard, 13-MAR-2002 ABB07123 RESULT 10 ABB07123 

sapiens.

Ношо

The invention provides thrombospondin (TSP)-binding molecules and fragments comprising regions of the TSP-1 binding domains of Histidine-CC fragments comprising regions of the TSP-1 binding domains of Histidine-CC Rich Glycoproteins (HRGP). The proteins are used for the regulation of earlier growth and proliferation, such as in the accretion of new blood vessels (angiogenesis), particularly for treatment of cardiovascular crample in embryogenesis, and in a wide range of disorders and diseases, including those involving tumours, malignancies, neoplastic and other pathological conditions and homeostatic imbalances in the control of growth and development, in particular anal cancer, bladder cancer, small ccell lung cancer, bradnessrooms (CC breast cancer, non-small cell lung cancer, bradnessrooms (DES), colorectal cancer, endometrial cancer, cesophageal cancer, cancer, cof the eye, eyelid, Kaposi 's sarcoma, kidney cancer, cancer, lymphoma, melanoma, mesothelioma, oral cancer, ovarian cancer, pancreatic cancer, cesticular cancer, skin cancer, ovarian cancer, paromach cancer, thyroid cancer, hepatoma, neuroendocrine cancer, testicular cancer, thyroid cancer, nepatoma, neuroendocrine cancer, testicular cancer and a cholangiocarcinoma. The present sequence represents the TSP-binding motif of HRGP Thrombospondin-binding molecules and fragments comprising regions of the TSP-1 binding domains of Histidine-Rich Glycoproteins, useful for treating cancers and cardiovascular diseases. Example; Fig 1; 22pp; English 2000US-00730379 99US-0169205P Silverstein SIMANTOV R. SILVERSTEIN R L. WPI; 2002-017220/02 75 AA; 06-DEC-1999; 05-DEC-2000; Simantov R, 15-NOV-2001. Sequence (SIMA/) 

97 GPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQPFP 148 . 0 Length 75; 0; Indels Query Match 31.3%; Score 302; DB 5; 1 Best Local Similarity 100.0%; Pred. No. 5.3e-20; Matches 52; Conservative 0; Mismatches 0; ð

448

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GPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQPFP Rabbit HPRG protein H/P rich domain. ADH10412 standard; protein; 101 AA. (first entry) 11-MAR-2004 ADH10412; RESULT 11 ADH10412 ID ADH g

Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit. 

Oryctolagus cuniculus.

WO2003077872-A2

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Homo
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ABG25331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                         The invention relates to an isolated tropomyosin (Tpm)-related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that corrivity of binding to the antiangiogenic polypeptide agent that binds to the isolated polypeptide or peptide is human histidine-proline rich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain of HK, or a Tpm-binding, the D5 domain of HK, or a Tpm-binding, the MC or its D5 domain. The Tpm-related antiangiogenic for inducing are useful for inhibiting endothelial cell apoptosis, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for increased angiogenesis is desired, e.g. coronary artery disease or conditions in which increased angiogenesis is desired, e.g. coronary artery disease to protein His-Pro (H/P) rich domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                         New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mapping; gene mapping; gene therapy; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.0%; Score 280.5; DB 8; Length 101; 51.6%; Pred. No. 6.4e-18; ive 1; Mismatches 24; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mazar AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 НСИНРИСИНРИСИРЕОРУСРЕРРИ
                                                                                                                                                                                                                       24; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic protein #28010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 245
                                                                                                            Juarez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             РНКННЅНЕОНРНСННРНА---
                                  17-MAR-2003; 2003WO-US008060
                                                          15-MAR-2002; 2002US-0364047P
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                                                                                   (ATTE-) ATTENUON LLC.
                                                                                                                                  WPI; 2004-090604/09.
                                                                                                                                                                                                                       Claim 6; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG28019 standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human
           25-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-FEB-2002
                                                                                                            저,
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                                                                                                                                                                                                cancer.
                                                                                                             Mccrae
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders of supplement. (II) and its binding partners are useful in medical imaging of polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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food supplement; medical imaging; diagnostic; genetic disorder
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Pred. No. 3.6e-15;
2; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 58378; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG25331 standard; protein; 330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAS92206.
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                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biodiversity.
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and to produce other types of data and products dependent on DNA and cain acid sequences. AbG00010-AbG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - НЕОНРИGНИРИАНИРИЕНОТИКОИРИСНИРИСНИРИСНИРИСНИР
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                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                   mapping; gene therapy; forensic;
g; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
26.0%; Score 251.5; DB 4;
Best Local Similarity 39.3%; Pred. No. 9.1e-15;
Matches 46; Conservative 5; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 55690; 103pp; English.
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                   Human; chromosome mapping; gene ma
food supplement; medical imaging;
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                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                               31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                Liu C,
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73
N-PSDB; AAS89518.
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                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 330 AA
                                                                                                              WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biodiversity.
                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                RT,
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ABG27250
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cactivity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal cactivity of (II) or to treat disease states involving (II). (II) as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations capporting social sequences of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and canno acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Act abouated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                  Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%; Score 248.5; DB 4
32.6%; Pred. No. 2.1e-14;
iive 3; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID NO 57609; 103pp; English.
               Novel human diagnostic protein #27241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LPLPEANFPSFPLPHHKH 138
                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                         31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                      Tang YT,
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                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAS91437
                                                                                                                                           WO200175067-A2
                                                                                                         Homo sapiens.
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                                                 Human;
유
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RESULT

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of supplement. (II) and states are useful for treating disorders of supplement of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in the printed pot_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 НИРИGНИРИСНОРОДУСРСОРРРИNДСИССИСНСЯРРЕНТЯВЯСРСКОРВРЕНСЯОТСЯУ 109
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                                                                                                                                                            i; gene mapping; gene therapy; forensic,
imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; SEQ ID NO 50126; 103pp; English
                                                                                                                      Novel human diagnostic protein #19758
                   Æ
                   protein; 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT
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23-AUG-2000; 2000US-00649167
                                                                                                                                                            Human; chromosome mapping;
food supplement; medical im
                                                                                        entry)
                                                                                   (first
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Best Local Similarity
Matches 57; Conserv
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N-PSDB; AAS83954.
                ABG19767 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 233 AA;
                                                                                                                                                                                                                                                 WO200175067-A2
                                                                                                                                                                                                                 Homo sapiens.
                                                                                      18-FEB-2002
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                                                  ABG19767;
ABG19767
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Search completed: June 15, 2005, 13:47:11 Job time : 142.273 secs

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GenCore version 5.1.6
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                Copyright
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- protein search, using sw model OM protein

June 15, 2005, 13:38:35 ; Search time 36.8514 Seconds (without alignments) 299.800 Million cell updates/sec Run on:

US-10-074-225A-5 966 1 HPHKHHSHEQHPHGHHPHAH......PSFPLPHHKHPLKPDNQPFP 148 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 seqs, 74649064 residues Searched:

513545 Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Patents AA: Issued

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 64, Appl	62	1,	7	7	equence 2,	-	13	6151,	2423	28819,		8369,	1953	19,	19,	19,	12	3920	Ŋ	6551,	Sequence 32753, A	47	ij	-	٦,	-
ΩI	US-09-976-594-6	US-09-919-039-62	-785-6	US-09-095-407-2	US-09-742-494-2	US-09-809-657-2	US-09-507-323B-13	US-09-902-540-13395	US-09-543-681A-6151	US-09-248-796A-24231	US-09-252-991A-28819	US-09-252-991A-25291	US-09-949-016-8369	09-248-796A-	US-09-281-766-19	09-612-858-1	US-09-957-995A-19	-323B-1	US-09-270-767-39206	ņ	US-09-328-352-6551	US-09-270-767-32753	US-09-270-767-47970	US-08-255-457-1	US-09-115-032-1	PCT-US95-05772-1	US-08-152-922A-6
DB	1	깍	m	m	4	4	ო	4	4	4	4	4	4	4	m	4	4	m	4	4	4	4	4	ч	N	Ŋ	Н
% Query Match Length	525	525	26	56	26	26	167	163	400	125	225	218	955	971	865	865	865	89	130	3	3	376		9	9	9	189
% Query Match	8.2	8	٠	19.2	•	•	19.1	•	•	16.8	16.7	16.4	16.4	٠	16.1	16.1	16.1	15.4	٠	•	15.2	•	•	•	15.0	•	14.5
Score	94	949	æ	185	œ	œ	٠	180	72.	162.5	61.	58.	15	S	ທ.	55.	55.	148.5	148	マ	4	4	145	144.5	144.5	144.5	140
Result No.	_ 	7	Ю	4	S.	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

2, Appli 1291, Ap								10641, A				• •	- •	6530, Ap	
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-08-161-406-2 US-09-538-092-1291	US-09-489-039A-12802	US-09-270-767-35326	US-09-270-767-50543	US-08-686-528A-3	US-09-456-287-3	US-08-686-528A-2	US-09-456-287-2	US-09-949-016-10641	US-09-252-991A-28004	US-09-949-016-7806	US-09-461-474-10	US-09-252-991A-24982	US-09-252-991A-22309	US-09-949-016-6530	US-09-270-767-44345
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309	297 49F	203	203	313	313	337	337	1343	413	693	474	613	754	623	264
14.5	14.0	13.7	13.7	13.7	13.7	13.7	13.7	13.6	13.5	13.4	13.3	13.3	13.3	13.2	13.1
140	135.5	132	132	132	132	132	132	131.5	130	129	128.5	128.5	128.5	127.5	127
7 8 7 8 7 8 7 8	30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Sequence 64, Application US/09976594

| Sequence 64, Application US/09976594
| Patent No. 6673549
| GENERAL INFORMATION:
| APPLICANT: Furness, Michael
| APPLICANT: Buchbinder, Jenny
| TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
| FILE REFERENCE: PA-0041 US
| CURRENT APPLICATION NUMBER: US/09/976,594
| CURRENT FILING DATE: 2000-10-12
| PRIOR APPLICATION NUMBER: 60/240,409
| PRIOR PILING DATE: 2000-10-12
| NUMBER OF SEQ ID NOS: 1143
| SOFTWARE: PERL PROGram
| SEQ ID NO 64
| LENGTH: 525
| TYPE: PRT
| ORGANISM: Homo sapiens
| FATURE:
| NAME/KEY: misc feature
| OTHER INFORMATION: Incyte ID No. 6673549 085596CD1
| US-09-976-594-64

; Sequence 62, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; FILE REFERENCE: PA-0015 US
; CURRENT APPLICATION NUMBER: US/09/919,039

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            410 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPCPFHCRQIGSVYRLPPLRKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 НРИХНИЅНЕОНРИСНИРИАНИРНЕН ОТНКОНРИСНИРИСНИРИСНИРИСНИРИСНИРИСН
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.6%;
Matches 146; Conservative 0
RESULT 1
US-09-976-594-64
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US-09-919-039-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1. Application US/08785636
; Sequence 1. Application US/08785636
; Patent No. 6027942
; GENERAL INFORMATION:
; APPLICANT: Yip, Tai-Tung
; APPLICANT: Hutchens, T. William
; TITLE OF INVENTION: Method and Apparatus for Desorption and Ionization of
; TITLE OF INVENTION: Analytes
; FILE REFERENCE: Hutchens
; CURRENT APPLICATION NUMBER: US/08/785,636
; CURRENT FILING DATE: 1997-01-17
; EARLIER APPLICATION NUMBER: 08/068,896
; SOFTWARE: PatentIN Ver. 2.0
                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                           1 НРИКИНЅНЕОНРИGНИРИАНИРНЕНDТИКОНРИСНИРИСНИРИСНИРИСНИРИСНИРИСН
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US-09-095-407-2
; Sequence 2, Application US/09095407
; Patent No. 6124137
; GENERAL INFORMATION:
; APPLICANT: Hutchens, T. William
; APPLICANT: Ani-Tung
; TITLE OF INVENTION: Surface-Enhanced Neat Desorption for the
Detection of Analytes
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                                                                                                                                                                                        Incyte ID No. 6727066 085596CD1
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19.2%; Score 185; DB 3; I
Best Local Similarity 100.0%; Pred. No. 9.7e-12;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SFPLPHHKHPLKPDNOPFP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 62
LENGTH: 525
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                 ; NAME/KEY: misc_feature; OTHER INFORMATION: Inc)
US-09-919-039-62
                                                                                                                                       ena
                                                                                                                  TYPE: PRT
ORGANISM: Homo sapi
FEATURE:
                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 146; Conser
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HPHKHHSHE
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COTHER INFORMATION:
US-08-785-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-785-636-1
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LENGTH: 26
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Sequence 2, Application US/09742494
; Sequence 2, Application US/09742494
; Sequence 3, Application US/09742494
; GENERAL INFORMATION:
; APPLICANT: HUTCHENS, WILLIAM
; APPLICANT: YIP, TAI-TUNG
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES
; FILE REFERENCE: P00798USE/09306611
; CURRENT APPLICATION NUMBER: US/09/742,494
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                         COUNTRY: USA
ZIP: 77010-3095
ZIP: 77010-3095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,407
FILING DATE: 10-Jun-1998
CLASSIFICATION NUMBER: US 08/068,896
FILING DATE: 28-MAY-1993
APPLICATION NUMBER: WO PCT/US94/06064
FILING DATE: 27-MAY-1994
APPLICATION NUMBER: US 08/556,951
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: 32,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 26;
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHHPHGHHPHGHHPHGHHPH 25
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MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-095-407-2
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STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                            CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-494-2
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LENGTH: 26
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Sequence 6151, Application US/09543681A
Sequence 6151, Application US/09543681A
Sequence 6151, Application US/09543681A
Sequence 615709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6151
LENGTH: 400
                                                                                                                                                                              US-09-902-540-13395

US-09-902-540-13395

Sequence 13395, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

TITLE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 13395

LENGTH: 163

WARDEN DATE: 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 HDHHHHSHDHDHDHGHHHHGHHHHHGHDHHHEHNATPANTVHKYIDKSEQKHKHNYETH
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Pred. No. 3e-09;
4; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.6%; Score 180; DB 4; ilarity 40.0%; Pred. No. 2.1e-10; Conservative 3; Mismatches 19
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----HGPAEEH-KARAP
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     GHCCHGHGPPPGHLRRRGPGKGPRPFH
                                                                   128 HH--HSGLDPSGHHHHHHSGLDPSGHH
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Best Local Similarity 29.9%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Myxococcus xanthus US-09-902-540-13395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Proteus mirabilis
US-09-543-681A-6151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-543-681A-6151
  92
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                                                                                                                                                           RESULT 6
US-09-809-657-2
; Sequence 2, Application US/09809657
; Patent No. 6734022
; GENERAL INFORMATION:
; APPLICANT: WILLIAM
; APPLICANT: YIP, TAI-TUNG
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES
; FILE REFERENCE: P00798USF/09306611
; CURRENT APPLICATION NUMBER: US/09/809,657
; CURRENT FILING DATE: 1993-05-28
; PRIOR APPLICATION NUMBER: 08/068,896
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 26
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09507323B

Sequence 13, Application US/09507323B

Patent No. 6274345

GENERAL INFORMATION:

APPLICANT: Choi, Jong Hyun

APPLICANT: Lee, Sang Yup

APPLICANT: Lee, Sang Yup

TITLE OF INVENTION: EXPRESSION VECTORS COMPRISING A GENE

TITLE OF INVENTION: MOTIF

TITLE OF INVENTION: MOTIF

TITLE OF INVENTION: MOTIF

TITLE OF INVENTION: MOTIF

FILE REFERENCE: HYLEE39.001AUS

TITLE OF INVENTION: WHMBER: CASO0-02-18

PRIOR APPLICATION NUMBER: CASO0-02-18

PRIOR APPLICATION NUMBER: KR 10-1999-0005773

PRIOR APPLICATION NUMBER: RA 10-1999-0005773

PRIOR APPLICATION NUMBER: MINGOWE VERSION 4.0

SEQ ID NO 13

LENGTH: 167

TYPE: PRY

CORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.2%; Score 185; DB 4; Length 26; 100.0%; Pred. No. 9.7e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 СИНРИСКИРНСКИРНСКИРН 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               СИНРИСКИРИСКИРИСКИРИ
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US-09-809-657-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 25; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-09-507-323B-13
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Best Local S
Matches 48
34
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Sequence 8369, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                    APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25291

LENGTH: 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
85 PPG---HLRRRG--PGKGPRPFHCRQIGSVYRLPPLRKGEV 120
                                       -GVQGALPRRRGRV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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Pred. No. 3.8e-08;
5; Mismatches 50
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                                                                                                                                               Sequence 25291, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25291
                                          158 VPAVLLHAWRAGPAPGAGALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.4%;
Best Local Similarity 32.0%;
Matches 49; Conservative
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Best Local Similarity 30.7%;
Matches 46; Conservative
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US-09-949-016-8369
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                                                                          RESULT 10
US-09-248-796A-24231
; Sequence 24231, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-12
; CURRENT FILING DATE: 1999-02-13
; PRIOR FILING DATE: 1998-08-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24231
; LENGTH: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
US-09-252-991A-28819
; Sequence 28819, Application US/09252991A
; Sequence 28819, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABSCIOLING NOWBER: US/09/252,991A
; CURRENT APPLICATION NUMBER: US 60/074,788
; FRICH REPIRED APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEG ID NO 28819
; LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Pred. No. 8.4e-09;
2; Mismatches 22
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--HSHEH 155
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, 32.4%;
vative
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US-09-248-796A-24231
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Best Local Similarity
Matches 52; Conser
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                     148
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Best Local S
Matches 34
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Search completed: June 15, 2005, 13:53:03 Job time : 38.8514 secs
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                                                                                                                                                                                                                                                                    RESULT 14
US-09-248-796A-19531
is Sequence 19531, Application US/09248796A
is Sequence 1951, Application US/09248796A
is General Incordation:
is Patent No. 6747137
is General Incordation:
is APPLICANT: Reith Weinstock et al
it TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN:
is TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
is TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS
is FILE REFERENCE: 107196.132
is CURRENT APPLICATION NUMBER: US 60/074,725
is PRIOR APPLICATION NUMBER: US 60/074,725
is PRIOR PILING DATE: 1998-02-13
is PRIOR PILING DATE: 1998-08-13
is NUMBER OF SEQ ID NOS: 28208
is SEQ ID NO 19531
is TYPE: PRT
is ORGANISM: Candida albicans
                                766 HRPHEGPGGGMGNSSGHRPHEGPGGMGSGHRPHEGPGGSMGGGGGGHRPHEGPGGGISGG 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416
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                                                                                    GНИРН---GH-НРНСНИРНСНО РОДУС
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09281766
; Patent No. 6376196
; Patent No. 6376196
; GENERAL INFORMATION:
; APPLICANT: Conrad, Patricia C.
; APPLICANT: Louie, Kitland
; APPLICANT: Louie, Kitland
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Recombinant Neospora Antigens and Their Uses
; TITLE OF INVENTION: Recombinant Neospora Antigens and Their Uses
; TITLE REFERENCE: 023070-082510US
; CURRENT APPLICATION NUMBER: US/09/281,766
; CURRENT FILING DATE: 1999-03-30
; PRIOR FILING DATE: 1996-05-10
; PRIOR FILING DATE: 1996-05-10
; SOFTWARE: PatentIN Ver. 2.1
; SOFTWARE: PatentIN Ver. 2.1
; SEQ ID NO 19
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Neospora 8P.
; OTHER INFORMATION: NC-p65 CDNA
---QHPHGHHPH------AHHPHE-----HDTHRQHP--
                                                                                                                             826 SGHRPHEGPGGGMGAGGGHRPHEGPGGSMGGSGGHRPHEGPGPGHCGPHGHRPH
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Pred. No. 2.9e-07;
6; Mismatches 26;
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                                                                                                                                                                      67 PCDPPPHNQGHCCHGH-GPPP-GHLRRRGPGKG 97
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Best Local Similarity 27.8%;
Matches 35; Conservative
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US-09-281-766-19
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                                                                                                Gaps
                                                                                          17;
                                                   Length 865;
                                                                                              88; Indels
                                                                                                                                                                                                                                                                                                                                                                             110 YRLP----PLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQP 146
                                           Score 155.5; DB 3;
Pred. No. 3.2e-07;
9; Mismatches 88;
                                             Query Match 16.1%;
Best Local Similarity 29.2%;
Matches 47; Conservative ;
US-09-281-766-19
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein June 15, 2005, 13:51:11; Search time 124.225 Seconds (without alignments) 456.700 Million cell updates/sec Run on:

US-10-074-225A-5 966 1 HPHKHHSHEQHPHGHHPHAH.....PSFPLPHHKHPLKPDNQPFP 148 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

seqs, 383334425 residues 1710399 Searched:

1710399 Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries 2000000000

Database

Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*

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16: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

19: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

20: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

21: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\*

22: /cgn2\_6/ptodata/1/pubpaa/USOO8\_PUBCOMB.pep:\* 

# Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES

Description	Sequence 5, Appli	Sequence 1, Appli	Sequence 42, Appl	Sequence 62, Appl	Sequence 3, Appli	Sequence 166051,	Sequence 1, Appli	Sequence 6, Appli	Sequence 33892, A	Sequence 37944, A	Sequence 9, Appli
ID	US-10-074-225A-5	US-10-074-225A-1	US-10-868-577A-42	US-09-919-039-62	US-10-074-225A-3	US-10-424-599-166051	US-09-730-379B-1	US-10-074-225A-6	US-10-029-386-33892	US-09-864-761-37944	US-09-730-379B-9
80	14	14	17	10	14	15	σ	14	14	σ	σ
% Query Match Length DB	148	525	525	525	526	67	75	101	378	292	38
% Query Match	100.0	100.0	100.0	98.2	56.2	33.6	31.3	29.0	25.1	22.9	22.0
Score	996	996	996	949	543	325	302	280.5	242.5	221	213
Result No.	-	7	m	4	υ.	9	7	œ	თ	10	11

Sequence 13, Appl Sequence 2423, Ap Sequence 2422, Ap Sequence 2422, Ap Sequence 2422, Ap Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 37352, A Sequence 191894, Sequence 191894, Sequence 185164, Sequence 185164, Sequence 34744, A Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 18528, Sequence 18528, Sequence 31727, A Sequence 160290, Sequence 160290, Sequence 160290, Sequence 1014, Ap Sequence 1106, A Sequence 37882, A Sequence 37882, A Sequence 31185, A Sequence 31185, A Sequence 320892, Sequence 320892, Sequence 320892, Sequence 320892, Sequence 320892, Sequence 320892,
US-09-730-379B-13 US-09-864-761-3313 US-10-389-566-2423 US-10-389-566-2422 US-10-389-566-2422 US-10-389-566-2422 US-10-424-599-281824 US-09-864-761-41679 US-09-864-761-41679 US-09-864-761-3732 US-09-864-761-3732 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-191894 US-10-425-115-307018 US-10-425-115-307018 US-10-425-115-307018 US-10-425-115-307018 US-10-425-115-307018 US-10-425-115-307018 US-10-425-115-30892 US-10-425-115-30892 US-10-425-115-30892 US-10-425-115-320892 US-10-425-115-320892 US-10-425-115-320892
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113 113 113 113 113 113 113 113 113 113
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## ALIGNMENTS

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Sequence 5, Application US/10074225A
; Sequence 5, Application US/20030082740A1
; GENERAL INFORMATION:
; APPLICANT: DOWNTE, Fernando
; APPLICANT: PLUNKETT, Marian L
; APPLICANT: PLUNKETT, Marian L
; APPLICANT: MAZAR, Andrew P
; TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC;
; TITLE OF INVENTION: ANTI-TUMOR AGENT
; FILE REFERENCE: 38342-178463
; CURRENT APPLICATION NUMBER: US/10/074,225A
; CURRENT FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 148
; ORGANISM: Homo sapiens
US-10-074-225A-5
RESULT 1
US-10-074-225A-5
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DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120

61

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APPLICANT: PUNATE, Fernando
APPLICANT: PUNATE, Fernando
APPLICANT: PUNATE, Scott
APPLICANT: PLUNKETT, Marian L
APPLICANT: HARRIS, Scott
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC ?
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFERENCE: 38342-178463
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2002-02-14
PRIOR PILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                   Sequence 62, Application US/09919039

Sequence 62, Application US/09919039

Publication No. US20030108871A1

GENERAL INFORMATION:

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES

TITLE OF INVENTION UMBER: US/09/919,039

CURRENT APPLICATION NUMBER: 06/222,113

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR PILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 62

LENGTH: 525

TYPE: PRT

ORGANISM: Homo sapiens

FANTINE: APPLICATION: APPLICATION

SEQ ID NO 62

LENGTH: 525

TYPE: PRT

ORGANISM: Homo sapiens
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                                                                                                                                 350 HPHKHISHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGHHPHGHHPHGHHPHGHHPHGHHPHCH
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US-09-919-039-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                              LPLPEANFPSFPLPHHKHPLKPDNOPFP 148
                                                                                                                                                                                                                        470 LPLPEANFPSFPLPHHKHPLKPDNOPFP 497
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 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120
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100.0%; Pred. No. 3.4e-70;
iive 0; Mismatches 0;
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Pred. No. 3.4e-70;
; Mismatches 0;
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JOS-10-868-5//A-42

Sequence 42, Application US/10868577A

Publication No. US20050032697A1

GENERAL INFORMATION:

APPLICANT: Alitalo et al.

TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIG

FILE REFERENCE: 28967/39359A

CURRENT APPLICATION NUMBER: US/10/868,577A

CURRENT APPLICATION NUMBER: US 60/478,390

PRIOR APPLICATION NUMBER: US 10/669,176

PRIOR PILING DATE: 2003-09-23

PRIOR PILING DATE: 2003-09-23

NUMBER OF SEQ ID NOS: 69

SOFTWARE: Patentin Version 3.2

LENGTH: 525

TYPE: PRT

ORGANISM: Homo sapiens

US-10-868-577A-42
                                                                LPLPEANFPSFPLPHHKHPLKPDNOPFP 148
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US-10-074-225A-1

Sequence 1, Application US/10074225A

Publication No. US20030082740A1

GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: PLUNKETT, Marian L
APPLICANT: PLUNKETT, Marian L
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH
TITLE OF INVENTION: ANTI-TUMOR AGENT
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFERENCE: 38342-178463
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT APPLICATION NUMBER: US 60/268,370
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 525
TYPE: PRT

TYPE: PRT

CORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER: US/10/074,225A
2002-02-14
                                          LPLPEANFPSFPLPHHKHPLKPDNQPFP
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Best Local Similarity
Matches 148; Conser
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Best Local Similarity
Matches 148; Conser
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US-10-868-577A-42
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; ORGANISM: Lepus americanus US-10-074-225A-6
                                          TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION: P
JOURNAL: Biochemistry
VOLUME: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-029-386-33892
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Best Local S
Matches 52
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US-10-424-599-166051
Sequence 166051
Septicant: Royalic David K
Septicant Application Number: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SEQ ID NO 166051
SEQ ID NO 16605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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; Sequence 1, Application US/09730379B
; Patent No. US20010041670A1
; GENERAL INFORMATION:
; APPLICANT: Simantov M.D., Ronit
; APPLICANT: Silverstein M.D., Roy L.
; TITLE OF INVENTION: THROMBOSPONDIN-BINDING REGION OF HISTIDINE-RICH
; TITLE OF INVENTION: GLYCOPROTEIN AND METHODS OF USE
; FILE REFERENCE: 955-7P/CON
; CURRENT APPLICATION NUMBER: US/09/730,379B
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 HPHXCHSHEQHPHGHHPHACHPHENDTHRQHPHGHPKGNHPHGHP 67
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                                                                                                                                                                                                                                DB 14; Length 526; 5.7e-36;
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                                                                                                                                                                                                                                   Score 543;
Pred. No. 5
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nilarity 57.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              2 РИКНИЯНЕОНРИСИНРИА-
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Lepus americanus
US-10-074-225A-3
                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 47; Conser
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Best Local S
Matches 47
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Sequence 6, Application US/10074225A;
Sequence 6, Application US/10074225A;
Sequence 6, Application US/20030082740A1

Publication No. US20030082740A1

GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

APPLICANT: MAZAR, Andrew P

TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC F

TITLE OF INVENTION: ANTI-TUMOR AGENT

FILE REFERENCE: 38342-178463

CURRENT APPLICATION NUMBER: US/10/074,225A

CURRENT FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/268,370

PRIOR APPLICATION NUMBER: US 60/268,370

PRIOR SEQ ID NOS: 11

SOFTWARE: PATENTIN Version 3.1

LENGTH: 101

LENGTH: 101

LENGTH: 101
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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                                                                                                                                                                                                                                            / Match 31.3%; Score 302; DB 9; Length 75; Local Similarity 100.0%; Pred. No. 3e-17; les 52; Conservative 0; Mismatches 0; Indels
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Pred. No. 2.2e-15;
1; Mismatches 24; Indels
PUBLICATION INFORMATION
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                                                                         ; ISSUE: 8
; PAGES: 2220-2225
; DATE: 1986
; DATABASE ACCESSION NUMBER: GenBank/P04196
US-09-730-379B-1
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Best Local Similarity 51.6%;
Matches 47; Conservative
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3 ИХНИЅНЕОНРИСИНРИАНИРИЕНОТИКОНРИСИИРИСИНРИСИ - ИРИСИИРИСИРИСИ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Simantow M.D., Ronit
APPLICANT: Simantow M.D., Roy L.
APPLICANT: Silverstein M.D., Roy L.
TITLE OF INVENTION: THROMBOSPONDIN-BINDING REGION OF HISTIDINE-RICH
TITLE OF INVENTION: GLYCOPROTEIN AND METHODS OF USE
FILE REFERENCE: 955-7P/CON
CURRENT APPLICATION NUMBER: US/09/730,379B
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
LENGTH: 38
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WE EXPRESSED IN PLACENTA, SIGNAL = 5.5

WE EXPRESSED IN HEL100, SIGNAL = 6.2

WE EXPRESSED IN HEART, SIGNAL = 7.1

WE EXPRESSED IN FETAL LIVER, SIGNAL = 6.1

WE EXPRESSED IN HELA, SIGNAL = 8.2

WE EXPRESSED IN HELA, SIGNAL = 7.7

WE EXPRESSED IN ADULT LIVER, SIGNAL = 7.7

WE EXPRESSED IN ADULT LIVER, SIGNAL = 3.1

WE EXPRESSED IN LUNG, SIGNAL = 7.9

WE EXPRESSED IN LUNG, SIGNAL = 7.9
              PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 37944
LENGTH: 292
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION: PUBLICATION INFORMATION
JOURNAL: Biochemistry
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; PAGES: 2220-2225

; DATE: 1986

; DATABASE ACCESSION NUMBER: GenBank/P04196

US-09-730-379B-9
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                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: BOTHER INFORMATION: EOTHER 
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Matches 41; Conser
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US-09-730-379B-13
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HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.1%; Score 242.5; DB 14; Length 47.1%; Pred. No. 8.5e-12; vative 1; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                           EXPRESSED IN PLACENTA, SIGNAL = EXPRESSED IN HELA, SIGNAL = 2.7 EXPRESSED IN LUNG, SIGNAL = 3.6
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US-0864-761-37944

i Sequence 37944, Application US/09864761

j Patent No. US20020048763A1

j GRUNEAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Penn, Sharron G.
 APPLICANT: Hanzel, David K.
 APPLICANT: Hanzel, David K.
 APPLICANT: Hanzel, David K.
 APPLICANT: Hanzel, David K.
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINN TITLE OF INVENTION: HUMAN GENOME-DERIVED SINN TITLE OF INVENTION: HUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-06-04

PRIOR FILING DATE: 2000-06-04

PRIOR FILING DATE: 2000-06-04

PRIOR FILING DATE: 2000-06-04

PRIOR FILING DATE: 2001-01-30

PRIOR PRIOR PRILCATION NUMBER: PCT/US01/00665

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01
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; SEQ ID NO 33892
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP T;
; OTHER INFORMATION: EXPRE
; OTHER INFORMATION: EXPRE
; OTHER INFORMATION: EXPRE
; OTHER INFORMATION: EXPRE
US-10-029-386-33892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity
41; Conserv
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Best Local S
Matches 41
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                                            Gaps
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0
 Length 38;
Query Match 22.0%; Score 213; DB 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 38; Conservative 0; Mismatches 0;
                                                                                                                GPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLP
                                                                                       GPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLP
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Sequence 2423, Application US/10389566;
Sequence 2423, Application US/10389566;
Bublication No. US20040025202A1
GENERAL INFORMATION:
APPLICANT: Laurie, Cathy C
TITLE OF INVENTION:
FILE REFERENCE: 38-77(52900)D
CURRENT APPLICATION NUMBER: US 60/365,301
PRIOR PPLICATION NUMBER: US 60/365,301
PRIOR PILING DATE: 2002-03-15
PRIOR PPLICATION NUMBER: US 60/391,786
PRIOR FILING DATE: 2002-06-25
PRIOR FILING DATE: 2002-06-26
PRIOR FILING DATE: 2002-06-26
NUMBER OF SEQ ID NOS: 2459
SOFTWARE: Patentin version 3.2
SEQ ID NO 2423
LENGTH: 130
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HIT: Q12329, EVALUE 4.90e+00
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N: EXPRESSED IN HELA, SIGNAL = 8.1

N: EXPRESSED IN HELA, SIGNAL = 8.8

N: EXPRESSED IN PLACENTA, SIGNAL = 9.5

N: EXPRESSED IN HEART, SIGNAL = 9.5

N: EXPRESSED IN HEART, SIGNAL = 9.2

N: EXPRESSED IN BRAIN, SIGNAL = 9.2

N: EXPRESSED IN BRAIN, SIGNAL = 7.6

N: EXPRESSED IN BT474, SIGNAL = 7.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 6

N: EXPRESSED IN BONE MARROW, SIGNAL = 6
                                   PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33313
LENGTH: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 15;
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20.7%; Score 199.5; DB 1!
l Similarity 44.6%; Pred. No. 9.7e-09;
45; Conservative 2; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 210; DB 9
Pred. No. 9e-10;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.7%;
Best Local Similarity 56.9%;
Matches 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 45; Conservat
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GENERAL INFORMATION:

APPLICANT: Simantov M.D., Ronit
APPLICANT: Simantov M.D., Ronit
TILE OF INVENTION:
TILE OF INVENTION: THROMBOSPONDIN-BINDING REGION OF HISTIDINE-RICH
TILE OF INVENTION: GLYCOPROTEIN AND METHODS OF USE
FILE REFERENCE: 955-7P/CON
CURRENT APPLICATION NUMBER: US/09/730,379B
CURRENT FILING DATE: 2000-12-05
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 38
TYPE: PRT
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N: HUMAN GENOME-DERIVED SINGLE EXON NOTES
N: GENE EXPRESSION ANALYSIS BY MICROARRAY
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Pred. No. 2.5e-10;
0; Mismatches 0;
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PUBLICATION INFORMATION: PUBLICATION INFORMATION
JOURNAL: Biochemistry
VOLUME: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER: GenBank/P04196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWBER: US 60/180,312

TWBER: US 60/180,312

2000-05-26

TWBER: US 09/632,366

2000-08-03

TWBER: GB 24263.6

2000-10-04

TWBER: US 60/236,359

2000-10-04

TWBER: US 60/236,359

2000-09-27
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2001-05-23
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001-01-30
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001-01-30
MBER: PCT/USO1/00665
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001-01-30
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MBER: PCT/US01/00667
001-01-30
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US-09-864-761-33313
; Sequence 33313, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pi
Matches 38; Conservative 0;
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENC
TITLE OF INVENTION: GENE EXPF
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US
CURRENT APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
PRIOR PILING DATE: 2000-02-04
PRIOR PILING DATE: 2000-06-20
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/PRIOR APPLICATION NUMBER: PCT/PRIOR APPLICATION NUMBER: PCT/PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PAGES: 2220-2225
; DATE: 1986
; DATABASE ACCESSION
US-09-730-379B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
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RESULT 15
US-10-389-566-2424

i Sequence 2424, Application US/10389566

i Publication No. US200400025202A1

i GENERAL INFORMATION:

APPLICANT: Monsanto Technology, LLC

TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants

FILE REFERENCE: 38-77(52900) D

CURRENT APPLICATION NUMBER: US 60/305,301

PRIOR APPLICATION NUMBER: US 60/305,301

PRIOR FILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-03-15

PRIOR FILING DATE: 2002-06-25

PRIOR APPLICATION NUMBER: US 60/392,018

PRIOR FILING DATE: 2002-06-26

NUMBER OF SEQ ID NOS: 2459

SOFTWARE: PatentIn version 3.2

LENGTH: 133

LENGTH: 133

TYPE: PRT

ORGANISM: Bacillus anthracis

US-10-389-566-2424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.7%; Score 199.5; DB 15; Length 133; 44.6%; Pred. No. 9.9e-09; vative 2; Mismatches 35; Indels 19;
                           69 HHGHH-HIHPQAILYQTH-----QGHQGHHDHHGHGHQGH 103
53 - НСИНРИСИD---- РОДУСРСДРРИНОСИСИСИСИСРРСИ 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 45; Conserv
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 1. ИРИКИНЅНЕОИРИСИНРИАНИРИЕН ОТИРИ - СИНРИ - СИНР - СИНРИ - СИ 53 -НGННРИСИВ---- РОДУ СРСВРРИМОСИСИСИ ВР 

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РОАІТУОТН-----ОСНОСННОННСНИСНОСН 103

15, 2005, 14:09:35 Search completed: June 1 Job time : 125.225 secs

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5.1.6
Compugen Ltd
version
- 2005
GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

, 2005, 13:37:20 June 15 Run on:

; Search time 28.5301 Seconds
 (without alignments)
 499.124 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-074-225A-5 966 1 HPHKHHSHEQHPHGHHPHAH.....PSFPLPHHKHPLKPDNQPFP 148

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

seqs, 96216763 residues 0.5 283416 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

number of results predicted by chance to have a or equal to the score of the result being printed analysis of the total score distribution. Pred. No. is the number score greater than or eq and is derived by analys

#### STIMMEDIES

	Description	histidine-rich gly		histidine-rich gly	•	ď		hypothetical prote	knob-associated hi	hypothetical prote	cation efflux fami	cAMP responsive el	cAMP response elem	hypothetical prote	zinc finger protei	MHC H-2K/t-w5-link	female-specific do	male-specific doub	zinc resistance pr	alpha-amylase homo	hypothetical prote	S59/2 homeotic pro	carboxypeptidase C	hypothetical prote	probable membrane	conserved hypothet	hypothetical prote	knob-associated Hi	cal r	probable histidine
SUMMARIES	ID	каниан	A60488	KGZÕHL	A54523	T45059	T14155	T33997	A29454	H83994	F87286	178877	A45477	T23089	T30173	149714	A32372	B32372	T27544	T39539	T48099	A36664	T43236	H82061	AD0262	AB3110	B98177	B71623	T13741	C64698
	DB	-	7	-	7	7	7	7	~	7	7	7	~	7	7	7	7	7	7	7	~	~	7	7	~	~	~	7	~	7
	Length	525	445	351	140	735	1571	471	657	380	361	369	208	515	1378	436	427	549	428	774	199	629	1002	242	373	375	375	654	1398	9
d	Query Match	100.0	52.1	25.0	22.5	ö	18.2	18.0	7.	7.	17.3	17.2	17.2	17.2	7	ė	ė.	16.6	16.4	ė.	è.	15.5	'n.	15.4	S.	د.	S.	ŝ	15.1	س
	Score	996	503.5	241.5	217	193	176	173.5	171.5	170.5	167	166.5	166.5	166.5	166.5	162	160	160	158	155.5	155	149.5	149.5	148.5	147	147	147	145.5	145.5	144.5
	Result No.		7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

histidine-rich cal	probable copper-tr	hypothetical prote	knob protein - mal	knob-associated hi	histidine-rich pro	knob protein precu	HRPII protein - ma	hypothetical prote	hypothetical prote	hypothetical prote	proline-rich prote	histidine/alanine-	extensin class I (	nodulin Enod2 - Se
A34373	JC2464	T30119	A26480	A54494	A28412	A54495	S31782	T28872	AC2680	A97462	S23737	A25942	S14983	S22140
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		14.8 10								•				
14.9	14. B. a.		14.8	14.8	14.8	14.8		14.7		14.6	14.5	14.5	14.4	14.4

# ALIGNMENTS

Nightdine-rich glycoprotein precursor - human
Nightdine-rich glycoprotein precursor - human
Nighternate names: HRG
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 09-Jul-2004
C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 09-Jul-2004
C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 09-Jul-2004
C;Date: 04-Dec-1986 #sequence of human histidine-rich glycoprotein derived from the nuclec A;Reference number: A01287; MUID:86216149; PMID:3011081
A;Reference number: A01287
A;Rocession: A01287
A;Residues: 1-525 < KOIX
A;Residues: 1-525 < KOIX
A;Residues: 1-525 < KOIX
A;Residues: 1-526 < KOIX
A;Residues: 1-526 < KOIX
A;Residues: 2-526 < Rounding A;Residues: 2-526 < Rounding A;Residues: 829669
A;Recession: S29669
A;Recession: S29669
A;Recession: S29669
A;Recession: S29669
A;Recession: S29669
A;Residues: 214-247 < KHEN>
A;Residues: Cermment: Although its physiological function is not yet known, HRG does bind heme, dyet din, and the lysine-binding site of plasminogen. On the basis of its homology with HMW A;Residues: Cermment: The amino half of this protein is homologous to the first two cystatin-like dc ould not have inhibitory activity.
C;Comment: The amino half of this protein is homologous to the first cho cystatin-like dc content in addition to having a high histidine and proline content, this protein has necession.

e-rich' region.
C;Genetics:
A;Gene: GDB:HRG
A;Cross-references: GDB:120055; OMIM:142640
A;Gene: GDB:HRG
A;Cross-references: GDB:120055; OMIM:142640
A;Map position: 3q27-3q27
C;Superfamily: histidine-rich glycoprotein; cystatin homology
C;Superfamily: histidine-rich glycoprotein #status predicted \*SIG>
F;1-18/Domain: signal sequence #status predicted \*SIG>
F;19-525/Product: histidine-rich glycoprotein #status predicted \*MAT>
F;19-131/Domain: cystatin homology \*CY1>
F;19-246/Domain: cystatin homology \*CY2>
F;140-246/Domain: cystatin homology \*CY2>
F;140-246/Domain: proline-rich
F;348-437/Region: proline-rich
F;348-437/Region: proline-rich
F;348-437/Region: proline-rich
F;348-437/Region: proline-rich
F;63,125,344,345/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;78-89,105-126,218-241/Disulfide bonds: #status predicted

Gaps ö Length 525; Indela 100.0%; Score 966; DB 1; 100.0%; Pred. No. 1.4e-74; iive 0; Mismatches 0; Query Match Best Local Similarity 100. Matches 148; Conservative

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1 НРНКИНЅНЕДИРИСИНРИАНИРИЕНОТИКОНРИСИИРИСИИРИСИИРИСИИРИСИ 60

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Thu Jun 16 13:0

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Local Similarity
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Best Local S
Matches 38
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                                                                                                  PPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.1%; Score 503.5; DB 2;
49.2%; Pred. No. 1.7e-35;
ive 15; Mismatches 26;
                                                                                                                                                                      LPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                                                                                                    ----HEOH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rative
                                                                                                                                                                                                  470 LPLPEANFP
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Best Local Similarity
Matches 91; Conser
                                                                          DFQDYGPCD
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HPHESYNFR
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                                                                                                                  DFQDYGPCD
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                                                                                                                      410
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Assession: Assession - Plasmodium lophurae (fragment)
C;Species: Plasmodium lophurae
C;Species: Plasmodium lophurae
C;Species: Plasmodium lophurae
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54523
R;Irving, D.O.; Cross, G.A.M.; Feder, R.; Wallach, M.
Mol. Biochem. Parasitol. 18, 223-234, 1986
Mol. Biochem. Parasitol. 18, 223-234, 1986
A;Title: Structure and organization of the histidine-rich protein gene of Plasmodium loph
A;Reference number: A54523; MUID:86174893; PMID:3007981
A;Accession: A54523
A;Accession: A54523
A;Accession: A54523
A;Residues: 1-140 <IRV>
A;Residues: 1-140 <IRV>
A;Residues: 1-140 <IRV>
A;Cross-references: UNIPROT:Q26056; GB:M15317; NID:g160331; PIDN:AAA29616.1; PID:g552196
C;Superfamily: plasmodium histidine-rich protein
C;Keywords: tandem repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              РИКИНЅНЕОНРИСИН - - - - РИАНИРИЕН - - ОТНЯОНРИСИИРИСИИРИСИИРИС
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 РИНИНИНАРИНИНИНИНАРИНИНАРИНИНАРИНИНИНАРИНИНИРМЕН
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;124-138,139-153/Region: 15-residue repeats
F;173-301,312-331/Region: 10-residue repeats
F;40/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.5%; Score 217; DB 2; Length 140; 39.6%; Pred. No. 1e-11; ive 2; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indela
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histidine-rich glycoprotein precursor - Plasmodium lophurae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 241.5; DB 1;
Pred. No. 2e-13;
1; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 РИСИНРИСИРРИСИВРОДУСРОРРИМОСИСИСИ
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Best Local Similarity 47.7%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       НИННРМЕННИННИВАНН:
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T45059
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hypothetical protein Y39B6B.gg [imported] - Caenorhabditis elegans

RESULT KGZQHL

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TASOUL /
TAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein BH2760 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83994
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-657 <TRI>
A;Cross-references: UNIPROT:P06719; GB:Y00060; NID:g9908; PIDN:CAA68268.1; PID:g9909
C;Superfamily: knob-associated histidine-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 18.0%; Score 173.5; DB 2; Best Local Similarity 40.6%; Pred. No. 1.5e-07; Matches 39; Conservative 2; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.8%; Score 171.5; DB 2; 39.0%; Pred. No. 3.1e-07; tive 5; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
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                     1037 PIDQEMRSEEPHSE----ESHGDEP 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
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Best Local Similarity 39.0
Matches 32, Conservative
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H83994
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C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45059
R;Wilson R:, Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burton, raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Johns B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-39, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; Stock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.; Stock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Aritle: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A;Reference number: S43531; MUID:94150718; PMID:7906398
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-735 *WIL.>
A;Cross-references: UNIPROT:Q9NES7; EMBL:AL132896; NID:g6434440; PIDN:CAB60938.1; PID:g6
A;Experimental source: clone Y39B6B
C;Genetics:
A;Note: Y39B6B.gg
A;Note: Y39B6B.gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 6
T14155
zinc finger protein Peg3 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C; Date: 20-Sep-1999 #sequence_revision 7.; Di, L.L.; Tada, M.; Suzuki, R.; Kuroiwa, Y.; Kaneko-Ishino, T.; Kagitani, F.; Kohda, T.; Li, L.L.; Tada, M.; Suzuki, R.
A; Title: Peg3 imprinted gene on proximal chromosome 7 encodes for a zinc finger protein.
A; Reference numbary; translated from GB/EMBL/DDBJ
A; Residues: 1-1571 < kUR>
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: 7
C; Keywords: zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 ROIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ннннарннен 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 2;
5.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 193; DB
Pred. No. 5.2e-
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ГОДУСРСОРРРНИДСИСИСИСРРР 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 20.0%;
Best Local Similarity 27.9%;
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 31; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 НАРАНИСНИ
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Query Match
Best Local Similarity
Matches 48; Conserv
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C; Species: Homo sapiens (man)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C; Accession: I78877
R; Zu, Y.L.; Maekawa, T.; Nomura, N.; Nakata, T.; Ishii, S.
Oncogene 8, 2749-2758, 1993
A; Title: Regulation of trans-activating capacity of CRE-BPa by phorbol ester tumor promc A; Accession: I78877
A; Accession: I7887
A; Accession: I7887
A; Cross-references: UNIPROT: Q02930; GB: L05912; NID: g181053; PIDN: AAC37527.1; PID: g181054
C; Genetics:
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C;Genetics:
A;Gene: CC0303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cation efflux family protein [imported] - Caulobacter crescentus
Cation efflux family protein [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: F87286
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87286
A;Accession: F87286
A;Accession: P87286
A;Accession: P87286
A;Accession: P87286
A;Accession: F87286
        and
                                                                                                                                                                   GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H83994
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <STO>
A;Cross-references: UNIPROT:Q9K990; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAA;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2760
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                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                     Length 380;
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                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                   Score 170.5; DB 2;
Pred. No. 2.3e-07;
6; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 EHGHEEDDHHHHDEDPHVWLDP 217
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Best Local Similarity
Matches 33; Conser
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Best Local Similarity
Matches 33; Conser
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--KDFG 74
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A;Accession: 178878
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 34-508 < ZUY2>
A;Residues: 34-508 < ZUY2>
A;Cross-references: GB:L05913; NID:g181055; PIDN:AAC37526.1; PID:g181056
C;Genetics:
A;Gene: GDB:CRE-BPA
A;Cross-references: GDB:9957436
A;Cross-references: GDB:9957436
A;Map position: 7p15-7p15
C;Superfamily: cAMP response element-binding protein 1; fos/jun DNA-binding domain homolc F;370-410/Domain: fos/jun DNA-binding domain homology <FUD>
                              domain homold
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A;Residues: 1-508 <NOM>
A;Cross-references: UNIPROT:Q02930; GB:L05515; NID:g181049; PIDN:AAA52072.1;
A;Experimental source: KG-1 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:125836, NCBIP:125837)
B;Zu, Y.L.; Maekawa, T.; Nomura, N.; Nakata, T.; Ishii, S.
Oncogene 8, 2749-2758, 1993
A;Title: Regulation of trans-activating capacity of CRE-BPa by phorbol ester A;Reference number: I58379; MUID:93390949; PMID:8378084
A;Accession: I58379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the gene family
                              fos/jun DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAMP response element-binding protein CRE-BPa - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 21-Sep-1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004 C;Accession: A45477; I58379; \(\overline{1}\)78878 R;Nomura, N.; Zu, Y.L.; Maekawa, T.; Tabata, S.; Akiyama, T.; Ishii, S. J. Biol. Chem. 268, 4259-4266, 1993 A;Title: Isolation and characterization of a novel member of the gene family A;Reference number: A45477; MUID:93179432; PMID:8440710
                                                                                                                                                                                                                                                                                                                                                                  55 H------GPGKGPRDPPHNQGHCCHGHGPPPGHLRRR----GPGKGPRPF--
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                                                                                                                                                                                    Gaps
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                                                                                                                         Length 369;
                                                                                                                                                                               Indels
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                                                            < FJD;
A,Gene: CREBPA
C,Superfamily: cAMP response element-binding protein 1;
F,231-271/Domain: fos/jun DNA-binding domain homology <F
                                                                                                                  Query Match 17.2%; Score 166.5; DB 2; Best Local Similarity 32.7%; Pred. No. 4.8e-07; Matches 48; Conservative 8; Mismatches 52;
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Pred. No. 6.5e-07;
8; Mismatches 52;
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RNRAAATRCRQKRKVWVMSLEKKAEEL
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A;Molecule type: mRNA
A;Residues: 8-508 <ZUY1>
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nilarity 32.7%; E
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MHC H-2K/t-w5-linked ORF precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 149714
R;Han, S.
Mol. Cell. Biol. 10, 138-145, 1990
A;Title: A putative transmembrane protein with histidine-rich charge clusters encoded in A;Reference number: 149714; MUID:90097821; PMID:2294398
A;Accession: 149714
A;Reference number: 149714
A;Ccession: 149714
A;Ccession: 143714
A;Cross-references: GB:M32010; NID:g193738; PIDN:AAA37767.1; PID:g309286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.8%; Score 162; DB 2; Best Local Similarity 42.9%; Pred. No. 1.3e-06; Matches 39; Conservative 2; Mismatches 32
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                                                                                                                                                           hypothetical protein H13N06.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23089
R;Lennard, N.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z19673
A;Accession: T23089
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A;Co
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Pred. No. 6.5e-07;
6; Mismatches 29
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Matches 39; Conser
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RESULT 14

2

Gaps

5.

Indels

DB 2; Length 1378;

17.2%; Score 166.5; DB 2; 36.0%; Pred. No. 1.6e-06; iive 5; Mismatches 45;

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Query Match Best Local Similarity Matches 31; Conser

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842 9

783 PLDQEMRSEEPHDDKPHGQEPHDDMRPHGQEPHDDEPHGDEPHGDEPHGDEPHGDEPHDDK

61 DFQDYGPCDPPHNQGHCCHGHGPPP 86

15

RESULT 149714

2 РИКИНЅНЕОНРИСНИРИАНИРИЕН- DTHROHPHGHHPHGHHPHGHHPHGHHPHGHHPHCH

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43 HCHSHGHSHBDFHHGHSHGHSH----EDFHHGHGHTHESIWHGHAHSHDHGHSREELH-H 97
1 НРНКИ-НЅНЕОНРНGН-НРНАНИРНЕНОТНRОНРНGН----НРНGН-ИРНGНИРН
                                                                                                                                                                                                                                   GHSHGHSHDSLHHG-----GHGHAHREHSHG 123
                                                                                                                                                             54 СН-НРИСИВРОДУСРСВРРИМОСИСИСИС
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8

Gaps

32; Indels

Length 436;

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5.1.6
Compugen Ltd.
version - 2005
GenCore (c) 1993
        Copyright
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OM protein - protein search, using sw model

2005, 13:32:29; Search time 133.141 Seconds (without alignments) 569.231 Million cell updates/sec June 15, Run on:

US-10-074-225A-5 966 1 HPHKHHSHEQHPHGHHPHAH......PSFPLPHHKHPLKPDNQPFP Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

segs, 512079187 residues 1612378 Searched:

1612378 Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	пошо вар	Q68dr3 homo sapien	mus m	Q99ps6 mus musculu	Q9esb3 mus musculu	mus	Q6yka2 mus musculu	Q99ps8 rattus norv	Q9bgul bos taurus	Q99ps7 rattus norv	Ω	Q28640 oryctolagus	33		_		Q26056 plasmodium			Q632v3 bacillus ce			Q72yz0 bacillus ce	Q7syh2 xenopus lae		Q816t1 bacillus ce		Q9vsz7 drosophila		Q9ki77 bacillus an	Q9ki76 bacillus an
SUMMARIES	ΙD		Q68DR3	Q99PS5	Q99PS6	Q9ESB3	Q6YK32	Q6YKA2	Q99PS8	Q9BGU1	Q99PS7	Q9ESB2	HRG RABIT	HRG_BOVIN	Q8M <u>P</u> 30	HRPX PLALO	Q9KI\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	<b>Q26056</b>	Q9KI89	Q801E5	Q632V3	Q6HCE3	Q9K188	Q72YZ0	Q7SYH2	Q7ZY91	Q816T1	Q8T0B3	V3V8Z7	Q6NBF4	Q9KI77	Q9KI76
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<b>19ki91 bacillus an</b>	Oddits xenopus tro	<pre>29v3a4 drosophila</pre>		29vv44 drosophila		076876 drosophila	275dj5 ashbya goss	298h88 rhizobium l	26ei04 cucurbita m	29ki82 bacillus an	29ki80 bacillus an	29ki78 bacillus an	19ki79 bacillus an
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2 Q9KI	2 Q6DI	1 CSUF	2 Q9NE	2 Q9V	2 Q7K1	2 0768	2 Q75D	2 Q98H	2 Q6EI	2 Q9KI	2 Q9KI	2 Q9KI	2 Q9KI
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#### ALIGNMENTS

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TISSUE=Plasma;

MEDLINE=93092937; PubMed=1459097;

Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,

Asanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,

Hochstrasser D.F.;

Hochstrasser D.F.;

Hochstrasser D.F.;

Electrophoresis 13:707-714(1992).

Electrophoresis 13:707-714(1992).

L. FUNCTION: The physiological function is not yet known. It binds heme, dyes and divalent metal ions. It can inhibit rosette formation and is known to interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HMW kininogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood coagulation cascade.

C. -- SUBCELLULAR LOCATION: Secreted.

C. -- SUBCELLULAR LOCATION: Expressed by the liver and secreted in plasma.

C. -- LISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
                                                                                                                                                                                                                                                                                                                                             Koide T., Foster D.C., Yoshitake S., Davie E.W.; "Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA."; Biochemistry 25:2220-2225(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n plasma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 214-247 FROM N.A.
MEDLINE=94245171; PubMed=8188234;
Hennis B.C., Frants R.R., Bakker E., Vossen R.H., van der Poort E.!
Blonden L.A., Cox S., Khan P.M., Spurr N.K., Kluft C.;
"Evidence for the absence of intron H of the histidine-rich
glycoprotein (HRG) gene: genetic mapping and in situ localization (HRG to chromosome 3q28-q29.";
Genomics 19:195-197(1994).
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                      20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich
glycoprotein) (HPRG).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Wakabayashi S., Takahashi K., Tokunaga F., Koide T.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                    525 AA
                                    PRT;
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=86216149; PubMed=3011081;
                                    STANDARD;
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RESULT 1
HRG HUMAN
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us-10-074-225a-5.rup

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Q99PS5;
Q99PS5;
01-JUN-2001
01-JUN-2001
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                                                                                                                         entry is copyright. It is produced through a collaboration ss Institute of Bioinformatics and the EMBL outstation - informatics Institute. There are no restrictions on its fit institutions as long as its content is in no way statement is not removed. Usage by and for commercial s a license agreement (See http://www.isb-sib.ch/announce/to license@isb-sib.ch).
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protein has many internal repeats. 12 tandem repetitions of a 5-residue sequence (GHHPH, consensus) form a histidine-rich region. SIMILARITY: Contains 2 cystatin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.
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(Potential).
(Potential).
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EMBL; AB005803; BAA21613.1; -...
EMBL; Z17218; CAA78925.1; -...
EMBL; Z17218; CAA78925.1; -...
PIR; A01287; KGHUGH.
SWISS-2DPAGE; P04196; HUMAN.
Genew; HGNC:5181; HRG.
MIM; 142640; -...
InterPro; IPR000010; Prot inh cystat.
Pfam; PF00031; Cystatin; 1...
Pfam; PF00031; Cystatin; 1...
Direct protein sequencing; Glycoprotein; Heparin-binding; Polymorphism; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Histidine-rich glycoprotein.

Cystatin-like 1.

Cystatin-like 2.

Pro-rich.

His/Pro-rich.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlCNAC. ..) (Potent N-linked (GlCNAC. ...) (Potent N-lin
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/PTId=VAR 014528.
A2B124D6CE93114F CRC64;
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Q68DR3;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp779H1622 (Fragment).
Name=DKFZp779H1622;
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 966; DB 1;
100.0%; Pred. No. 1.2e-67;
vative 0; Mismatches 0;
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STRAIN=FVB/N; TISSUE=Liver;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MAIschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MAISCHON M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

MAISCHON M., Soares M.B., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Norley D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Norlessley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

Matring M., Madan A., Young A.C., Shevchenko Y., Butterfield Y.S.,

Matring M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

Marra M.A., Schmutz J., Myers R.M., Butterfield M.S.,

Jones S.J., Marra M.A.;

Madan A., Schmutz J., Myers R.M., Butterfield Y.S.,

Macharation and initial analysis of more than 15,000 full-length human
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                                                                                                                Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, CR749302; CAH18157.1; -. Hypothetical protein.

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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.6%; Pred. No. 1.6e-66;
Matches 146; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                       08522797450AFA1F CRC64;
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Last annotation update)
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01-JUN-2001 (TrEMBLrel. 17, La
25-OCT-2004 (TrEMBLrel. 28, La
Histidine-rich glycoprotein.
Name=Hrg; Synonyms=MMHRG;
Mus musculus (Mouse)
SEQUENCE FROM N.A.
TISSUE-Liver;
The German cDNA Consortium;
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STRAIN=FVB/N; TISSUE=Liver;
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DFQDYGPCDPPPHNQ---GHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRK 117
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                                                                                                                                                                                                                                                                                            Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;
"Murine histidine-rich glycoprotein: cloning, characterization and cellular origin.";
Immunol. Cell Biol. 78:280-287(2000).
EMBL; AF194028; AAG28416.1; -.
MGD; MGI:2146636; Hrg.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
SEQUENCE 525 AA; 59132 MW; 6E55F2A439CFB123 CRC64;
                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                         Q9ESB3;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Histidine-rich glycoprotein.
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Q6YK32;

O5-JUL-2004 (TrEMBLrel. 27, Created)

O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)

O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)

Histidine-rich glycoprotein HRG.
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MEDLINE=20307726; PubMed=10849117;
                         PRELIMINARY;
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Matches 105; Conser
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Histidine-rich glycoprotein.
Name=Hrg; Synonyms=MMHRG;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                          525;
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STRAIN=BALB/c; TISSUE=Liver;
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S., Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055897; BAB33094.1; -.
MGD; MGI:2146636; Hrg.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000010; Prot_inh_cystat.
Ffam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
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                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                      59162 MW; A83E93A439CFB126 CRC64;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; AB055898; BAB33095.1; -.
EMBL; BC011168; AAH11168.1; -.
MGD; MGI:2146636; Hrg.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR00010; Prot_inh_cystat.
Pf00031; Cystatin; 1.
SMART; SM00043; CY; 2.
SEQUENCE 525 AA; 59162 MW; AB3E93A439CFB1
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GEVLTLPEANFPSFSLPNCNRSLQPEIQPFP 497
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Best Local Similarity
Matches 105; Conser
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Gaps ω ; SEQUENCE FROM N.A.
HSU S.J., Balmain A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY137504; AAN27996.1; -.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot inh\_cystat.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 2.
SEQUENCE 536 AA; 60439 MW; CCF14FC08DD53D7C CRC64; 66.8%; Score 645.5; DB 2; Length llarity 69.5%; Pred. No. 1.3e-42; Conservative 9; Mismatches 34; Indels

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(FEB-2001) to the EMBL/GenBank/DDBJ databases.
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ses 104; Conserv
                                                                                                                                                                                                                                                                                                                          Name=BTHRG;
Bos taurus
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Best Local S
Matches 104
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Q99PS7
ID Q99PS
AC Q99PS
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Q9BGU1
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                                     DPQDYGPCDPPPHNQ---GHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRK 117
                                                        477
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DFQDYGPCDPPPHNQ---GHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRK 117
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          1 ненкнизнедириснирианиривнотиконенскирискириснириснириснирисн
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Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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kahashi K., Hirokado Y., Togo Y., Izumi
, Hirata D., Tsuchida N., Koide T.;
                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                        60492 MW; 71CE4FC6DF3A3D72 CRC64;
                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Histidine-rich glycoprotein Hrg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                         Score 645.5; DB 2;
Pred. No. 1.3e-42;
9; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148
                                                                                               508
                                                                           GEVLPLPEANFPSFPLPHHKHPLKPDNOFFP 148
                                                                                                                                               536 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 525 AA
                                                                                                                                                                                                                                                                                                                 extracellular space; TAS
                                                                                      GEVLPLPEANFPSFPLPHHKHPLKPDNQPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SILLY STRAIN STRAIN STRAIN SUBJUSTED SUBMITTED (JUL-2002) to the EMBL/GenBan EMBL; AY13562; AAN10183.1; -. GO; GO:0005615; C:extracellular space; InterPro; IPR000010; Prot inh_cystat. Pfam; PF00031; Cystatin; I. SMART; SM0043; CY; 2. SEQUENCE 536 AA; 60492 WW; 71CE4FC6
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q99PS8
Q99PS8;
Q1-JUN-2001 (TrEMBLrel. 17, C1 01-JUN-2001 (TrEMBLrel. 17, L6 01-JUN-2003 (TrEMBLrel. 24, L6 Histidine-rich glycoprotein 1. Name=RNHRG1;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                         66.8%;
/ 69.5%;
cvative
                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A.
STRAIN=Sprague-Dawle
Wakabayashi S., Take
Ohashi T., Sato N.,
                                                Query Match
Best Local Similarity
Matches 105; Conser
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                        Name=Hrg1;
                                                                                              478
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                                      61
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Q6YKA2
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Q99PS8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 HPHGHDFLDYGPCDPPSNSQELKGQYHRGHGPPHGHSRKRGPGKGLFPFHQRQIGYVYRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         413 HPYGHHPHGHHPHDNDFYDHGPCDPPPHRQDPQDHHRQGRDPPPRHSKERGPGKGHFRFY
                                                                                                                                                                                                                                                                                                                                                      1 НРНКИНЅНЕОНРИGНИРНАНИРИЕНОТНКОНРИСНИРИСНИРИСНИРИСНИРИСН
                                                                                                                                                                                                                                                                                                                                                                                                                               HPHCHDFQDYGPCDPPPHNQ --- GHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRL
                                                                                                                                                                                                                                                                     Gaps
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NCBI_TaxID=9913;
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Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.
Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055894; BAB33091.1; -.
GO; GO:0004869; F:Cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot_inh_Cystat.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 2.
SEQUENCE 546 AA; 61948 MW; 26264858824D89EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 546;
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                                                                                                                                                                                                                 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.7%; Score 644; DB 2; Length 54 ilarity 62.7%; Pred. No. 1.7e-42; Conservative 10; Mismatches 34; Indels
                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                 Length
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ database: EMBL; AB055895; BAB33092.1; -. GO; GO:0004869; F:cysteine protease inhibitor activity InterPro; IPR000010; Prot inh_cystat.
Pfam; PF00031; Cystatin; I. SMART; SM00043; CY; 2. SMART; SM00043; CY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9BGU1;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNOPFP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    462 PPLNVGEVLTPPEANFPIFSLPNCNRPPQPEIRPFP 497
                                                                                                                                                                                                             Query Match 66.7%; Score 644; DB 2;
Best Local Similarity 68.6%; Pred. No. 1.6e-42;
Matches 107; Conservative 7; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         НРНКНИЅНЕО́НРНСНИРНАННРНЕНОТНКО́НРНСНИРНСНИРНСНИРНСНИРНСНР
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                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Rođentia; Sciurognathi; Muridae; Murinae; Rattus
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STRAIN=Lewis;
MEDLINE=20307726; PubMed=10849117;
Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;
Immunol. Cellular origin.";
Immunol. Cell Biol. 78:280-287(2000).
EMBL; AF194029; AAG28417.1; -.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot inh_cystat.
Pfam; PF00031; Cystatin; I.
Pfam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 510;
                                                                                                                                                                                               STRAIN-Sprague-Dawley; TISSUE-Liver;
STRAIN-Sprague-Dawley; TISSUE-Liver;
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.
Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055896; BAB33093.1; -.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot inh_cystat.
Ffam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
SMART; SM00043; CY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 626; DB 2; Length 515;
Pred. No. 4e-41;
6; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.6%; Score 614.5; DB 2; Length 68.9%; Pred. No. 3.1e-40; vative 7; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9ESB2,
Q9ESB2;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
(TrEMBLrel. 17, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||| ||: | :|: ||||
NFPSFSLPNCNRPPQPEIQPFP
                                                                                                 Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                   64.8%;
69.5%;
               01-JUN-2003 (TrEMBLrel. 24,
Histidine-rich glycoprotein
Name=RNHRG2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histidine-rich glycoprotein
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                                                                                 (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Hrg;
Rattus norvegicus (E
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 HPHKHHSHE
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Best Local Similarity
Matches 102; Conser
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Best Local Similarity
Matches 105; Conser
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                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                         NCBI_TaxID=10116;
                                                                                 Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
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Q9ESB2
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                                           454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coagulation cascade.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
-!- DOMAIN: In addition to having a high His and Pro content, this protein has many internal repeats. 15 tandem repetitions of a 5-
residue sequence (G[H/P][H/P]PH, consensus) form a His/Pro-rich
                           DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             glycoprotein.",
Biochemistry 35:1925-1934(1996).
-!- FUNCTION: The physiological function is not yet known. It binds
heme, dyes and divalent metal ions. It can inhibit rosette
formation and is known to interact with heparin, thrombospondin,
and the lysine-binding site of plasminogen. On the basis of its
homology with HMW kininogen, the His-rich region of this protein
may mediate the contact activation phase of intrinsic blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U32189; AAC48516.1; -.
InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; I.
Direct protein sequencing; Glycoprotein; Heparin-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich glycoprotein) (HPRG) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE OF 9-23; 301-313 AND 422-429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Serum;
MEDLINE=96229917; PubMed=8639676; DOI=10.1021/bi952061t;
Borza D.-B., Tatum F.M., Morgan W.T.;
"Domain structure and conformation of histidine-proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histidine-rich glycoprotein.
Cystatin-like 1.
Cystatin-like 2.
Pro-rich.
His/Pro-rich.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Py similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region.
SIMILARITY: Contains 2 cystatin-like domains.
                                                                                          LPLPEANFPSFPLPHHKHPLKPDNQPFP 148
                                                                                                                    LTPPEANFPIFSLPNCNRPPOPEIRPFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
8
1126
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106
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116
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ID HRG RABIT
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61
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SIGNAL
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CC coagulation cascade.

CC coagulation cascade.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

CC -!- DOMAIN: In addition to having a high His and Pro content, this protein has many internal repeats. 12 tandem repetitions of a 5-

Tesidue sequence (GHHPH, consensus) form a histidine-rich region.

CC -!- SIMILARITY: Contains 2 cystatin-like domains.

M DIRECT protein sequencing; Glycoprotein: Henarin-bindin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGHPPHGPPPHGHPPHGHGFHDHGPCDPPSHKEGPQDLH-QHAMGPPPKHPGKRGPGKGH
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MEDLINE=93351678; PubMed=8348977; DOI=10.1016/0014-5793(93)80945-Q; Soerensen C.B., Krogh-Pedersen H., Petersen T.E.; "Determination of the disulphide bridge arrangement of bovine histidine-rich glycoprotein."; FEBS Lett. 328:285-290(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28, Last sequence update)
44, Last annotation update)
coprotein (Histidine-proline rich glycoprotein)
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Cetartiodactyla; Ruminantia; Pecora; Bovidae
                               (Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDNQPFP 148
         (Potential)
                                                                                                                          (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FPFHWRIGSVYQLPPLQKGEVLPLPEANFPQLLLRNHTHPLKPEIQPFP
                                                                                                                                                                                                                                                                       Length 526;
                                                                                                                                                                                                                                                                                                                            40; Indels
N-linked (GlCNAC. .) (Pot Cleavage (by plasmin). Cleavage (by plasmin).
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Pred. No. 1.2e-34;
8; Mismatches 40;
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P3343;
01-FEB-1994 (Rel. 26
01-FEB-1994 (Rel. 26
05-JUL-2004 (Rel. 44
Histidine-rich glycc
(HPRG) (Fragments).
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Mammalia; Eutheria;
Bovinae; Bos.
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 98; Conser
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  CARBOHYD
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HRG BOVIN

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ار A.A.;
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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEVLPLPEANFPSFPLPHHKHPLKPDN
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Similar to Plasmodium lophurae. Histidine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=AX4;
Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                Length
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128A8223499DE6FC CRC64;
                                                                                                ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein).
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                            Similarity 47.8%; Score 489; DB 1; I Similarity 47.8%; Pred. No. 1.5e-30; SB; Conservative 16; Mismatches 26;
                       (GlcNAc.
                                                                                                (GlcNAc
                                                                                                                                              (GlcNAc
                                                                                                                                                                                               (GlcNAc
                                                                                              N-linked
                                                                                                                                                                                               N-linked
                                                                                                                                            N-linked
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                                                                                                                                                                                                                                                                                                                                               44470 MW;
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Submitted (MAR-2003) to the
EMBL; AC123513; AAM44363.1;
EMBL; AC117070; AAM09303.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
Hypothetical protein.
                                        77.
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78
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103
122
263
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Best Local Simi
Matches 88;
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SEQUENCE
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NON CONS
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Q8MP30
ID Q8MP30
DT Q8MP3
DT Q1-OC
DT O1-OC
DT O1-OC
DT O2-JU
DE HYPOT
DE G1/C
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                 υ,
                                                                                                                                                                                          61 DFQDYGPCDPPPHNQGHCCHGHGPPPGHLRRRGPGKGPRPFHCRQIGSVYRLPPLRKGEV 120
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                                                                                                 Gaps
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MEDLINE=85061618; PubMed=6095114;
Ravetch J.V., Feder R., Pavlovec A., Blobel G.;
Ravetch J.V., Feder R., Pavlovec A., Blobel G., Feder R., Fed
                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Histidine-rich glycoprotein.
N-linked (GlcNAc. .) (Probable)
2 X 16 AA tandem repeats.
                                                  DB 2; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.0%; Score 241.5; DB 1; Length 351; 47.7%; Pred. No. 2.8e-11; vative 1; Mismatches 34; Indels 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Histidine-rich glycoprotein precursor.
Plasmodium lophurae.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5853;
                                             Score 281.5; DB 2; Length
Pred. No. 1.5e-14;
3; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 X 10 AA tandem repeats
D19A48D47D890453 CRC64;
28937 MW; AD4C7A2F86BB14B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-2.
2 X 15 AA tandem repeats.
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16-2.
2 X 17 AA tandem repeats.
17-1.
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PIR; A22692; KGZQHL.
HSSP; P13231; 1HCE.
Glycoprotein; Malaria; Repeat, SIGNAL.
1 23
PROPEP 24 47
CHAIN 48 351
CARBOHYD 40 40
DOMAIN 59 90
REPEAT 75 90
DOMAIN 91 123
REPEAT 91 107
REPEAT 108 123
DOMAIN 124 153
REPEAT 124 138
REPEAT 139 153
                                                  29.1%;
38.3%;
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Nature 312:616-620(1984).
-!- MISCELLANEOUS: In the
P.lophurae in ducks, t
accumulates to compris
histidine rich proteir
                                           Query Match
Best Local Similarity 38.3
Matches 57; Conservative
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Best Local Similarity
Matches 42; Conserv
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233
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HRPX_PLALO
ID HRPX_PLALO
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(c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein Run on:

June 15, 2005, 13:31:29 ; Search time 95.7269 Seconds (without alignments) 408.065 Million cell updates/sec

US-10-074-225A-6 697 1 SVNIIHRPPPHGHHPHGPPP.......HPPHGHGFHDHGPCDPPSHK 101 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

seqs, 386760381 residues

2105692

Searched:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003as:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	Adh10412 Rabbit HP	Abb79805 Rabbit hi			Ade76897 Human pro		Adl12335 Human ste	Abb79807 Rabbit hi	Abb79806 Human his	Adh10411 Human HPR	Abg09949 Novel hum	N	Ade57105 Rat Prote	0 Rat	Add48703 Rat Prote	9 ORF2	Aar04116 ORF1 of E	Add45740 Human Pro	Abo52997 Human spl	5 Tumour	Aao30246 Human Sap	Aao30188 Human cP3	Adj68263 Human hea	Aao30408 Human sec	
QI 1	ADH10412	ABB79805	ADH10410		ADE76897	ADH10409	ADL12335	ABB79807	ABB79806	ADH10411	ABG09949	ADD45442	ADE57105	ADD47240	ADD48703	AAR04119	AAR04116	ADD45740	ABO52997	ABM80186	AAO30246	AAO30188	ADJ68263	AA030408	CO. CO. L. S. K. K.
Length DB	!			525 5						148 8	491 4	296 7	296 7	274 7	•				_			_	173 7		
% Query Match	100.0	100.0	100.0	45.1	45.1	45.1	45.1	40.2	40.2	40.2	7.	7	37.2	35.3	35.3	ო	ش	•	٠	33.5	•	•	33.1	•	ני ני
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Result No.		7	m	4	ß	Q	7	œ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	u

Adg15008 Human SEC	• • •	Abb68218 Drosophil	Abull891 Human ABC	Abb61183 Drosophil	Abb61362 Drosophil	Abp73921 Candida a	Adg15007 Human SEC	Abb57176 Mouse isc	Adn43006 Human sec	Abb78538 Ser-Pro-P	Aao30407 Human sec	Adn43007 Human sec	Ads23375 Bacterial	Adn20587 Bacterial	Aar22380 Antigen m	Abr39650 A. thalia	Adm80808 Human CAD	Aab26153 Neospora
ADG15008	AAB71654	ABB68218	ABU11891	ABB61183	ABB61362	ABP73921	ADG15007	ABB57176	ADN43006	ABB78538	AAO30407	ADN43007	ADS23375	ADN20587	AAR22380	ABR39650	ADM80808	AAB26153
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230	9 6	102	247	80	594	1130	272	1378	220	104	162	202	449	518	487	205	163	865
32.9	32.8	32.8	32.7	32.3	32.0	32.0	31.9	31.7	31.6	30.9	30.8	30.8	30.6	30.3	30.1	30.1	29.9	29.8
229	228.5	228.5	228	225	223	223	222	221	220	215.5	215	214.5	213.5	211	210	209.5	208.5	208
26	78	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit. Rabbit HPRG protein H/P rich domain ADH10412 standard; protein; 101 AA (first entry) 11-MAR-2004 ADH10412; ADH10412 

Oryctolagus cuniculus. WO2003077872-A2. 25-SEP-2003.

2002US-0364047P (ATTE-) ATTENUON LLC 15-MAR-2002;

17-MAR-2003; 2003WO-US008060

ם, Juarez Donate F, Mccrae K,

AP

Mazar

WPI; 2004-090604/09

New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer

Claim 6; SEQ ID NO 24; 117pp; English.

The invention relates to an isolated tropomyosin (Tpm) -related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agents, as does the

us-10-074-225a-6.rag

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binds to the isolated polypeptide or peptide is human histidine-proline

binds to the isolated polypeptide or peptide is human histidine-proline

crich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic

homologue, variant, domain of human or rabbit HPRG, two chain

chuman kininogen (HK), the D5 domain of HK, or a Tpm-binding,

antiangiogenic homologue, variant, domain or fragment of the HK or its D5

domain. The Tpm-related antiangiogenic receptor polypeptide or peptide,

antibodies and compositions are useful for inhibiting endothelial cell

migration, invasion, proliferation or angiogenesis, for inducing

endothelial cell apoptosis, or for treating tumours or cancer, diabetic

retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis,

psoriasis, or scleroderma. The antibody may be also used for detecting

the presence of a Tpm polypeptide or peptide in a biological sample, for

promoting wound healing, or for treating diseases or conditions in which

increased angiogenesis is desired, e.g. coronary artery disease or

protein His-Pro (H/P) rich domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histidine proline rich glycoprotein; HPRG; rabbit; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
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  The antiangiogenic polypeptide agent that
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251. .296
/note= "Proline-rich domain"
321. .421
/note= "Histidine-proline-rich domain, region also
specifically claimed in Claim 1"
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0
                                                                                                                                                                                                                                                                                                            Length 101;
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      61 СИРРИСРРИСИРРИСРРИСИРРИСИСЕНИНСРСОРРЅНК 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 697; DB 8;
Pred. No. 1.9e-51;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 526
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Best Local Similarity 100.
Matches 101; Conservative
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P-PSDB; ABN84911.
  native Tpm interna
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SVNIIHRPP
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ABB79805
ID ABB79805 standard;
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                                                                                                                                                                                                                                                                                 Sequence 101 AA
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The present sequence is the protein sequence of rabbit histidine proline rich divoporatein (HPRG), a proteinaceous chelator that can be used to inhibit angiogenesis and treat cancer. Claimed anti-angiogenesis and treat cancer. Claimed anti-bibiting angiogenesis.

CC domain (see ABR99800) of human HPRG; and HP domain of trabbit HPRG of the seek that the following the generic sequence given in ABR99809. As a diagnostically or therapeutically produced anti-angiogenic polypeptide, peptide having the generic sequence given in ABR99808. Deptide multimers and a carrier; an antibody septide or peptide multimer and a carrier; an antibody peptide, peptide or peptide multimer and a carrier; an antibody peptide, peptide or peptide multimer and a carrier; an antibody peptide, peptide or peptide multimer and a carrier; an antibody peptide, peptide or peptide multimer and a carrier; an antibody companied, peptide or peptide multimer and a carrier; an antibody peptide, peptide or peptide multimer of the antibody; a method for inhibiting can an antigen-binding fragment of the antibody; a method for inhibiting an appleasis a method for treating a subject having a disease or condition associated with undesired cell migration, invasion, or an antigen-binding fragment of the antibody; a method for inhibiting angogenesis a method of effecting the presence of HPRG or the peptide or peptide or peptide multimer; an application associated with undesired cell migration, invasion, and angiogenesis and expectited multimer; and angiogenesis and angiogenesis and angiogenesis and may also be complex mixture. The compositions and embrods are useful in disease. Complex mixture. The compositions and methods are useful in disease, disbetic vertacting a disease or condition associated with undesired cell migration in pertinent disease states, and in veatuble or peptide multi
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 migration,
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                invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
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diagnosing or treating diseases associated with undesired cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 GHPPHGPPHGHPPHGPPPHGHPPHGHGFHDHGPCDPPSHK 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 697; DB 5;
Pred. No. 7.5e-51;
; Mismatches 0;
                                                         Claim 1; Page 12-13; 82pp; English.
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100.0%; Pr
vative 0;
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Best Local Similarity
Matches 101; Conserv
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The invention relates to an isolated tropomyosin (Tpm)-related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isolated antiangiogenic receptor polypeptide agents, The isolated antiangiogenic receptor polypeptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agents, as does the activity of binding to the antiangiogenic polypeptide agent that contains to the isolated polypeptide or peptide is buman histidine-proline rich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain or fragment of human or rabbit HPRG, two chain the Tpm-related antiangiogenic receptor polypeptide or peptide, antibodies and compositions are useful for inhibiting endothelial cell ampiration, invasion, proliferation or angiogenesis, for inducing migration, invasion, proliferation or angiogenesis, for inducing conductions in veitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm Polypeptide or peptide in a biological sample, for permipheral artery disease or conditions in which increased angiogenesis is desired, e.g. coronary artery disease or peripheral artery disease. The present sequence represents a rabbit HPRG process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
            ipm; tropomyosin; antiangiogenic receptor;
histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic;
ophthalmological; antiinflammatory; gynaecological; antiarthritic;
antipsoriatic; dermatological; cardiant; vasotropic; vulnerary;
angiogenesis; gene therapy; rabbit.
                                                                                                                                                                     Location/Qualifiers
251. .296
/note = pro-rich domain
321. .421
/note = His-Pro rich domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mazar AP
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                                                                                                                                  cuniculus
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                                                                                                                                    Oryctolagus
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Domain
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Gaps

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Indels

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Score 697; DB 8; Pred. No. 7.5e-51; ; Mismatches 0;

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Conservative

Query Match Best Local Similarity Matches 101; Conser

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100.0%;

Length 526;

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The present sequence is the protein sequence of human histidine proline rich glycoprotein (HPRG), a proteinaceous metal chelator that can be used to inhibit angiogensis and treat cancer. Claimed anti-angiogenic polypeptides comprise: the histidine-proline-rich (H/P) domain (see ABB79806) of human HPRG; an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or therapeutically labeled anti-angiogenic polypeptide, peptide or peptide multimer; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled by peptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any of the domains in a way which inhibits the anti-angiogenic activity of HPRG or the domain, or an antigen-binding fragment of the antibody; a method for inhibiting cell migration, cell proliferation or angiogenesis, or for inducing apoptosis; a method for treating a subject having a disease or condition associated with undesired cell migration, invasion, cell proliferation, or angiogenesis; a method of stimulating or inhibiting angiogenesis in a subject; a method of detecting the presence of HPRG or its cleavage product or its peptide in a biological sample; isolated
                                                                                                                                                                                                                                                                                                Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
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GHPPHGPPPHGPPHGPPPHGHPPHGHGFHDHGPCDPPSHK 101
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/note= "Proline-rich domain"
350. .497
                                                                                                                                                                                                                                                             Human histidine proline rich glycoprotein.
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                                                                                                                                        525
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                                                                                                                                       ABB79804 standard; protein;
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P-PSDB; ABN84910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
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expression vector; transformed or transfected cells; a method of expression vector; transformed or transfected cells; a method of providing to a cell, tissue or organ an angiogenesis inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an affinity ligand useful for binding to, or isolating, an HPRG-binding molecule or cells expressing the binding molecule, comprising the polypeptide, peptide or peptide multimer, immobilised to a solid support or carrier; and a method of isolating HPRG-binding molecule, or isolating or enriching cells expressing HPRG-binding site or receptor, from a complex mixture. The compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's disease, and amyotrophic lateral sclerosis. The antibodies are stimulators of angiogenesis and are useful for promoting in various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 ATFGTNGAQRHSHNNNSSDLÄPHKHHSHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHGPPPHGHPP----HGPPPHGHPPHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         45.1%; Score 314; DB 5; Length 525; 41.8%; Pred. No. 9.9e-19; vative 2; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --НИРИСРРИЧНИРИСРР-----НСИР-РИСРРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein expressed in a liver disorder #18
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encoding the polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 525
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N-PSDB; ADE76896.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE76897 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 525 AA;
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 nucleic acids
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Best Local Simi
Matches 64;
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ADE76897
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein concern several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically condition is useful for detecting and encoded by a cDNA differentially expressed in a sequence of a protein encoded by a cDNA differentially expressed in a sequence of a protein encoded by a cDNA differentially expressed in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 КРРГКРНGSRDHHHPHKP-----НЕНGPPPPPDERDHSHGPPLPQGPPPLLPMSCSSCQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----HGHP-PHGPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 314; DB 8; Length 52
Pred. No. 9.9e-19;
2; Mismatches 23; Indels
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/note = pro-rich domain
350. .497
/note = His-Pro rich domain
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                                    Claim 1; SEQ ID NO 62; 41pp; English.
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Best Local Similarity 41.8%;
Matches 64; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                                                                liver disorder
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ADH10409
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The invention relates to an isolated tropomyosin (Tpm)-related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agents, as does the native Tpm internal fragment. The antiangiogenic polypeptide agent that binds to the isolated polypeptide or peptide is human histidine-proline crich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic polypeptide or peptide or rich glycoprotein (HPRG), rabbit HPRG, or a Tpm-binding, antiangiogenic human kininogen (HK), the D5 domain of HK, or a Tpm-binding, to natiangiogenic homologue, variant, domain of fragment of the HK or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antiangiogenic antiangiogenic antiangiogenic receptor polypeptide or peptide, antiangiogenic nongositions are useful for inhibiting endothelial cell mostations are useful for inhibiting endothelial cell mostations are useful for inhibiting endothelial cell mostations are useful for inhibiting wound healing, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for increased angiogenesis is desired, e.g. coronary artery disease. The present sequence represents a human HPRG protein sequence.
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                                                                                                                                                                                                                                                                                    New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------RHP-----PHGPPPHGHPP-----HGPPPHGHPPHGP
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15-MAR-2002; 2002US-0364047P
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Best Local Similarity 41.8
Matches 64; Conservative
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steroid therapy; ci
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                                                                (ATTE-) ATTENUON
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                                                                                                                                          Mccrae K,
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The invention relates to a combination comprising cDNAs that are
differentially expressed in response to steroid treatment. Also included
are the following: a high throughput method for using a cDNA to detect
differential expression of nucleic acids in a sample; and a high
throughput method of screening molecules or compounds to identify a
ligand that specifically binds a cDNA. The sample is from a subject with
Wilson disease and comparison of a standard defines a stage of that
disease. The high throughput method of screening molecules or compounds
to identify a ligand that specifically binds a cDNA comprises: combining
the combination with molecules or compounds under conditions to allow
specific binding; and detecting specific binding between each cDNA and at
least one molecule or compound. The molecules or compounds are regulatory
proteins. The combination is useful for preparing a composition for
treating liver disorders associated with steroid therapy, e.g., cirrhosis
or hepatitis. The present sequence represents a human protein which is
differentially expressed in steroid-induced C3A liver cells. Note: The
sequence data for this patent did not form part of the printed
specification but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 КРРFКРHGSRDHHHPHKP----НЕНGPPPPDERDHSHGPPLPQGPPPLLPMSCSSCQH 329
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                                                                                                                                                                                                                                                                                                                                                               Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises CDNAs that are differentially expressed in response to steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----RHP-----PHGPPPHGHPP-----HGPPPHGHPPHGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 64; 141pp; English.
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                                                                                                                                               12-OCT-2001; 2001US-00976594
                                                                                                                                                                                          12-OCT-2000; 2000US-0240409P
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                        Homo sapiens.
                                                              US6673549-B1
                                                                                                         06-JAN-2004
                                                                                                                                                                                                                                                                              Furness LM,
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                                                                                                                                                                                                                                                                                                                                                                                                                               treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB79807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
ABB79807
ID ABB7
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teriosclerotic, antiinflammatory, antidiabetic, tiarthritic, antiulcer, osteopathic, antitumour, nootropic, neuroprotective, antiparkinsonian, chelator. antiangiogenic; HPGP; rabbit; cytostatic; antiar gynaecological; an ophthalmological; proline Histidine

Oryctolagus cunicu

WO200264621-A2

22-AUG-2002

14-FEB-2002; 2002WO-US004336

14-FEB-2001; 2001US-0268370P

(ATTE-) ATTENUON LLC.

Mazar AP; Plunkett ML, F, Donate

WPI; 2002-666989/7

P-PSDB; ABN84910

ine rich glycoprotein (HPRG) polypeptide, useful for ting diseases associated with undesired cell migration, attion, or angiogenesis, e.g. cancer, atherosclerosis. diagnosing or trea invasion, prolifer New histidine-prol

82pp; English. Claim 1; Page 13;

The present sequence is the protein sequence of the histidine-prolinecrich (HPP) domain of rabbit anti-angiogenic histidine proline rich
glycoprotein (HPRG, see also ABB79805). Claimed anti-angiogenic
colypebtides or peptides comprise: the H/P domain (see ABB79806) of human
colypebtides or peptides comprise: the H/P domain (see ABB79806) of human
colypebtides or peptides comprise: the H/P domain (see ABB79806) of human
cc thinbiting angiogenesis, endothelial cell proliferation or endothelial
cube formation in vitro or in vivo; or a pentapeptide having the generic
cube formation in ABB79800. Also claimed are: chemically synthesised or
recombinantly produced peptide multimers; a diagnostically labeled anti-angiogenic polypeptide to repetide or peptide
cc carrier; an antibody specific for an epitope of HPRG that is present in
the diagnostically labeled anti-angiogenic polypeptide or peptide or peptide
cc multimer; an antibody specific for an epitope of HPRG that is present in
the H/P domains in a way which inhibits the anti-angiogenic activity of
the H/P domains in a way which inhibits the anti-angiogenic activity of
c the H/P domains in a mantigen-binding fragment of the antibody; a
method for inhibiting call migration, call invasion, cell invasion, or angiogenesis; a method of
c migration, invasion, proliferation, or angiogenesis; a method of
c migration, invasion, proliferation, or angiogenesis; a method of
c migration, invasion, proliferation, or angiogenesis; a method of
c peptide multimer; an expression vector; transformed or
c transfected cells; a method of providing to a cell, tissue or organ an
expected cells; a method of providing to a cell, tissue or organ an
expected, cells; an enthod of providing to a cell, tissue or organ and
congressing HPRG-binding molecule, or solating, an HPRG-binding molecule or cells expressing
c moliferations and methods are useful in diagnosing or treating a disease
c composition as an angiogenesis, such as cancer, atherosclerosis, diabetic numation, endometriosis, arthritis, peptic ulcers, or especially useful in inhibiting the growth of primary uses, and may also be used in treating neurodegenerative leimer's or Parkinson's disease. The antibodies are loggenesis and are useful for promoting in pertinent disease states, and in various stimulators of ang neovascularization fractures. HPRG is proliferation, or retinopathy, infla immunoassays or tumours

Ź Sequence 148

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                                                                   ----нн-----рненотиконрисинр
                        19;
Length 148;
                        Indels
                       24;
DB 5;
Score 280.5; DB:
Pred. No. 2.3e-16
                                                                                               70 НGНРРНGРРРНGНРРНGНGFHDHGРCDPPSH 100
                       Mismatches
                      ..
H
 40.28;
                                                                || || | | | || || || || || || || PHKGHHSHEQHPHA-
            51.6%;
                       Conservative
            Similarity
                      47;
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 Query Match
           Best Local
Matches 4
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HCHHPHGHHPHGHHPHCHDFQDYGPCDPPPH

RESULT ABB7980

ABB79806 standard; protein; 148 AA

(first entry) 25-NOV-2002

Human histidine proline rich glycoprotein His/Pro-rich domain.

Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian.

Homo sapiens.

WO200264621-A2

22-AUG-2002

14-FEB-2002; 2002WO-US004336.

14-FEB-2001; 2001US-0268370P

(ATTE-) ATTENUON LLC

Plunkett ML, Harris S, Donate F,

WPI; 2002-666989/71.

P-PSDB; ABN84910

New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.

English Claim 1; Page 13; 82pp; The present sequence is the protein sequence of the histidine-prolinecrich (H/P) domain of human anti-angiogenic histidine proline rich
glycoprotein (HPRG, see also ABB79804). Claimed anti-angiogenic
glycoprotein (HPRG, see also ABB79804). Claimed anti-angiogenic
comparing of reabbit HPRG (see ABB12345); a variant of human HPRG; an H/P
commain of rabbit HPRG (see ABB12345); a variant of these that is capable
cof inhibiting angiogenesis, endothelial cell proliferation or endothelial
cube formation in vitro or in vivo; or a pentapeptide having the generic
sequence given in ABB79808. Also claimed are: chemically synthesised or
recombinantly produced peptide multimers; a diagnostically labeled anti-angiogenic polypeptide, peptide or peptide
cric multimer; a diagnostically useful HPRG-related composition, comprising
the diagnostically labeled polypeptide, peptide or peptide multimer and
carrier; an antibody specific for an epitope of HPRG that is present in
the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any
cof the domains in a way which inhibits the anti-angiogenic activity of
the HPRG or the domain, or an antigen-binding fragment of the antibody; a
method for inhibiting cell migration, cell invasion, cell proliferation
or angiogenesis, a method for treating a
method for inhibiting angiogenesis in a subject; a method of
stimulating or inhibiting angiogenesis in a subject; a method of
stimulating or inhibiting or its cleavage product or its peptide in

us-10-074-225a-6.rag

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a biological sample; isolated nucleic acids encoding the polypeptide, peptide or peptide multimer; an expression vector; transformed or transfected cells; a method of providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an affinity ligand useful for binding to, or isolating, an HPRG-binding molecule or cells expressing the binding molecule, comprising the polypeptide, peptide or peptide multimer, immobilised to a solid support or carrier; and a method of isolating HPRG-binding molecule, or isolating or enriching cells expressing HPRG-binding site or receptor, from a complex mixture. The compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, invasion, conditions or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's or Parkinson's disease. The antibodies are stimulators of angiogenesis and are useful for promoting in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 РНGННРНGРРРНGНИРНGРРНGНPРНGНPРНGРРКНPРНGРРРHGPPPHGPPHGPPHGPPPHGPPP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.2%; Score 280.5; DB 5; Length 148; 51.6%; Pred. No. 2.3e-16; ive 1; Mismatches 24; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 НGНРРНGРРРНGНРРНGНGРСDРРSH 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mazar AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H/P rich domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-MAR-2003; 2003WO-US008060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L5-MAR-2002; 2002US-0364047P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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transfected cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human HPRG protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angiogenesis; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH10411 standard
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                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 148 AA;
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                                                                                                                                                                                                                                                                                                                                                                                   immunoassays
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The invention relates to an isolated tropomyosin (Tpm)-related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of anotherlial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that binds to the isolated polypeptide or peptide is human histidine-proline rich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain of fragment of human or rabbit HPRG, two chain human kininogen (HK), the D5 domain of HK, or a Tpm-binding, the D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antiangiogenic homologue, variant, domain or fragment of the HK or its D5 antiangiogenic homologue, variant, domain or fragment of the high HPRG, two chain migration, invasion, proliferation or angiogenesis, for inducing endothelial cell apoptosis, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uvetifs, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, eg. coronary artery disease or peripheral artery disease. The present sequence represents a human HPRG protein His-Pro (H/P) rich domain.
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                            The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful in reations in olypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AbG00010-AbG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Pred. No. 1.3e-14;
2; Mismatches 35; Indels 41;
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                                                                                                                                                                        Claim 20; SEQ ID NO 40308; 103pp; English
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Best Local Similarity 41.8%;
Matches 56; Conservative
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The invention discloses a composition comprising two or more isolated rat cor human polymucleotides or a polymucleotide which represents a fragment, cor human polymucleotides or a polymucleotide, acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector comprising the nucleic polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence with differentially regulated in an animal subjected to pain and a kit to perform the method for identifying a nucleotide sequence that increases or decreases the expression of the polymucleotide sequence to that increases or decreases the expression of the polymucleotide sequence to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the polympotides the activity of one or more of the polympotides given in the specification, a method for identifying a compound useful in treating spain and a pharmaceutical composition complying the one or more of the polympotides given in the specification, and a pharmaceutical composition computed or more of the polympotides or their antibodies. The polymucleotide or the compound that composition comprising the one or more of pain and a pharmaceutical composition comprising the one or more of therapy). The sequence presented is a rat protein (shown in Table 2 of therapy). The sequence presented is a rat protein (shown in Table 2 of the sequence data for this patent did not form part of the printed construction, but was obtained in electronic form directly from WIPO at the sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for the sequence pain (seq
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                                                                                                                                                                                                                                                                                                                                                       New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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Pred. No. 2.3e-14;
1; Mismatches 27;
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(GEHO ) GEN HOSPITAL
(FARB ) BAYER AG.
                                                                                                                                  C, D'urso D,
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The invention discloses a composition comprising two or more isolated rat cor human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for identifying a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more compound that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound that composition comprising the one or more confining pain and a pharmaceutical composition comprising medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic pain (e.g. spinal segmental nerve injury (Chung), chronic pain pain (e.g. spinal segmental nerve injury (Chung), chronic pain (e.g. spinal segmental nerve injury (Chung), chronic pain (e.g. spinal seguence data for this patent did not form directly from MIPO at the sequence data for this patent did not form directly from MIPO at from inthum the sequence data for the sequence form directly 
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26-NOV-2001; 2001US-0333347P.
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                                                                      Rattus norvegicus
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(FARB )
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, amethod for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a compound that regulates the activity of one or more of the polynucleotides, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound use the compound that regulates the activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament (e.g. spinal segmental nerve injury (CMI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification) which is differentially expressed during pain.

The sequence data for this patent did not form date of the printed polyment of the speciment of the sequence data for this patent did not form part of the printed polyment of the sequence data for this patent did not form date of the speciment of the sequence of the sequence data for this patent did not form data for this patent did not form data for this 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                              Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
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Pred. No. 2.9e-13;
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                                                                                                                                                   Rat Protein AAA42064, SEQ ID NO 12934
ADD47240 standard; protein; 274 AA
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                                                                                                                         Unidentified.
                                                                                    02-DEC-2004
29-JAN-2004
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                                           ADD47240;
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more
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                                                           PPPGGPQQRPQGPPPPGGPQQGPQGPQGPQGPPPPGGPQQSPPQGPPPGGPQ 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                              l tissue; gene therapy; spinal segmental nerve injury; on injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                  54 --PHGPPPHG----HPPHGPPPHGHP---PHGPPPHGHPPHGHGFHDHGP-----CDP
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   34;
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  Mismatches
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(first entry)
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GENBANK; AAA42064.
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Unidentified.
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polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (described in Table 3 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 QGPQGPPPGGPQQSPPQGPPPGGPQGPPPPGGPQQGR----QGPPPPGGPQQDP
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Pred. No. 2.9e-13
1; Mismatches 2
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Best Local Similarity 47.1%;
Matches 57; Conservative
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Sequence 62, Appl
Sequence 845, Appl
Sequence 1338, Ap
Sequence 8196, Ap
Sequence 840, Appl
Sequence 890, Appl
Sequence 889, Appl
Sequence 889, Appl
Sequence 889, Appl
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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version 5.1.6
- 2005 Compugen Ltd.
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US-09-919-039-62
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US-09-538-092-845
US-09-949-016-8196
US-09-949-016-8196
US-09-538-092-840
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US-09-538-092-889
US-09-538-092-889
US-09-538-092-889
US-09-547-693-235
US-09-547-693-235
US-09-281-766-19
US-09-281-766-19
US-09-281-766-19
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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RESULT 2
US-09-919-039-62
; Sequence 62, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039

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Sequence 64, Application US/09976594

| Sequence 64, Application US/09976594
| Patent No. 6673549
| GENERAL INFORMATION:
| APPLICANT: Furness, Michael
| APPLICANT: Buchbinder, Jenny
| TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
| FILE REFERENCE: PA-0041 US
| CURRENT APPLICATION NUMBER: US/09/976,594
| CURRENT FILING DATE: 2000-10-12
| PRIOR PILING DATE: 2000-10-12
| PRIOR RILING DATE: 2000-10-12
| NUMBER OF SEQ ID NOS: 1143
| SOFTWARE: PERL Program
| SEQ ID NO 64
| LENGTH: 525
| TYPE: PRT
| ORGANISM: Homo sapiens
| FEATURE:
| NAME/KEY: misc feature
| OTHER INFORMATION: Incyte ID NO. 6673549 085596CD1
| US-09-976-594-64
          Sequence 42632, A Sequence 4, Appli Sequence 2, Appli Sequence 13, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli
 Sequence
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        US-09-270-767-43608
US-09-270-767-43608
US-09-270-767-43608
US-08-217-327-4
US-09-507-3238-13
US-09-507-3238-13
US-08-487-359-3
US-08-487-359-5
US-08-642-255-49
US-08-642-255-49
US-08-642-255-53
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US-08-487-359-8
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RESULT 1
US-09-976-594-64
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                                                                                                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 845, Application US/09538092
; Sequence 845, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- РИСРРИСИРР-----НСРРИСИРРИСР
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                                                                                                                                                                                                                                                                                                    45.1%; Score 314; DB 4; Length 525; 41.8%; Pred. No. 4.6e-21; vative 2; Mismatches 23; Indels

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                                                                                                                                                                                                                                        Incyte ID No. 6727066 085596CD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 РРНGНРРНGРРНGНРРНGНGFHDHGPCDPPSH 100
                                ,222,113
CURRENT FILING DATE: 2002-09-09;
PRIOR APPLICATION NUMBER: 60/222,1:
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 62
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: PolyE
                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incy
US-09-919-039-62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Homo sapiens
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Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      7 RPP--PHG-
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LENGTH: 331
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RESULT 4 US-09-538-092-1338

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Sequence 8196, Application US/09949016

Facerat No. 6812339

Facerat INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

FRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FEATURE FEATURE FILING WINDOWS VETSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346 PPPMGMPPRGPPFGSPMGHP--GPMPPHGMRGPPPLMPPHGYTGPPRPPPYG---YQRGP 400
Sequence 1338, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: 60/127,352

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (0) ... (0)
COTHER INFORMATION: Polypeptide Accession Number Q15427
US-09-538-092-1338
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Pred. No. 6.4e-14;
3; Mismatches 25;
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Pred. No. 8.4e-14;
6; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 PPHGH-HPHG-PP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.5%;
Best Local Similarity 46.0%;
Matches 57; Conservative
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Best Local Similarity 38.6%;
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 424
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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US-09-538-092-840
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                                                                                                                                    226 SOGPPRRPGKPEGSPSQGGNKPQGPPPHPGKPQGPPPQEGNKPQRPPPGRPPGRPPGG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Salivary Proteins And Fragments
Thereof Having Alpha-Glucosidase Inhibitory Activity
166 PPPHPGKPEGPPPQGGNQSQGPPPRPGKPEGPPPQGGNQSQGPPPRPGKPEGPPQGGNQ 225
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Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----
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CITY: M11.

STATE: WI
COUNTRY: USA

ZIP: 53202-4108

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/925,237
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Barta, Kent S.
REGISTRATION NUMBER: 96429/9002
FELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 257-3501
TELEPHONE: (608) 257-3501
TELEPHONE: AGINER: AGI
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ches 35;
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Pred. No. 4.8e-
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Azen, Edwin A.
APPLICANT: Azen, David
TITLE OF INVENTION: Human Salivary Protoner of INVENTION: Thereof Having All NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kent Barta
STREET: 100 East Wisconsin Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08925237 Patent No. 5981720 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.9%;
Best Local Similarity 44.9%;
Matches 48; Conservative
                                                                                                                                                                                                                                                       : | ||: |
286 NPQQPLPPPAGK 297
                                                                                                                                                                                                           90 HDHGPCDPPSHK 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 251;
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; Sequence 890, Application US/09538092
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfeld, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Usi;
; TITLE OF INVENTION NUMBER: US/09/538,092
; CURRENT APPLICATION NUMBER: 60/127,352
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; RIOR APPLICATION NUMBER: 60/178,965
; RIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 GPPPH-GHPPHGPPPHGHPPHGPPPHGH-----РРИСИСЕНDHGPCDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 247;
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Pred. No. 1.2e-13;
4; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P02812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 32.9%; Score 229.5; DB 4 Local Similarity 43.6%; Pred. No. 9.1e-14; les 48; Conservative 3; Mismatches 34
CURRENT APPLICATION NUMBER: C., C., C., C., CURRENT APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 840
LENGTH: 251
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Best Local Similarity 36.4%;
Matches 52; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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ORGANISM: Artificial/Unknown
                       Query Match
Best Local Similarity
Matches 47; Conserv
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ORGANISM: Human
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US-09-547-693-235
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Sequence 888, Application US/09538092

Patent No. 6753314

GENERAL INFORMATION:

APPLICANT: Giot, Loic

APPLICANT: Mansfield, Traci A.

TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

FILE REFERENCE: 15966-542

CURRENT APPLICATION NUMBER: US/09/538,092

CURRENT APPLICATION NUMBER: 06/127,352

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOFTWARE: CuraPatSeqFormatter Version 0.9

SEQ ID NO 888

LENGTH: 234
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                                                                                                                                                                                                                 and Method
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                                                                                                                                                         JUNEARL INFORMATION.

APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatSeqFormatter Version 0.9
SEQ ID NO 889
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 32.1%; Score 224; DB 4; Best Local Similarity 37.6%; Pred. No. 3.1e-13; Matches 50; Conservative 3; Mismatches 36.
   201 GKPQGPPPAGGNPQQPQDPPAGK 223
                                                                                                      Sequence 889, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polyp
US-09-538-092-888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (0)...(0) OTHER INFORMATION: Poly
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US-09-538-092-888
                                                                RESULT 9
US-09-538-092-889
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9409

LENGTH: 258
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Sequence 235. Application US/09547693
Batent No. 6639050
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kieliszewski, Marcia
TITLE OF INVENTION:
Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
TITLE OF INVENTION:
Glycoproteins
FILE REFERENCE: OHU-04089
CURRENT FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 236
SOFTWARE: Patentin version 3.0
SEQ ID NO 235
LENGTH: 104
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 PERPPPQGGNQSQGPPPHPGKPEGPPPQEGNKSRSARSPPGKPQGPPQQEGNKPQGPPPP 211
                                                                                                                                                                           74
                                                                                                                                                                        15 RPPPPGKPQGPPPQGGNQSQGPPPHPGKPERPPPQGGNQSQGPPPHPGKPERPPPQGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 QSQGPPPTPGKPEGPPPQGGNQSQGPPPHPGKPERPPPQGGNQSHRPPPPP 125
    Length 234;
                                                                                                                                                                                                                                      53 РРИСРРИСИРРИСРРИ-СИРРИСРРИ----СИРРИСИСЕНОНОРСОРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 258;
                                                                                                                    7 крррнднирндрри-синрндрррндирридррк--иррндрри-
                                                           Indels
    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 220; DB 4;
Pred. No. 6.7e-13;
4; Mismatches 40
31.8%; Score 221.5; DB 4.1 A 2.3%; Pred. No. 4.5e-13; Conservative 5; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 КРРРИСНИРИСРРРИСНИРИСРРИС---
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 31.6%;
Best Local Similarity 35.7%;
Matches 51; Conservative 4
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Sequence 19, Application US/09612858

Sequence 19, Application US/09612858

GENERAL INFORMATION:

APPLICANT: Conrad, Patricia C.

APPLICANT: Louie, Kitland

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Recombinant Neospora Antigens and Their Uses

FILE REFERENCE: 023070-082510US

CURRENT APPLICATION NUMBER: US/09/281,766

PRIOR PILING DATE: 1999-03-30

PRIOR FILING DATE: 1996-05-10

PRIOR FILING DATE: 1996-05-10

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 19
                                                                                                                                        9
                                                                                                  Length 104;
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es 41;
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US-09-281-766-19
is Sequence 19, Application US/09281766
js Patent No. 6376196
js GENERAL INFORMATION:
is APPLICANT: Conrad, Patricia C.
js APPLICANT: Louie, Kitland
js TITLE OF INVENTION: Recombinant Neospora Ant FILE REFERENCE: 023070-082510US
js CURRENT APPLICATION NUMBER: US/09/281,766
js CURRENT FILING DATE: 1999-03-30
js PRIOR APPLICATION NUMBER: US 08/645,951
js PRIOR APPLICATION NUMBER: US 08/645,951
js PRIOR PILING DATE: 1996-05-10
js NUMBER OF SEQ ID NOS: 23
js SOFTWARE: Patentin Ver. 2.1
js SEQ ID NO 19
js LENGTH: 865
js TYPE: PRT
js ORGANISM: Neospora 8p.
js OTHER INFORMATION: NC-p65 CDNA
US-09-281-766-19
                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                  Score 215.5;
Pred. No. 7.4
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Pred. No. 2
                                                                                                30.9%;
larity 45.1%;
Conservative
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Synthetic
US-09-547-693-235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 29.8%;
Best Local Similarity 37.9%;
Matches 39; Conservative
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Best Local Similarity
Matches 41; Conser
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US-09-612-858-19
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559 PPPEASPPESSPPDROHPHPPRPNPPEASPPEPSPPNWQHPHPPPRPNPPEASPPEP 618
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US-09-957-995A-19
; Sequence 19, Application US/09957995A
; Patent No. 6777192
; GENERAL INFORMATION:
; APPLICANT: Conrad, Patricia A.
; Barr, Bradd C.
; Anderson, Mark L.
; Sverlow, Karen W.
; TITLE OF INVENTION: Recombinant Neospora Antigens and Their
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                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                   SPPNWQHPHPPRPNPPGASPPESSPNWQHPHPPPRPNPP 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/957,995A
FILING DATE: 15-Apr-2002
CLASSIFICATION: <UNKNOWn>
                                                                                                    Length
                                                                                                                                                                                                                                                                                                  57 РРРИСИРРИСРРИСИРРИСРРИСИРРИСИРИСЕНОНСР-СОРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION: CONTRIGUED PRIOR APPLICATION NUMBER: US 08/215,858
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: US 08/327,516
FILING DATE: 20-OCT-1994
APPLICATION NUMBER: US 08/645,951
FILING DATE: 10-MAY-1996
APPLICATION NUMBER: US 09/281,766
FILING DATE: 30-MAR-1999
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-082512US
                                                                                                                                                                                                в рррисинрисрррисинрисррисиррисрррк----
                                                                                                Score 208; DB
Pred. No. 2.4e<sup>-</sup>
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 208;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-957-995A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
ORGANISM: Neospora sp. ; OTHER INFORMATION: NC-p65 cDNA US-09-612-858-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.8%;
                                                                                                Query Match 29.8%;
Best Local Similarity 37.9%;
Matches 39; Conservative
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SEQUENCE CHARACTERISTICS
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2;
                  Best Local Similarity 37.9%; Pred. No. 2.4e-11;
Matches 39; Conservative 5; Mismatches 47; Indels 12; Gaps
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Search completed: June 15, 2005, 13:53:03 Job time : 25.1486 secs

# version 5.1.6 - 2005 Compugen Ltd. GenCore Copyright (c) 1993

protein search, using sw model 1 OM protein June 15 Run on:

, 2005, 13:51:11 ; Search time 84.7751 Seconds (without alignments) 456.700 Million cell updates/sec

US-10-074-225A-6 697 1 SVNIIHRPPPHGHHPHGPPP.......HPPHGHGFHDHGPCDPPSHK 101 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

seqs, 383334425 residues 1710399 Searched:

1710399 Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published\_Applications

Leading Applications AA:\*

| cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO6\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO7\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO8\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO9\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO9\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO9\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Sequence 6, Appli	Sequence 3, Appli	Sequence 62, Appl	Sequence 1, Appli	Sequence 42, Appl	Sequence 320892,	Sequence 5, Appli	Sequence 171176,	Sequence 4, Appli	Sequence 8217, Ap	Sequence 252326,
ΩΙ	14 US-10-074-225A-6	US-10-074-225A-3	US-09-919-039-62	US-10-074-225A-1	US-10-868-577A-42	US-10-425-115-320892	US-10-074-225A-5	US-10-437-963-171176	US-09-850-887-4	US-10-732-923-8217	US-10-425-115-252326
DB	14	14	10	14	17	16	14	16	σ	11	16
% Query e Match Length DB ]	101	526	525	525	525	371	148	235	274	1643	149
& Query Match	100.0	100.0	45.1	45.1	45.1	41.0	40.2	35.7	35.3	34.6	34.0
Score	697	697	314	314	314	285.5	280.5	248.5	246	241.5	237
Result No.	П	7	e	4	ស	9	7	<b>c</b> o	თ	10	11

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-100-424-5999-100-	US-10-425-115-222187 US-10-425-115-276286 US-10-369-493-3240
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233.5 233.5 233.5 233.5 233.5 231.5 222.2 223.5 222.3 223.5 221.5 221.5 212.5 213.5	211 211 211
	4 4 4 5 4 4 5

#### ALIGNMENTS

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Sequence 6, Application US/10074225A

Publication No. US20030082740A1

GENERAL INFORMATION:

APPLICANT: DONATE, Fernando

APPLICANT: PLUNKETT, Marian L

APPLICANT: HARRIS, Scott

APPLICANT: MAZAR, Andrew P

TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC P

TITLE OF INVENTION: ANTI-TUMOR AGENT

FILE REFERENCE: 38342-178463

CURRENT APPLICATION NUMBER: US/10/074,225A

CURRENT APPLICATION NUMBER: US 60/268,370

PRIOR APPLICATION NUMBER: US 60/268,370

PRIOR APPLICATION NUMBER: US 60/268,370

PRIOR APPLICATION NUMBER: US 60/268,370

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1

LENGTH: DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Lepus americanus
US-10-074-225A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Le
US-10-074-225A-6
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ö ö Length 101; Indels Query Match 100.0%; Score 697; DB 14; Best Local Similarity 100.0%; Pred. No. 1.3e-42; Matches 101; Conservative 0; Mismatches 0;

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GHPPHGPPPHGHPPHGPPPHGHPPHGHGFHDHGPCDPPSHK 101 61

4:47 2005

Thu Jun 16 13:0

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PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC #
330 ATFGTNGAQRRSHNNNSSDLAPHKHHSHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 ATFGINGAQRHSHNNNSSDLHPHKHHSHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275 КРРГКРНGSRDHHHPHKP-----НЕНGРРРРDЕRDHSHGPPLPQGPPLLPMSCSSCQH
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FILE REFERENCE: 28967/39359A
CURRENT APPLICATION NUMBER: US/10/868,577A
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US 60/478,390
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
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6.1e-15;
ches 23;
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6.1e-15;
                                                                                                         68 РРИСИРРИСРРИСИРРИСИСЕН ТОО
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DONATE, Fernando
APPLICANT: DONATE, Fernando
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: HAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GL
TITLE OF INVENTION: HISTIDINE RICH GL
FILE REFERENCE: 38342-178463
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2002-02-14
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 525
TYPE: PRI
TYPE: PRI
TYPE: PRI
TYPE: PRI
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                                                                                                                                                              390 HPHGHHPHGHHPHGHHPHCHDFQDYGPCDPPPH
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US-10-868-577A-42
; Sequence 42, Application US/10868577A
; Publication No. US20050032697A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10074225A Publication No. US20030082740A1
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Best Local Similarity 41.8%;
Matches 64; Conservative
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Best Local Similarity
Matches 64; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-074-225A-1
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                                                                                                                                                                                                                                           Sequence 3, Application US/10074225A;
Publication No. US20030082740A1
GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: PLUNKETT, MARIAN L
APPLICANT: PLUNKETT, MARIAN L
TITLE OF INVENTION: ANTI-TUMOR AGENT
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFERENCE: 38342-178463
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 526
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US-09-919-039-62
i Sequence 62, Application US/09919039
j Publication No. US20030108871A1
general information:
i APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION:
FILLE REFERENCE: PA-0033 US
CURRENT FILING DATE: 2002-09-09
FRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2002-09-09
FRIOR PLICATION NUMBER: 60/222,113
FRIOR FILING DATE: 2000-07-28
INUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 62
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
FEITURE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 СИРРИСРРИСИРРИСРРИСИРРИСИРИСКИОНСРОПОРОЗНК 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 697; DB 14;
Pred. No. 4.6e-42;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.1%; Score 314; DB 10; Best Local Similarity 41.8%; Pred. No. 6.1e-15; Matches 64; Conservative 2; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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Best Local Similarity 100.
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 RPP--PHG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Lepus
US-10-074-225A-3
                                                                                                                                                  RESULT 2
US-10-074-225A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321
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SENERAL INFORMATION:

SEQUENCE 171176

SEQUENCE 171176, Application US/10437963

Publication No. US20040123343A1

SEQUENCE 171176, Application US/10437963

SERVERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: W. Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

APPLICANT: Li, Ping

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 171176

LENGTH: 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 РИКНИЅНЕОНРНОННРНА-------НН------РНЕНDТИКОНРНСНИР 42
                                                                                                                                                                                                                                                                                                                                                                                                                                  6 нк-рррнснирнсрриснирнсрру-нснрр--нсррик--ррнсрриснррнсрр
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                      Length 148;
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                                                                                                                                                                                                                                                                                                 Score 280.5; DB 14; Length
Pred. No. 5.5e-13;
1; Mismatches 24; Indels
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US-10-437-963-171176
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OTHER INFORMATION: unsure at all Xaa locations
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US-09-850-887-4
; Sequence 4, Application US/09850887
; Patent No. US20020009778A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Corley, Neil C.
; PRIOR FILING DATE: 2001-02-14; NUMBER OF SEQ ID NOS: 11; SOFTWARE: Patentin version 3.1; SEQ ID NO 5; LENGTH: 148; TYPE: PRT; ORGANISM: Homo sapiens US-10-074-225A-5
                                                                                                                                                                                                                                                                                                 Query Match 40.2%;
Best Local Similarity 51.6%;
Matches 47; Conservative
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ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: unsure
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US-10-074-225A-5
i Sequence 5, Application US/10074225A
j Publication No. US20030082740A1
j GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC
TITLE OF INVENTION: ANTI-TUMOR AGENT
TITLE OF INVENTION UMBER: US/10/074,225A
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/268,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-25-115-320892

i Sequence 320892, Application US/10425115

i Publication No. US20040214272A1

i GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongue

i APPLICANT: Cao, Yongue

APPLICANT: Cao, Yongue

I TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322)B

CURRENT PILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 320892

LENGTH: 371

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

NAME/KEY: unsure

LOCATION: (1) .. (371)

OTHER INFORMATION: Unsure at all Xaa locations

FEATURE:

FEA
                         130 PPQHQHVPPPPPRGYGPPPRGYGPPPPPPPHGHVPPPPPPRH-GHGPPPPGQHVLPPLL 188
                                                                                                                                                                                                                            330 ATFGTNGAQRHSHNNNSSDLHPHKHHSHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGH 389
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                                                                                                                                                                  ----НСРРНСНРРНСР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----НСРРРИСН--НРНСРРРИСНРРИСРРРКНРРИСРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
41.0%; Score 285.5; DB 16; Length Best Local Similarity 47.3%; Pred. No. 4.9e-13; Matches 62; Conservative 3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone ID: MRT4577_55716C.1.pep
                                                                                                                                                                                                                                                                                            РРИСИРРИСРРИСИРРИСИСЕН 100
                                                                                                                                                                                                                                                                                                                                    390 HPHGHHPHGHHPHGHPHCHDFQDXGPCDPPPH 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - БРРНСНИР-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: US-10-425-115-320892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-10-732-923-8217
; Sequence 8217, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: 10/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 8217
; LENGTH: 1643
         TITLE OF INVENTION, THYROID AND PITUITARY MEMBRANE PROTEIN NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                        TYPE: Floppy disk

TYPE: Floppy disk

SR: IBM PC compatible

ING SYSTEM: PC-DOS/MS-DOS

RE: Word Perfect 6.1 for Windows/MS-DOS 6.2

ICATION DATA:

ATION NUMBER: US/09/850,887

DATE: 07-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.3%; Score 246; DB 9; Length 274; Best Local Similarity 47.1%; Pred. No. 2.5e-10; Matches 57; Conservative 1; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                  ATION DATA:
TION NUMBER: 09/087,678
DATE: <Unknown>
NT INFORMATION:
ERRONE, MICHAEL C.
ATION NUMBER: 39,132
CC/DOCKET NUMBER: PF-0535 US
ATION INFORMATION:
NE: (650) 855-0555
: (650) 845-4166
EQ ID NO: 4:
RACTERISTICS:
274 amino acids
mino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPTION: SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
Gorgone, Gina
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106712
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                                                                                                                                  COUNTRY: US
ZIP: 94304
COMPUTER READABI
MEDIUM TYPE
COMPUTER: 1
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SOFTWARE:
CURRENT APPLICA
APPLICATION
FILING DATY
CLASSIFICA
PRIOR APPLICATION
APPLICATION
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;
SEQUENCE DESCR.
US-09-850-887-4
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SEQUENCE CHARA
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NAME: CER
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TELECOMMUNICAT
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GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 252326
LENGTH: 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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; OTHER INFORMATION: Clone ID: MRT4577_161704C.1.pep
US-10-425-115-252326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.0%; Score 237; DB 16; Best Local Similarity 49.0%; Pred. No. 6.7e-10; Matches 47; Conservative 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 РРНGРРРНGНРРНGЧРРНGНРРНGНGРСDРР 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(149)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 252326, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
US-10-424-599-223180
; Sequence 223180, Application US/10424599
; Publication No. US20040031072A1
; ORGANISM: Anopheles gambiae str. PEST
US-10-732-923-8217
                                                                Query Match
Best Local Similarity 39.8
Matches 64; Conservative
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ORGANISM: Zea mays
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NAME/KEY: ungure
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                                                                                                                                                                                                                                                         7 КРРРИСИНРИСРРИСИНРИСРРИСИРРИСРРИСЬРИИ-РРИ-СРРИСИРРИ-СРРРИСИР
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                                                                                                                                                                                          Length 241;
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                                                                                                                                                                                                                         39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39; Indels
                                                                                                                                                                                                                                                                                                                                                     64 РН-СРРРИСИРРИ-СРРРИСИРРИСИСЕН ОВРЅНК 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       РН-СРРРИСИРРН-СРРРИСИРРИСИСРНОНСРС-- ОРРБИК 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    РНЕКРРРЕХОРРНЕКРРРЕХОРРНЕКРРРЕНОРРНЕКРРЕНО 192
                                                                                                                                      Clone ID: PAT_MRT3847_43562C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.5%; Score 233.5; DB 16;
ilarity 48.0%; Pred. No. 2.1e-09;
Conservative 3; Mismatcher 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Franssen, Henk J
APPLICANT: Bisseling, Anton H
TITLE OF INVENTION: ENOD2 Gene Regulatory Region
FILE REFERENCE: MPS 4-87FD2
CURRENT APPLICATION NUMBER: US/10/751,014
CURRENT FILING DATE: 2004-01-02
PRIOR APPLICATION NUMBER: US/09/564,142A
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 309
TYPE: PRT

CORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-10-751-014-5
; Sequence 5, Application US/10751014
; Publication No. US20040172676A1
; GENERAL INFORMATION:
; APPLICANT: Franssen, Henk J
; TITLE OF INVENTION: ENOD2 Gene Regulatory Region
; FILE REFERENCE: MPS 4-87FD2
; CURRENT APPLICATION NUMBER: US/10/751,014
; CURRENT FILING DATE: 2004-01-02
; PRIOR APPLICATION NUMBER: US/09/564,142A
; PRIOR FILING DATE: 2000-05-03
                                                                                                                                                                                          DB 15;
                                                                                                                                                                                        Score 233.5; DB 1. Pred. No. 1.7e-09; 3; Mismatches 39
 NUMBER: US/10/424,599
: 2003-04-28
5: 285684
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-10-751-014-2
; Sequence 2, Application US/10751014
; Publication No. US20040172676A1
; GENERAL INFORMATION:
                                                                                                                                                                                        33.5%;
48.0%;
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                                                                                                         max
CURRENT APPLICATION NI
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 223180
LENGTH: 241
                                                                                TYPE: PRT
CRGANISM: Glycine ma
FEATURE:
CTHER INFORMATION: C
US-10-424-599-223180
                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 49; Conser
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49; Conser
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95 KPPPEYQPP
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Other Molecules Associated With
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 HLHPHPHPHPPPPKKPYYYHSPPPVHPHPYPH-PHPHPHPHPHPHPHPHVHS 291
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                                                                                                                                                                                                                                                                     Gaps
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i Sequence 281824, Application US/10424599

i Sequence 281824, Application US/10424599

j Publication No. US20040031072A1

j GENERAL INFORMATION:

j APPLICANT: La Rosa Thomas J

j APPLICANT: Cao Yongwei

j TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

j TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

j FILE REFERENCE: 38-21(5323) B

j CURRENT APPLICATION NUMBER: US/10/424,599

j CURRENT FILING DATE: 2003-04-28

j NUMBER OF SEQ ID NOS: 285684

j SEQ ID NO 281824

j LENGTH: 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                 11;
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es 39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                         151 РИЕКРРЕХОРИЕКРРЕХОРЕКЕКРРЕНОРРНЕКРРЕНО 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT

ORGANISM: Glycine max

FEATURE:

LOCATION: (1)..(342)

OTHER INFORMATION: unsure at all Xaa locations

FEATURE:

FEATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_96507C.1.pep
US-10-424-599-281824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 15;
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Pred. No. 2.6e-09;
1; Mismatches 25
                                                                                                                                                                                                                       Score 233.5; I
Pred. No. 2.1e-
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 15, 2005, 14:09:36
Job time : 85.7751 secs
PRIOR APPLICATION NUMBER: 08/859,555 PRIOR FILING DATE: 1997-05-20 NUMBER OF SEQ ID NOS: 6 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.4%;
                                                                                                                                                                                                                     Query Match 33.5%;
Best Local Similarity 48.0%;
Matches 49; Conservative
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                                                                                                                            ; TYPE: PRT
; ORGANISM: Glycine max
US-10-751-014-5
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Best Local Similarity
Matches 61; Conservat
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                                                                                 SEQ ID NO 5
LENGTH: 309
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#### 5.1.6 Compugen Ltd. version - 2005 GenCore (c) 1993 Copyright

sw model - protein search, using OM protein

June 15, 2005, 13:37:20 ; Search time 19.4699 Seconds (without alignments) 499.124 Million cell updates/sec Run on:

US-10-074-225A-6 697 1 SVNIIHRPPPHGHHPHGPPP........HPPHGHGFHDHGPCDPPSHK 101 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext Scoring table:

283416 seqs, 96216763 residues 0.5 Searched:

Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

number of results predicted by chance to have a in or equal to the score of the result being printed, analysis of the total score distribution. Pred. No. is the numbe score greater than or and is derived by anal

#### SUMMARIES

		do				
Result		Query				
No.	Score	Match	Length	DB	QI	Description
	31	S	l	-		histidi
α	260.5	37.4	445	~	A60488	histidine-rich gly
m		37.2	295	~	B48013	proline-rich prote
4	in	35.9	128	N	D38355	basic proline-rich
ß	<b>T</b>	35.6	278	7	B39066	proline-rich prote
9		35.5	206	Н	PIRT3	acidic proline-ric
7	246.5	35.4	227	~	C29149	proline-rich prote
80		35.4	240	N	A24264	
თ	•	35.4	317	N	A28996	proline-rich prote
10	m	34.3	240	~	B24264	
11	E	33.9	330	~	S22140	nodulin Enod2 - Se
12		33.8	392	Н	PIHUB6	salivary proline-r
13	235.5	33.8	432	N	T06782	extensin - soybean
14		33.8	580	N	T10863	extensin precursor
15		33.6	173	N	T51469	glycine/proline-ri
16	233.5	33.2	309	7	S08343	nodulin precursor
17		33.2	424	~	A54964	spliceosome-associ
18		33.4	1571	~	T14155	zinc finger protei
19		32.9	251	Н	PIHUPF	salivary proline-r
20	228.5	32.8	188	N	D29149	proline-rich prote
21	225.5	32.4	212	7	B36298	proline-rich prote
22	224	32.1	310	Н	PIHUSD	salivary proline-r
23	•	31.9	220	N	A36298	proline-rich prote
24	221	ä	309	~	S10889	proline-rich prote
25	2	ä	1378	N	T30173	zinc finger protei
26		ö	117	7	D40750	proline-rich prote
27	213.5	30.6	301	~	E29149	proline-rich prote
28		ö	434	~	119	nodule-specific hy
29	210	30.1	297	0	S23737	proline-rich prote

rhodopsin - Allote hydroxyproline-ric	nodulin - alfalfa	proline-rich prote	hypothetical prote	nodulation protein	hypothetical prote	proline-rich prote	basic proline-rich	rhodopsin - northe	proline-rich prote	hypothetical prote	proline-rich prote	proline-rich prote	hypothetical prote	carboxypeptidase C
S60755 S06733	S04554	A42817	C84534	S10101	T28770	A48013	JH0481	S14332	B29149	T49482	A30496	\$22373	T32402	T43236
ч 2	7	~	~	~	~	7	N	Н	~	~	N	~	~	7
440 620	97	223	727	112	539	170	188	452	172	1176	164	260	592	1002
30.1	30.0	29.8	29.7	29.6	29.3	29.1	29.0	28.8	28.6	28.5	28.4	28.3	28.3	28.3
	60	808	207	6.5	4.5	2.5	202	201	39.5	98.5	198	7.5	7.5	7.5
210	ñ	•	•	20	20	7			ä	ä		13	13	13

#### ALIGNMENTS

	ıman			-Dec-1	
	istidine-rich glycoprotein precursor - human	1;Alternate names: HRG	;;Species: Homo sapiens (man)	g	
GHUGH	istidine	, Alterna	;Species	;Date: 0	

RESULT I
MUNICAL
MIGHINA
MISTIGNAN—TICH Glycoprotein precursor - human
Nistigna—rich glycoprotein precursor - human
Nistigna—rich glycoprotein precursor - human
Cipbete: 04-Dec=1986
Requence\_revision 04-Dec-1986 #text\_change 09-Jul-2004
Cipbete: 04-Dec=1986
Requence\_revision 04-Dec-1986 #text\_change 09-Jul-2004
Cipbete: 04-Dec=1986
Requence\_revision 04-Dec-1986 #text\_change 09-Jul-2004
Richies The Forest. D. 12-20-2225, Jag66
AirLies Amino acid sequence\_of human histidine-rich glycoprotein derived from the nuclec
AirReference number: A01287; MUID: 86216149; PMID: 301081
AirCession and A01287
AirCession and A01287
AirCession and Air Reference of human histidine-rich glycopi
AirCession and Air Reference are Reference of AirCession of AirCession and AirCession are AirCession and AirCession and AirCession are AirCession and AirCession are AirCession and AirCession and

Gaps 64; Query Match 45.1%; Score 314; DB 1; Length 525; Best Local Similarity 41.8%; Pred. No. 1.7e-16; Matches 64; Conservative 2; Mismatches 23; Indels

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40 7 RPP--РИG----НИРИGРРРНGНИРИGРРР-----ИGИР-РИGРРР---

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200

4:47

13:0

16

Thu Jun

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RESULT 5
B39066
proline-rich protein 15 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 09-Jul-2004
C;Accession: B39066
R;Lin, H.H.; Ann, D.K.
Genomics 10, 102-113, 1991
A;Title: Molecular characterization of rat multigene family encoding proline-rich protein A;Reference number: A39066; MUID:91257817; PMID:2045095
A;Accession: B39066
A;Accession: B39066
A;Accession: Laye: DNA
A;Molecule type: DNA
A;Residues: 1-278 <LIN>
R;Castle, A.M.; Castle, J.D.
J. Biol. Chem. 268, 20490-20496, 1993
A;Title: Novel secretory proline-rich proteoglycans from rat parotid. Cloning and charact A;Reference number: A48013; MUID:93388626; PMID:8376404
A;Reference number: A48013; MUID:93388626; PMID:8376404
A;Reference number: A48013
A;Reference number: A48013
A;Residues: Dreliminary
A;Molecule type: mRNA
A;Residues: 1-295 < CAS>
A;Residues: 1-295 < CAS>
A;Residues: 1-295 < CAS>
A;Cross-references: UNIPROT:Q07611; GB:L17318; NID:g310199; PIDN:AAA03074.1; PID:g310200
C;Superfamily: proline-rich protein
C;Keywords: extracellular protein; glycoprotein; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
D38355
basic proline-rich peptide IB-8a - human (fragments)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 09-Jul-2004
C;Accession: D38355
R;Kauffman, D.L.; Bennick, A.; Blum, M.; Keller, P.J.
Biochemistry 30, 3351-3356, 1991
A;Title: Basic proline-rich proteins from human parotid saliva: relationships on A;Reference number: A38355; MUID:91190884; PMID:1849422
A;Accession: D38355
A;Accession: D38355
A;Accession: D38355
A;Katus: proliminary
A;Molecule type: protein
A;Residues: 1-128 <KAU>
C;Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141 PPQPGSPQGPPPPGGPQQRPPQGPPPQGPPQGPQSPQPPPPPPPPPGGPQRAPQGPPPQG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 VNRPERPPOHGGNHHHPHHPPPAAGPORPPOPGSPQGPPPPGGPQORPPQGPPQGGPQR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 saliva: relationships
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --- PHGPPPHGHP---- PHGPPPHG
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                                                                                                                                                                                                                                                                                                                                                                           Length 295;
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                                                                                                                                                                                                                                                                                                                                                                           Score 259.5; DB 2; Length
Pred. No. 1e-12;
1; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201 СРОКРРОРСЯРОСРРРССРООКРРОСРРРОС----СРОКРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- РРНGHРРHGHGFHDHGPCDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 35.9%; Score 250; DB 2; L Best Local Similarity 45.0%; Pred. No. 2.5e-12; Matches 50; Conservative 5; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNI IHRPPPHG---HHPH---
                                                                                                                                                                                                                                                                                                                                                                           37.2%;
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 38.4
Matches 63; Conservative
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A60488

A6048
       330 ATFGTNGAQRHSHNNNSSDLHPHKHHSHEQHPHGHPHAHHPHEHDTHRQHPHGHPHGH 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40
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proline-rich proteoglycan 2 precursor, parotid - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 HEHSPAGRPPFKPSGSKOHG-HPHESYNFRCPPPLEHKNHSDSPPFQARAPLPFPPPGLR
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                                                                                                   --- РНСРРРНСНРР-----НСРРРНСНРРНСР
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                                                                                                                                                                                                                             68 РРНСИРРНСРРИСИРРНСИРРНСТИВНСТОРРЅИ 100
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 53; Conser
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PPPHR 352
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A;Accession: A28996
A;Molecule type: DNA
A;Residues: 1-317 <ANN>
A;Cross-references: UNIPROT:Q62103; GB:M23236; GB:J03891; NID:g200535; PIDN:AAA53048.1; E
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse multige
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 03-May-1996
C;Accession: A24264
R;Ann, D.K.; Carlson, D.M.
J. Biol. Chem. 260, 15863-15872, 1985
A;Title: The structure and organization of a proline-rich protein gene of a A;Reference number: A92508; MUID:86059475; PMID:2999141
A;Accession: A24264
A;Molecule type: DNA
A;Residues: 1-240 <ANN>
C;Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proline-rich protein M14 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28996
R;Ann, D.K.; Smith, K.; Carlson, D.M.
J. Biol. Chem. 263, 10887-10893, 1988
A;Title: Molecular evolution of the mouse proline-rich protein multigene fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- ВНДС---- ВНДСБРИСЬ---- ВНДСБРИСЬ---- НЕВНСВРИСЬ---- ВНДСТВИСЬ---- ВНДСТВИСЬ---- ВНДСТВИСЬ---- ВНДСТВИСЬ---
                                                                                                                                                                                                                          33 RPPPSGFQFRPPVNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPPPPQ
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                                                                                                                                                                                                                                                                                                  ---ВНДС----НРРИСР----НРРИСР----НРРИСР----НРРИСР-----
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                                                                                   Gaps
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                                                                                   41;
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C; Superfamily: proline-rich protein
C; Keywords: saliva
C; Keywords: saliva
F;1-15/Domain: signal sequence #status predicted <SIG>
F;1-15/Product: proline-rich protein M14 #status predicted <MAT>
           Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 240;
                                                                                                                                                     -----HGABHG----HHBHGBBHC----HGAGBH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length
                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 35.4%; Score 246.5; DB 2; 1 Similarity 43.6%; Pred. No. 7.6e-12; 58; Conservative 0; Mismatches 34;
     35.4%; Score 246.5; DB 2;
.larity 43.6%; Pred. No. 7.2e-12;
Conservative 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.4%; Score 246.5; DB 2; llarity 43.6%; Pred. No. 9.6e-12; Conservative 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 PAGPQPRPPQGPP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGPQPRPPQGPP 144
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  Query Match
Best Local Similarity
Matches 58; Conser
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                     RPPPHGHHP
                                                                                                                                                                                                                                                                                                     46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROT:P04474; GB:K02247; NID:g206395; PIDN:AAA1949.1; PID:g206396

contains six 18- to 19-residue repeats.

may protect teeth by binding to tannins.

rich protein

parotid gland; saliva; tandem repeat
equence #status predicted <SIG>
c proline-rich protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT: Q62107; GB: M11902; NID: 9200544; PIDN: AAA40003.1; PID: 9200545 Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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PIRT3
acidic proline-rich protein precursor - rat
Nalternate names: PRP
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C; Accession: A03296
R; Ziemer, M.A.; Swain, W.F.; Rutter, W.J.; Clements, S.; Ann, D.K.; Carlson, D.N.
J. Biol. Chem. 259, 10475-10480, 1984
A; Title: Nucleotide sequence analysis of a proline-rich protein cDNA and peptide
A; Reference number: A03296; MUID:84289443; PMID:6547951
A; Reference rumber: A03296
A; Accession: A03296
A; Rose-references: UNIPROT:P04474; GB:K02247; NID:g206395; PIDN:AAA1949.1; PIIC
C; Comment: This protein contains six 18- to 19-residue repeats.
C; Comment: This protein may protect teeth by binding to tannins.
C; Comment: This protein may protect
C; Comment: This protein may protect
C; Comment: This protein may protect
C; Comment: Signal sequence #status predicted <SIG>
F; 1-13/Domain: signal sequence #status predicted <AT>
F; 1-206/Product: acidic proline-rich protein #status predicted <AT>
F; 80-189/Region: 18-residue repeats
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                                                                                                                                                                                                                                                                                                                            112 GPQQRPQGPPPPGGPQQGPQGPPPPGGPQQFQGPPPPGGPQQSPPQGPPGGPPGGPQQGPQ 171
                                                                                                                                                                                                                                                                                                                                                                                                       52 HP---PHGPPPHGHP---PHGPPPHGHP---PHGPPPHG----HGFHDHGPC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 КРРРИСИНРИСРРИСИНРИСРРРИСИР------РИСРРРИСИРРИСРРИСИРРИСРР 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W.J.; Clements, S.; Ann, D.K.; Carlson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cispecies: Mus musculus (fragment)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 09-Jul-2004
CiAccession: C29149
Riclements, S.; Mehansho, H.; Carlson, D.M.
J. Biol. Chem. 260, 13471-13477, 1985
A; Title: Novel multigene families encoding highly repetitive peptide sequench; Riclements: Clone pUMP40
A; Reference number: A92501; MUID:86033799; PMID:3840480
A; Contents: Clone pUMP40
A; Accession: C29149
A; Molecule type: mRNA
A; Residues: 1-227 < CLE>
A; Residues: 1-227 < CLE>
A; Cross-references: UNIPROT:Q62107; GB:M11902; NID:g200544; PIDN:AAA40003.1, C; Superfamily: proline-rich protein
                                                                                                                                                                                                                                                       8 рего----нирисрерис----нирисрерис-----киррисрерис
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                                                                                                                                                                                           Gaps
                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206;
                                                                                                             Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 247.5; DB 1; Length
Pred. No. 5.6e-12;
4; Mismatches 30; Indels
                                                                                                                                                                                     32; Indels
                                                                                                             Score 248; DB 2;
Pred. No. 6.7e-12;
1; Mismatches 32
A;Cross-references: UNIPROT:Q04154; GB:M36414 C;Superfamily: proline-rich protein
                                                                                                             35.6%;
llarity 47.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.5%;
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                                                                                                    Query Match
Best Local Similarity
Matches 58; Conser
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53; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DPP
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Best Local 9
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C29149
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GB:S6

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A,Accession: B40750
A,Molecule type: DNA
A,Residues: 35-392 AAZE
A,Cross-references: UNIPROT:P04280; UNIPROT:P04281; UNIPROT:P02811; UNIPROT:Q16038; GB:S6
A,Cross-references: UNIPROT:P04280; UNIPROT:P04281; UNIPROT:P02811; UNIPROT:Q16038; GB:S6
A,Experimental source: subject C.J. (large allele)
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 35-127, 'R',129-148,'R',150-151,153-187,'K',189-272,'S',274-336,'S',338-392 

A,Cross-references: GB:S62929
A,Experimental source: subject M.V.O. (large allele)
A,Accession: A40750
A,Accession: A40750
A,Molecule type: DNA
A,Residues: 35-183,245-270,'Q',272-392 <AZ3>
A,Cross-references: GB:S62928
A,Experimental source: subject C.J. (medium allele)
A,Experimental source: subject C.J. (mediu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-183,245-392 < MAE>
A; Cross-references: GB: K03204; NID: g190485; PIDN: AAA60185.1; PID: g190486
A; Cross-references: GB: K03204; NID: g190485; PIDN: AAA60185.1; PID: g190486
A; Note: alternatively splice forms lacking portions of the repeat region were also found R; Carties: Length polymorphisms in human proline-rich protein genes generated by intragenic A; Reference number: S02127; MUID: 89121440; PMID: 2851479
A; Reference number: S02127
A; Residues: 35-127, 250-273, R', 275-277, R', 279-336, S', 338-392 < LYO>
A; Residues: 35-127, 250-273, R', 275-277, R', 279-336, S', 338-392 < LYO>
A; Residues: S02127
A; Recession: S02127
                                                                                                                           salivary proline-rich phosphoprotein precursor PRB1 (large allele) [validated] - human N; Contains: peptide IB-1; peptide P-E (peptide IB-9); peptide P-F; peptide P-H C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 04-Dec-1986 #sequence revision 12-Apr-1996 #text change 09-Jul-2004
C; Accession: B40750; C40750; A40750; C25372; S02128; S02127; A03293; A90502; A91974; A055 R; Azen, E.A.; Latreille, P.; Niece, R.L.
Am. J. Hum. Genet. 53, 264-278, 1993
A; Title: PRBI gene variants coding for length and null polymorphisms among human salivary
A; Reference number: A40750; MUID: 93304421; PMID: 8317492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cleavages in the human salivary
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A;Molecule type: protein
A;Residues: 'S',338-392 <SAI>
R;Azen, E.; Lyons, K.M.; McGonigal, T.; Barrett, N.L.; Clements, L.S.; Maeda, N.; Vanin,
Proc. Natl. Acad. Sci. U.S.A. 81, 5561-5565, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             saliva
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A; Residues: 17-38,'AP',41-51,92-148,'R',150-152 < KA2>
A; Note: among nine basic proline-rich peptides isolated from the saliva, this peptihological system of protein
A; Rocession: A90502
A; Molecule type: protein
A; Residues: 275-336,'S',338-392 < KAU>
R; Saitch, E.; Isemura, S.; Sanada, K.
J. Biochem. 94, 1991-1999, 1983
A; Title: Further fractionation of basic proline-rich peptides from human parotid
A; Reference number: A91974; MUID: 84161824; PMID: 6671974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 35-183,245-392 <LY2>
A; Residues: 35-183,245-392 <LY2>
A; Cross-references: EMBL:X07516
R; Kauffman, D.; Hofmann, T.; Bennick, A.; Keller, P.
Biochemistry 25, 2387-2392, 1986
A; Title: Basic proline-rich proteins from human parotid
A; Reference number: A90502; MUID:86243355; PMID:3521730
A; Accession: A03293
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S22140
nodulin Enod2 - Sesbania rostrata
C; Species: Sesbania rostrata
C; Species: Sesbania rostrata
C; Species: Sesbania rostrata
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C; Accession: S22140
R; de Bruijn, F.J.
submitted to the EMBL Data Library, November 1991
A; Reference number: S22140
A; Reference number: S22140
A; Accession: S22140
A; Accession: S22140
A; Accession: Janary
A; Molecule type: DNA
A; Residues: 1-330 < DEB>
A; Residues: 1-330 < DEB>
A; Cross-references: UNIPROT: Q41402; EMBL: X63339; NID: g21372; PIDN: CAA44939.1; PID: g21373
C; Superfamily: proline-rich protein 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse multig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
B24264
proline-rich protein MP3 - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 09-Sep-1987 #sequence_revision 09-Sep-1987 #text_change 03-May-1996
C; Accession: B24264
R; Ann, D.K.; Carlson, D.M.
J. Biol. Chem. 260, 15863-15872, 1985
A; Title: The structure and organization of a proline-rich protein gene of a mouse, A; Reference number: A92508; MUID:86059475; PMID:2999141
A; Residues: 1-240 < ANN>
C; Superfamily: proline-rich protein
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                                                                                   33 ŘPPSGSQPRPPVNGSQQGPPPPGGPQPRPPQGPPPPGGPQPRPPQGPPPPGGPQPRPPQ
                                                                                                                                                                                         ---БНДЧС----НРРИСРРИС----ПРРИСРЕНС----НРРИС----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----HGPPPHG----HPPHGPPPHG-----RPPHGPPP----RHPPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 кРРНЕКРРНЕКРРУДКРРУЕКРРНЕКРРНЕКРРНЕКРРЕУКРРНЕК 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.9%; Score 236; DB 2; Length 330; Best Local Similarity 41.1%; Pred. No. 5.8e-11; Matches 44; Conservative 10; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 34.3%; Score 239; DB 2; Best Local Similarity 42.6%; Pred. No. 2.7e-11; Matches 58; Conservative 0; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 PAGPHLRPTQGP--PP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 ----НGFHDHGPCDPP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 PGGPQPRPPQGPP 165
                                                                                                                                                                                                                                                                                                                                                                          87 -HGFHDHGPCDPP 98
   RPPPHGHHP
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                                                                                                                                                                                     GPPPHG--
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Best Local S
Matches 58
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A,Reference number: A05401
A,Redestence number: A05401
A,Recasidous: A05401
A,Recasidous: A05401
A,Recasidous: A05401
A,Recasidous: A05402
A,Accessidous: A05402
A,Accessidous: A05402
A,Accessidous: A05402
A,Accessidous: A05402
A,Accessidous: A05402
A,Residues: AN,-57-59
A,Residues: AN,-57-59
A,Tille: Basid prolline-rich proteins from human parctid saliva: complete covalent struct A,Reference number: A0444; MUD: 83101329; PMID: 6924859
A,Tille: Basid prolline-rich proteins from human parctid saliva: complete covalent struct A,Reference number: A90444; MUD: 83101329; PMID: 6924859
A,Tille: Basid prolline-rich proteins from human parctid saliva: complete covalent struct A,Reference number: A90444; MUD: 83101329; PMID: 6924859
A,Tille: Basid prolline-rich proteins
A,Residues: 32-2127, R.129-148, R., 150-152 cKA3>
A,Rocessidous: A91566
A,Rocessidous: 
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T06782
extensin - soybean
N;Alternate names: hydroxyproline-rich glycoprotein
C;Species: Glycine max (soybean)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06782
R;Ahn, J.H.; Choi, Y.; Kwon, Y.M.; Kim, S.G.; Choi, Y.D.; Lee, J.S.
R;Ahn, J.H.; Choi, Y.; Kwon, Y.M.; Kim, S.G.; Choi, Y.D.; Lee, J.S.
Plant Cell 8, 1477-1499, 1996
A;Title: A novel extensin gene encoding a hydroxyproline-rich glycoprotein requires sucr A;Reference number: Z15809; MUID:96434536; PMID:8837503
A;Reference number: Z15809; MUID:96434536; PMID:8837503
A;Residues: 1-432 AHN>
A;Residues: 1-432 AHN>
A;Residues: UNIPROT:Q39835; EMBL:U44838; NID:g1165321; PIDN:AAB53156.1; PID:g116
C;Genetics:
A;Gene: HRGP3
C;Superfamily: proline-rich protein 3
C;Keywords: glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNIPROT: Q39835; EMBL: U44838; NID: g1165321; PIDN: AAB53156.1; PID: g116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bucz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---- СИРРИСРРРИСИРРИСРРИ - СИРРИСРРИСИР - - РИСИСЕНОНСРСОРР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 235.5; DB 1; Length 392; Pred. No. 7.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.8%;
larity 41.4%;
Conservative 4
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Best Local Similarity
Matches 48; Conser
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extensin precursor - kidney bean

NiAlternate names: cell wall protein; hydroxyproline-rich glycoprotein
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Date: 109-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10863; B29356
R;Wycoff, K.L.; Powell, P.A.; Gonzales, R.A.; Corbin, D.R.; Lamb, C.; Dixon, R.A.
Plant Physiol. 109, 41-52, 1995
A;Title: Stress activation of a bean hydroxyproline-rich glycoprotein promoter is superin A;Reference number: 217192; MUID:96061709; PMID:7480331
A;Restus: preliminary; translated from GB/EMBL/DDBJ
A;Restus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-580 cWYC
A;Reference number: A29356; MUID:88142825; PMID:3437892
A;Reference number: A29356
A;Molecule type: mRNA
A;Residues: N', 1-229
A;Residues: N', 1-229
A;Residues: N', 1-229
A;Residues: VN', 1-29, Textisboon Koekoek
C;Superfamily: hydroxyproline-rich glycoprotein
C;Keywords: glycoprotein; hydroxyproline
C;Keywords: glycoprotein; hydroxyproline
C;Keywords: glycoprotein; hydroxyproline
F;1-29/Domain: signal sequence #status predicted cMAT>
F;30-580/Product: extensin #status predicted cMAT>
                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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N;Alternate names: protein K10A8 130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51469
                                                                                                                                                                                                                                                                                                                                                  107 PPPYYYHSPPPKHSPPPYYYHSPPPPKHSPPPPYYYHSPPPPKHSPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 РРРҮҮҮҮН БРРРКН БРРРУҮҮН БРРРРКН БРРРГҮҮҮН БРРРКН БРРРГҮҮҮН БРРРР
                                                                                                                                                         6 ИКРРРИСИИР----НGРРРИСИИР-----НGРРРИСИИР
                                                                                                                                                                                                                                                                                             PP----HGHPP----HGPPP----HGHPP---HGPPP----HGHPPH
                                                                                                                                                                                                                      49 НЅРРРКИЅРРРУҮҮНЅРРРКИЅРРРКИЅРРРУҮҮНЗРРКИЅРРРУҮҮНЅРРР--РКИЅР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 НЅРРРРКИЅРРРРҮҮҮНЅРРРКИЅРРРРҮҮҮНЅРРРРКИЅРРРУҮҮНЅРРР--РКНЅР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRPPPHGHHP----HGPPPHGHHP----HGPPP--HGHPP----HGPPPHGP
                                                                                         Gaps
                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
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                                                                                       Indels
Score 235.5; DB 2;
Pred. No. 8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32;
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                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHG----FHDHGPCDPPSH 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHSPPPYYYHSP-PPPKH
                     33.8%;
l Similarity 41.7%;
58; Conservative
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R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Accession: T51469
A;Accession: T51469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <SAT>
A;Cross-references: UNIPROT:Q9LF59; EMBL:AL391151
A;Experimental source: cultivar Columbia; BAC clone K10A8
C;Genetics:
A;Map position: 5
A;Introns: 97/1
A;Note: K10A8_130
                                                                                                                                                                                                                                                                                                                                                                                                    5;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                   Query Match 33.6%; Score 234.5; DB 2; Length 173; Best Local Similarity 51.7%; Pred. No. 4.3e-11; Matches 45; Conservative 7; Mismatches 22; Indels 13
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1|||| 26 PPHGH---

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15, 2005, 13:51:56

Search completed: June 1 Job time : 20.4699 secs

us-10-074-225a-6.rup

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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 15, 2005, 13:32:29 ; Search time 90.8594 Seconds (without alignments) 569.231 Million cell updates/sec Run on:

US-10-074-225A-6 697 1 SVNIIHRPPPHGHHPHGPPP.......HPPHGHGFHDHGPCDPPSHK 101 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Uniprot\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	oryctolagus	bos taurus	rattus norv	mus musculu	rattus norv	rattus norv	homo sapien	homo sapien	bos taurus	rattus norv	sus scrofa	sus scrofa	sus scrofa	homo sapien	neurospora	rattus norv	mus musculu	mus musculu	mus musculu	mus musculu	rattus norv	anopheles g	oryza sativ	sesbania ro	phaseolus v	homo sapien	glycine max				
	Description	028640	Q9bgu1	Q99pa8	Q99ps5	98d660	Q9egb3	Q6yk32	Q6yka2	099ps7	Q9esb2	Q68dr3	P04196	P33433	007611	Q95jd0	095jd1	095309	Q7m4q5	Q78fa3	P04474	062107	P05142	P05143	062103	004154	Q7prh5	Q61517	041402	Q7dmv8	P04280	Q39835
SUMMARIES	ID	HRG RABIT	Q9BGU1	Q99PS8	Q99PS5	Q99PS6	Q9ESB3	Q6YK32	Q6YKA2	Q99PS7	Q9ESB2	Q68DR3	HRG HUMAN	HRG_BOVIN	Q07611	Q95JD0	Q95JD1	Q95JC9	Q7M4Q5	Q7SFA3	PRP3_RAT	Q621 <u>0</u> 7		PMP3_MOUSE	Q621 <u>0</u> 3	Q04154	Q7 PRH5	Q61517	Q41402		PRP1_HUMAN	Q398 <u>3</u> 5
	DB	-	(7)	~	N	~	~	~	~	~	7	~	-	-	~	~	~	7	~	~		~	Н	Н	~	~	~	~	~	~	~	N
	Length	526	546	525	525	525	525	536	536	515	210	312	525	396	295	511	266	9/9	128	1109	206	227	261	296	317	274	1646	257	n	230	σ	432
dŧ	Query	100.0	60.3	53.8	47.8	47.8	47.8	47.8	47.8	46.3	45.2	45.1					37.1	36.5	35.9	35.7	35.5	35.4	35.4	35.4	υ.	35.3	34.4	щ		33.8	•	33.8
	Score	697	420.5	375	333	333	333	333	333	323	315	314	314	260	259.5	258.5	258.5	254.5	250	249	247.5	246.5	246.5	246.5	246.5	246		~	~	235.5	_	
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33 phaseolus v 59 arabidopsis				79 m splicing	15 rattus norv	78 yarrowia li	78 mus musculu	10 mus musculu				
Q09083 091 f59	P0829	Q86ya1	Q1542	Q8qzy	Q6ayl	Q6cay	05497	Q8r5n0	Q80u4	015214	P02812	969890
209083 091,F59	NO75 SOYBN	286YĀ1	3B4 HUMAN	08QZ <u>Y</u> 9	6AYL5	6CAY8	054978	PRSNO	180047	15214	RB2 HUMAN	268D <u>9</u> 6
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~ ~	309 1	338 2	424 1	424 2	424 2	586 2	1571 2	1572 2 C	1617 2 Q	173 2 Q	382 1 E	
580 2	33.5 309 1	33.5 338 2	33.5 424 1	33.5 424 2	33.5 424 2	33.5 586 2	33.4 1571 2	33.4 1572 2 Q	33.4 1617 2 Q	33.1 173 2 Q	382 1 E	33.0

#### ALIGNMENTS

ABIT HRG_RABIT STANDARD; PRT; 526 AA. Q28640; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Histidine-rich glycoprotein precursor (Histidine-proline rich	NameshRG; Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	LIJ SEQUENCE FROM N.A., AND SEQUENCE OF 9-23; 301-313 AND 422-429 TISSUE=Serum; MEDLINE=96229917; PubMed=8639676; DOI=10.1021/bi952061t; Borza DB., Tatum F.M., Morgan W.T.; "Domain structure and conformation of histidine-proline-rich	glycoprotein."; Biochemistry 35:1925-1934 (1996). Biochemistry 35:1925-1934 (1996).	-!- DOWAIN: In addition to having a high His and Pro content, this protein has many internal repeats. 15 tandem repetitions of a 5-residue sequence (G[H/P][H/P]PH, consensus) form a His/Pro-rich region!- SIMILARITY: Contains 2 cystatin-like domains. This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.	the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).  EMBL; U32189; AAC48516.1;  EMBL; U32189; AAC48516.1;  InterPro; IPR000010; Prot inh_cystat.  Pfam; PF00031; Cystatin; I.  Potential.  Signal.  Signal.  A Potential.  CHAIN  9 526 Histidine-rich glycoprotein.  CHAIN  9 126 Cystatin-like 1.
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us-10-074-225a-6.rup

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Matches
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                                                                                                                                                                                                                                                                                                                                                                                       Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.
Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055894; BAB33091.1; -.
GO; GO:0004869; F:Cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot inh cystat.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 2.
SEQUENCE 546 AA; 61948 MW; 26264858824D89EE CRC64;
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   Cystatin-like 2.

Pro-rich.

His/Pro-rich.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

Notential.

N-linked (GlCNAC...) (Pot.

Cleavage (by plasmin).

Cleavage (by plasmin).

Cleavage (by plasmin).
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                   Score 697; DB 1;
Pred. No. 2.6e-38;
0; Mismatches 0;
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251 296
129 498
14 505
68 79
95 116
93 415
7 230
2 302
115 115
192 240
310
310
485
485
642
58877 MW;
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Best Local Similarity 100.
Matches 101; Conservative
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Eukaryota, Metazoa, C
Mammalia, Eutheria, C
Bovinae, Bos.
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        DOMAIN
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525

PRELIMINARY;

**Q99PS8** 

RESULT 3 Q99PSB ID Q99P

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SIGNIER C. STRAIN=FVB/N; TISSUE=Liver;

STRAIN=FVB/N; TISSUE=Liver;

STRAIN=FVB/N; TISSUE=Liver;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

B Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Sprague-Dawley, TISSUE=Liver,
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.
Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AB055895; BAB33092.1; -.
GO; GO:0004869; F:Cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot inh_cystat.
Pfam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
SMART; SM00043; CY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381 QHPHGH-----HPHGHHPHGDHPHGHHPHGHDFLDYGPCDPPSN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 РРРИСИРРИСРРИСИРРИСРРИСИРРИСИРЕНСИСРИВИСРСПРРЅИ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Indels
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(TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%; Score 375; DB 2; ilarity 63.5%; Pred. No. 2.3e-17; Conservative 2; Mismatches 24;
                                                                                                                                  Histidine-rich glycoprotein 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Histidine-rich glycoprotein.
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Mus musculus (Mouse).
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                                                                                                                                                                                                                        Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                         01-JUN-2003
   01-JUN-2001
01-JUN-2001
                                                                                                                                                                           Name=RNHRG1
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                    322 ИКТНК-РЅУИНЅСИЕНРСНGНКРНGНИРНSННРРGННSHG----НИРНGНИРНSHHSHGH 376
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Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                    3 NIIHRPPPHGH----HP-HGPPPHGHHPHGPPPHGPPPRHPPHGPPHGPPHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NIIHRPPPHGH----НР-НGPPPHGHHPHGPPPHGPPPRHPPHGPPHGPPHGPPHGP
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Chordata; Craniata; Vertebrata; Euteleostomi; ; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

STRAIN=BALB/c; TISSUE=Liver;
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.,
A Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055897; BAB33094.1; -.
R MGD; MGI:2146636; Hrg.
R GO; GO:0005615; C:extracellular space; TAS.
R ThterPro; IPR00010; Prot_inh_cystat.
R InterPro; IPR00031; Cystatin; I.
R SMART; SM00043; CY; 2.
R SMART; SM00043; CY; 2.
                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055898; BAB33095.1; -.
EMBL; BC011168; AAH11168.1; -.
R GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000010; Prot inh_cystat.
R Ffam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
SEQUENCE 525 AA; 59162 MW; A83E93A439CFB126 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.8%; Score 333; DB 2; Length 525; 58.3%; Pred. No. 1.2e-14; ive 3; Mismatches 30; Indels
                                                                                                                                                                                                                                           Score 333; DB 2; Length 525;
Pred. No. 1.2e-14;
3; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                                                                                                                         377 HPPGHHPHGHHPHGHHPHGHHPHGHDFLDYGPCDPPSN 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 РРНСНРРНСРРРНСНРРНСРРНСРРНСНРРНСРСБРБЯН 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oggps6 PRELIMINARY; PRT; 525 AA.

Oggps6;
Ol-JUN-2001 (TrEMBLrel. 17, Created)
Ol-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Ol-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Histidine-rich glycoprotein.
Name=Hrg; Synonyms=MMHRG;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Muchi
                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                              47.8%;
                                                                                                                                                                                                                                                                          Conservative
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Best Local Similarity 58.3
Matches 60; Conservative
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 60; Conser
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Q99PS6
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X MEDLINE=20307726; PubMed=10849117;
X Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;

Murine histidine-rich glycoprotein: cloning, characterization and cellular origin.";
Immunol. Cell Biol. 78:280-287(2000).

EMBL; AF194028; AAG28416.1; -.

R MGD; MGI:2146636; Hrg.

R GO; GO:0005615; C:extracellular space; TAS.

R GO; GO:0005615; C:extracellular space; TAS.

R ThterPro; IPR000010; Prot_inh_cystat.

R Ffam; PF00031; Cystatin; I.

R SMART; SM00043; CY; 2.

R SEQUENCE 525 AA; 59132 MW; 6E55F2A439CFB123 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 NIIНRPPPHGH----НР-НGPPPHGHPHGPPPHGHPPHGPPPHGPPHGPPHGP
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                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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HBU S.J., Balmain A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY137504; AAN27996.1; -.
GO; GO:0004869; F:Cysteine protease inhibitor activity; IEA.
InterPro; IPR00010; Prot inh_Cystat.
Pfam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
SEQUENCE 536 AA; 60439 MW; CCF14FC08DD53D7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 РРИСИРРИСРРРИСИРРИСРРИСИРРИСИСИНОНСРСОРРЯН 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              377 HPPGHHPHGHHPHGHHPHGHHPHGHDFLDYGPCDPPSN 419
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(TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Histidine-rich glycoprotein HRG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 47.8%; Score 333; DB 2; Best Local Similarity 58.3%; Pred. No. 1.2e-14; Matches 60; Conservative 3; Mismatches 30,
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58.3%; Pred. No. 1.3e-14;
iive 3; Mismatches 30;
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                                                                                 Histidine-rich glycoprotein.
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Best Local Similarity 58.3
Matches 60; Conservative
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                                                                                                                                      Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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RESULT Q9ESB3

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RESULT Q6YKA2

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Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hulett M.D., Parish C.R.;
"Murine histidine-rich glycoprotein: cloning, characterization and cellular origin.";
Immunol. Cell Biol. 78:280-287(2000).
EMBL; AF194029; AAG28417.1; -.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; 1.
SMART; SM0043; CY; 2.
SEQUENCE 510 AA; 57581 MW; 508E6E06AA2ED58E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         лошо варлепь (пимап).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 510;
                                                                                  58 РРИСИРРИСРРИСИРРИСИРРИСИРРИСИРРИСИСРИВНО 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Liver;
The German cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osan Fobo G., Han M., Wiemann S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR749302; CAH18157.1; -.
Hypothetical protein.
NON TER
1 1 1
SEQUENCE 312 AA; 35124 MW; 08522797450AFAIF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 PRGH-----HPHGHHPHGDHPHGHPHGHDFLDYGPCDPPSN 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   РНСИРРИСРРИСИРРИСРРИСИРРИСИРРИСИСЕНОИСРСОРРЅИ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 NRSHRPPRNHSCNEHPCHRQHPHGHHPHGQHPHGHHPHGQHPR---
                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Name=Hrg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          068DR3;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp779H1622 (Fragment).
322 NRSHR-PPHNHSCNEHPCHGQHPHGHHPHGHPHGHPHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.2%; Score 315; DB 2; ilarity 55.9%; Pred. No. 1.8e-13; Conservative 3; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Lewis;
MEDLINE=20307726; PubMed=10849117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Q9ESB2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIIHRPPPHGH----HP-HGPPPHGHIPHGPPPHGHPPHGPPRHDPHGPPHGHPPHGP
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Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Sprague-Dawley; TISSUE=Liver; Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S. Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB055896; BAB33093.1; -. GO; GO:0004869; F:cysteine protease inhibitor activity; IEA. InterPro; IPR000010; Prot_inh_cystat.

Ffam; PF00031; Cystatin; I. SMART; SM00043; CY; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th 46.3%; Score 323; DB 2; Length 515; Similarity 57.3%; Pred. No. 5.5e-14; 59; Conservative 3; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30; Indels
388 HPPGHHPHGHHPHGHHPHGHHPHGHDFLDYGPCDPPSN 430
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                                                                                                                                                                                                                                                                                                                                                                            STRAIN=NIH/Ola;
HSU S.J., Balmain A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY135662; AAN10183.1; -.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 2.
SEQUENCE 536 AA; 60492 MW; 71CE4FC6DF3A3D72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.
58055 MW; 7CEBA3A1A3678966 CRC64;
                                                                                                                                      O6YKA2;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Histidine-rich glycoprotein Hrg.
Name=Hrg1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.8%; Score 333; DB 2; Best Local Similarity 58.3%; Pred. No. 1.3e-14; Matches 60; Conservative 3; Mismatches 30;
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                                                                                                                     PRT;
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a; Chordata; C
a; Rodentia; S
                                                                                                                     PRELIMINARY;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; R
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Best Local S
Matches 59
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RESULT Q99PS7 ID Q9

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MEDLINE=86216149; PubMed=3011081;
Koide T., Foster D.C., Yoshitake S., Davie E.W.;
"Amino acid sequence of human histidine-rich glycoprotein derived from the nucleotide sequence of its cDNA.";
Biochemistry 25:2220-2225(1986).
                                                                                                                                                                                 117 ATFGTNGAQRHSHNNNSSDLHPHKHHSHEQHPHGHHPHAHHPHEHDTHRQHPHGHHPHGH
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                                                                                                                                                  -----RHP-----RHP------PHGPPPHGHPP-----HGPPPHGP
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                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714 (1992).

-!- FUNCTION: The physiological function is not yet known. It binds heme, dyes and divalent metal ions. It can inhibit rosette formation and is known to interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HMW kininogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood coagulation cascade.

-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Sereted.
-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma protein has many internal repeats. 12 tandem repetitions of a 5-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEDLINE=94245171; PubMed=8188234;
Hennis B.C., Frants R.R., Bakker E., Vossen R.H., van der Poort E.
Blonden L.A., Cox S., Khan P.M., Spurr N.K., Kluft C.;
"Evidence for the absence of intron H of the histidine-rich
glycoprotein (HRG) gene: genetic mapping and in situ localization
HRG to chromosome 3q28-q29.";
Genomics 19:195-197(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                         64;
                                                                                                                                                                                                                                                                                                                                                                                  20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich glycoprotein) (HPRG).
    Length 312,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ပ
                                                                         --HGHP-PHGPPP
  Score 314; DB 2; Length 31 Pred. No. 1.4e-13; 2; Mismatches 23; Indels
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MEDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
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Wakabayashi S., Takahashi K., Tokunaga F., Koide T.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                           177 HPHGHHPHGHHPHGHDFQDXGPCDPPPH 209
                                                                                                                                                                                                                                                                                                                                                     525 AA
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
Query Match
Best Local Similarity 41.8%;
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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62 KPPFKPHGSR
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collaboration
                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Histidine-rich glycoprotein.
Cystatin-like 1.
Cystatin-like 2.
Pro-rich.
His/Pro-rich.
By similarity.
Compare the second of the second o
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InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; I.
Direct protein sequencing; Glycoprotein; Heparin-binding;
Polymorphism; Repeat; Signal.
SIGNAL
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A2B124D6CE93114F CRC64;
 residue sequence (GHHPH, consensus) form a h. SIMILARITY: Contains 2 cystatin-like domains.
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01-FEB-1994 (Rel. 28, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein (Histidine-proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     396 AA
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                                                                                                                                                                                                                                                      EMBL; M13149; AAA52694.1; -.
EMBL; AB005803; BAA21613.1; -.
EMBL; Z17218; CAA78925.1; -.
PIR; A01287; KGHUGH.
SWISS-2DPAGE; P04196; HUMAN.
Genew; HGNC:5181; HRG.
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254
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Best Local Similarity
Matches 64, Conserv
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Search completed: June 15, 2005, 13:51:03
 Proline-rich proteoglycan.
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                            MEDLINE=93351678; PubMed=834897; DOI=10.1016/0014-5793(93)80945-Q; MEDLINE=93351678; PubMed=834897; DOI=10.1016/0014-5793(93)80945-Q; MEDLINE=93351678; PubMed=834897; DOI=10.1016/0014-5793(93)80945-Q; MEDLINE=93351678; PubMed=81897; DOI=10.1016/0014-5793(93)80945-Q; MEDLINE=93351678; PubMed=81897; DOI=10.1016/0014-5793(93)80945-Q; MEDLINE=10.0016; PubMed=81980; Pu
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ses 52; Conservative
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                      SEQUENCE, AND DISULFIDE MEDLINE=93351678; PubMed
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ID Q0761
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                                                                                                                                                         STRAIN=Sprague-Dawley, TISSUE=Parotid, MEDLINE=93388626; PubMed=8376404; Castle A.M., Castle J.D.; Castle A.M., Castle J.D.; "Novel secretory proline-rich proteoglycans from rat parotid. Cloning and characterization by expression in AtT-20 cells."; J. Biol. Chem. 268:20490-20496(1993). EMBL; L17318; AAA03074.1; -. EMBL; EA88013; B48013. SEQUENCE 295 AA; 30026 MW; EEA44BD8B38E1B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 VNRPERPPQHGGNHHHPHHPPPAAGPQRPPGSPQGPPPGGPQQRPPQGPPQGGPQR
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        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCSI_TaxID=10116;
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Sus.
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Zhang Q., Szalay A.A., Kyeyune-Nyombi E., Sands J.F., Oberg
Zhang Q., Szalay A.A.,
Tieche J.-M., Leonora J.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX035848; AAK61382.1; -.
GO; GO:0005199; F:structural constituent of cell wall; IEA.
InterPro; IPR003882; Pistil extensin.
PRINTS; PR01218; PSTLEXTENSIN.
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    095JD0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Basic proline-rich protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 37.2%; Score 259.5; DB 2; Best Local Similarity 38.4%; Pred. No. 4.8e-10; Matches 63; Conservative 1; Mismatches 27;
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Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 AA;
                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9823;
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Job time : 92.8594 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

, 2005, 13:52:01 , Search time 90 Seconds (without alignments) 21.487 Million cell updates/sec June 15

US-10-074-225A-7 23 1 XXPHG 5

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

seqs, 386760381 residues 2105692 Searched:

Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
4: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Targettin	Pentapept	Mimotope	Pentameri	Melanotro	Peptide 5	Antidepre	sta 6	Histidine	Histidine	Histidine	Histidine	me cl	int VL	prot		oit HP	oit HP	oit HP	HPRG prot	p pri	coli m	Hexapepti	Hexanenti
	Description	ı												338 Enzyme	9	419 HPRG	422 HPRG	417 Rabbit	415 Rabbit	416 Rabbit	8		Ш	0	
	Desci	Abg77500	Aar12701	Aar51565	Aar69933	Aar89833	Aar98679	Aaw78934	Aay23419	Abb 79810	Abb79808	Abb79809	Abb79811	Aag8033	Aao15016	Adh10419	Adh10422	Adh1041	Adh1041	Adh10416	Adh1041	Ado81122	Adr03627	Aaw7537	Daw75302
		! ! ! ! !																							
OUMBAKIES		00	.01	65	33	33	79	34	19	10	90	601	111	38	16	19	22	17	15	16	18	22	27	70	00
S O	ID	ABG77500	AAR12701	AAR51565	AAR69933	AAR89833	AAR98679	AAW78934	AAY23419	ABB79810	ABB79808	ABB79809	ABB79811	AAG80338	AA015016	ADH10419	ADH10422	ADH10417	ADH10415	ADH10416	ADH10418	AD081122	ADR03627	AAW75370	A 2 W 7 G 3 D 2
	DB		~	~	~	~	~	7	~	ហ	Ŋ	ß	Ŋ	ហ	ഹ	8	œ	ω	80	æ	æ	æ	œ	7	c
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ф	Query Match	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3
	Score	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
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	Adpsisse Camploine Adn12399 Peptide # Ado37172 Binding p	Ado37904 Binding p Ado37705 Binding p Ado37180 Binding p	Binding	Capture Capture	Ado28426 Capture s Ado27694 Capture s	Ado27702 Capture s Ado28220 Capture s	Adr49685 6-mer pep Adr50404 6-mer pep	Adr49871 6-mer pep Adr49871 6-mer pep
ហហ	0 1 0	6 8 ADO37904 6 8 ADO37705 6 8 ADO37180	88	<b>ω</b> ω	<b>∞ ∞</b>			
91.3	1 91.3 1 91.3	21 91.3 21 91.3 21 91.3	91.3		91.3 91.3	91.3 91.3	91.3 91.3	91.3 91.3
226		32 32 33	3 3 4 5 4	36 37	8 6 8 6	40	42 43	44 45

## ALIGNMENTS

Targetting peptide selective for human organ, tissue or cell type #33. Human, cytostatic, antiinflammatory, antidiabetic, cardiovascular, immunomodulator, antibacterial, antiviral, gene therapy, cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease, degenerative disease. ABG77500 standard; peptide; 4 AA (first entry) 05-NOV-2002 ABG77500; ABG77500 RESULT 1 

Homo sapiens.

WO200220723-A2.

14-MAR-2002

07-SEP-2001; 2001WO-US028044.

08-SEP-2000; 2000US-0231266P. 17-JAN-2001; 2001US-00765101.

(TEXA ) UNIV TEXAS SYSTEM.

Pasqualini R; Arap W,

WPI; 2002-599247/64.

ಥ New targeting peptides identified by phage display, useful for treating disease state, e.g. cancer, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial or viral infection or cardiovascular disease.

Claim 16; Page 63; 269pp; English.

The invention describes an isolated peptide of 100 amino acids or less in size. The peptide is useful for treating a disease state, e.g. cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease. This sequence represents a human targeting peptide selective for human organs, tissues or cell types

Sequence 4 AA;

assay;

screening

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mimotope panel; rational drug design; candidate drug; hydrophobicity; antibody repertoire.
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                          WPI; 1994-109390/13
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                          Sequence 5 AA;
                                            Key
Modified-site
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11-OCT-1988;
                                                                                                               06-DEC-1989;
                                                                                             05-APR-1994
                                                                             US5300425-A
                                                                                                                                                                                                                                              Example 3;
                                                                                                                                                                          Kauvar LM;
                           Synthetic
                                                                                                                                                                                                                            receptor.
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                                                                                                                                                                                                                                                                                                                                                                             Peptide is one of a panel, each of which have systemicly varied values of at least two parameters. A test protein is matched against the panel, and the paralogues with highest binding affinity are selected. Selected paralogues are bound to a matrix which is incorporated into the HPLC gel and used as affinity ligands. Technique is useful in chromatographic separation, purification and binding assay
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                               Identifying paralogueueueueue with specific affinity for analyte candidate paralogues with systematically varied values of at least
                                                                                                                                                        chromatographic affinity ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 from panel of maximally diverse mimotopes.
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          Length 4;
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        Score 21; DB 5; Le
Pred. No. 1.8e+06;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             91.3%; Score 21; DB 2; L6
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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         91.3%;
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                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                        paralogue for
                                                                                                                                                                                                                                                                             (TERR-) TERRAPIN TECHN INC
                                                                                                                                        entry)
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       Query Match
Best Local Similarity
Matches 3; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                     AAR12701 standard;
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                                         PHG 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5 AA;
                                                                                                                                                         Pentapeptide
                                                                                                                                                                                                                                            31-OCT-1989;
                                                                                                                                                                                                                                                            31-OCT-1989;
                                                                                                                                                                                                                          16-MAY-1991.
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19-OCT-1994
                                                                                                                                                                                                           WO9106356-A.
                                                                                                                                                                                                                                                                                                                                                 parameters.
                                                                                                                                       31-JUL-1991
                                                                                                                                                                                                                                                                                               Kauvar LM;
                                                                                                                                                                                          Synthetic
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                                                                                                                      AAR12701;
                                                                                    RESULT 2
AAR12701
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AAR51565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mimotope; antibody; production; high specificity; detection; immunoassay; high performance liquid chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening of candidate drugs for binding to receptor - by comparing inverse image antibody profile of drug with mimotope-binding profile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pentameric mimotope 59 used to obtain highly specific antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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. 1.8e+06;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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88US-00255906
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J.

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AAR89786-R89858 are small peptide compounds based on the tripeptide hormone melanotrophic release inhibiting factor (MIF), also known as L-propyl L-leucyl glycine and melanocyte stimulating inhibitory factor. The peptides are used for treating depression and can be administered so as to achieve a circulating plasma level of 30-90 mg per average human adult. The peptides show greater anti-depressant activity than MIF. They can be administered at lower dosage than known anti-depressants which reduces potential deleterious side effects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panel; mimotope; decreasing hydrophobicity; periodic variation; hydrophobic moment; antibody; repertoire; identification; drug; candidate; receptor; binding; ligand; rational; design; selection; treatment; tumour; production; immunological reagent; analyte; detection; trace contaminant; mimetope.
                                                                                                                                                                                                         New tri-, tetra-, penta- and poly-peptide cpds. - based on the tri:peptide hormone melanocyte stimulating inhibitory factor, used for treating depression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide 59 from 88 member diverse mimotope panel.
                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 21; DB 2; Le
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                 Claim 63; Page 32; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "acylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR98679 standard; peptide; 5 AA.
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88US-00255906.
89US-00447009.
                                                                      95WO-US005560.
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(first entry)
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                    Noble JF,
                                                                                                                          (INNA-) INNAPHARMA INC
                                                                                                                                                                                WPI; 1995-403936/51
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Modified-site
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11-OCT-1988;
06-DEC-1989;
                                                                                               04-MAY-1994;
                 WO9530430-A1
                                                                      02-MAY-1995;
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11-MAR-1997
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                                          16-NOV-1995
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AAR98679
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                                                                                                                                                                                                                                                                                                 AAR69875-969 are pentameric mimotopes designed on the basis of decreasing hydrophobicity and periodic variation of hydrophobic moment. All the pentapeptides are acetylated at the N-terminus except E12 (for FITC) (sic). E12 is not identified in the specification. The mimotopes are used in the method of the invention to obtain antibodies specifically and strongly reactive with a desired analyte. The mimotope is obtd. by reacting a panel of starting antibodies (Abs) representative of the resting B cell repertoire of a mammal with an analyte (so as to identify analyte-reacting Abs) and then reacting each of a panel of candidate mimotopes representative of a random set of 3D contours with the analyte-reacting Abs. A subject is immunised with one or more mimotopes identified and the product Abs are recovered from the serum of the subject. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Melanotrophic release inhibiting factor (MIF) modified peptide analogue.
                                                                                                                                                                                                                     Producing antibodies with high specificity and affinity for an analyte by immunisation with selected mimotope, also analyte detection kits, useful for immunoassay of materials usually analysed by HPLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIF; melanotrophic release inhibiting factor; modified; analogue; hormone; depression; low dosage; L-propyl L-leucyl glycine; melanocyte stimulating inhibitory factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             may be in cis- or trans- form"
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1.8e+06;
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1
/label= OTHER
/note= "4-F-Phe"
2
/label= 4Hyp
/note= "4-OH-Pro, may
5
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/note= "amidated"
                                                                                                                                    (TERR-) TERRAPIN TECHNOLOGIES INC.
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88US-00255906
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3; Conservative
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AAR89833
ID AAR89833 standard;
                                                                                                                                                                                                                                                                           Example 3; Fig 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5 AA;
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Modified-site
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                                                                  04-JUN-1993;
             JS5384263-A
                                                                                             13-OCT-1987
11-OCT-1988
                                       24-JAN-1995
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Best Local S
Matches 3
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                                                                                                                  The present peptide is a member of a panel of 88 pentapeptide mimotopes designed on the basis of decreasing hydrophobicity, and periodic variation of hydrophobic moment. The panel was synthesised using the method of Geysen, H. M., et al, Proc. Natl. Acad. Sci. USA (1984), which uses lots of 96 pins; the remaining 8 polyethylene pins being controls. The mimotopes were then mixed, 125-I labelled and tested with individual members of a basal antibody (Ab) repertoire. Nearly uniform binding to all members of a nalyte. A small number showed greatly increased defined amt. of analyte. A small number showed greatly increased labelling, these Ab representing the successful result of an initial screen for those that pref. bind analyte. The above is an example of a claimed method for identifying members of a panel of candidate drugs, that bind to a receptor having a known ligand. It is useful in rational drug design, e.g. selection of monoclonal Ab for treating individual tumours, and for the prodn. of immunological reagents for any analyte, including those not normally detectable by immunoassay, e.g trace
                                                                                                                                                                                                                                                                                                                                                         ö
                                                                   ind a specific receptor by competitive - useful in rational drug design.
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antidepressant; depression; tripeptide MIF; hormone; bovine; ramelanocyte stimulating inhibitory factor; psychiatric disorder; neurochemical; central nervous system.
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                                                                                                                                                                                                                                                                                                                                    91.3%; Score 21; DB 2; Length 5;
100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0; Indels
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2 /label= 4Hyp
/note= "4-hydroxyproline"
5 /note= "amidated"
                                                                    Identifying candidate drugs that bind reaction with panel of mimetope(s) - v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            based peptide #64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide; 5 AA.
                                                                                                   27pp; English
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        (KAUV/) KAUVAR L M
                                                                                                                                                                                                                                                                                                                                              Similarity 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antidepressant MIF
                                                WPI; 1996-361955/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW78934 standard;
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                                                                                                  Example 3; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                            PHG 5
                                                                                                                                                                                                                                                                                                                Sequence 5 AA;
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Modified-site
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Bos taurus.
Rattus sp.
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                            Kauvar LM
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Best Local Si
Matches 3,
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AAW78934
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Peptides given in AAW78922 to AAW79000 are based on the tripeptide MIF (melanocyte stimulating inhibitory factor), which was initially isolated from bovine and rat hypothalmic extracts. The peptides from the present invention are useful for treating depression, optionally together with other antidepressants e.g. fluoxetine, amitriptyline or sertraline. The peptides avoid the serious side effects of the prior art tricyclics, MAO oxidase inhibitors and second generation antidepressants. They are also lipid soluble and easily cross the blood-brain barrier, but are not so easily metabolised as the parent MIF (the tripeptide Pro-Leu-Gly-NH2) and so allows a lower dosage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5; V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                     treatment
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                                                                                                                                                                                                                                                 - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.3%; Score 21; DB 2; Le 100.0%; Pred. No. 1.8e+06; cive 0; Mismatches 0;
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                                                                                                                                                                                                                                                 peptides based on structure of MIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Page 85; 104pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (IMMU-) IMMUNE RESPONSE CORP. (KIMM-) KIMMEL CANCER CENT SIDNEY.
                                                                                                                                                  Abajian HB
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                                                                                                                                                                                                                                                                                                                           Claim 14; Col 99; 56pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-US023147.
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95US-00432651
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                                                                                                 (INNA-) INNAPHARMA INC
                                                                                                                                                Hlavka JJ, Noble JF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-404801/34.
                                                                                                                                                                                                WPI; 1998-361753/31
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Best Local Similarity
Matches 3; Conserv
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02-MAY-1995;
                                                04-MAY-1994;
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                                                                                                                                                                                                                                                                          depression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY23419;
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The specification describes vaccines which comprise immunologically effective amounts of T cell receptor (TCR) peptides. The TCRs are present on the surface of T cells. The TCRs are chosen from V beta 6.2/3, V beta 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta 5/6, V beta 6.7, V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vitro or in vivo; or a pentapeptide having the generic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Histidine proline rich glycoprotein; HPRG; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian.
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Pred. No. 1.8e+06;
0; Mismatches 0;
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Best Local Similarity
Matches 3, Conser
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antiarteriosclerot
antiarthritic, ant
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ABB79810
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sequence given in ABB79808, such as the present peptide, or its variant having an additional 1 to 4 amino acids comprising His, Pro or Gly at its neving an additional 1 to 4 amino acids comprising His, Pro or Gly at its recombinantly produced peptide anti-angiogenic polypeptide, peptide or peptide or peptide multimers; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled patient angles peptide or peptide multimer and a carrier, an antibody specific for an epitope of HPRG that is present in the HJP domain of human or rabbit HPRG, and which binds to HPRG or to any complex in a way which inhibits the anti-angiogenic activity of HPRG or the domains in a way which inhibits the anti-angiogenic activity of HPRG or the domain, or an antigen-binding fragment of the antibody; a method for inhibiting cell migration, cell invasion, cell proliferation subject having a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis; a method of transfected cells an ample; isolated nucleic acids encoding the polypeptide, peptide or habitimer; an expression vector; transfermed or transfected cells; a method of providing to a cell; tissue or organ an expression vector; transfermed or transfected cells; a method of providing to a cell; tissue or organ an expression vector; transfermed or indication, or isolating an element of cells and the peptide multimer; an expression vector; transfermed or isolating or isolated multimer; an expression vector; transfermed or isolating an element of cells expressing the binding molecule, compression vector; transferior or isolating an element of sells expressing the binding molecule, compressing HPRG-binding molecule, or isolating an element of sells expressing the binding molecule, or isolating and element of sells expressing the binding molecule, or isolating and element of sells encorry attended with undesired cell migration, invasion, or angiogenesis, such as cancer, atheroseclerosis, cretinopathy, inflammetrion, en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histidine proline rich glycoprotein; HPRG; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian.
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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Matches 3; Conser
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ABB79808
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The present sequence is a generic sequence (see also ABB79809-11) of isolated anti-angiogenic polypeptides of the invention. Claimed anti-angiogenic polypeptides comprise: the histidine proline-rich (H/P) domain of human histidine proline rich glycoprotein (HPRG, see ABB79806); an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; and the present peptide, or its variant having an additional 1 to 4 amino acids comprising His. Pro or Gly at its N· or C-terminus. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically useful HPRG-related composition, comprising the diagnostically useful HPRG-related composition, comprising the diagnostically useful HPRG-related cor peptide multimer; a diagnostically useful HPRG-related cor peptide multimer and a carrier; an antibody specific for an epitope of cor peptide multimer and a carrier; an antibody specific for an epitope of cor peptide multimer; and operation or an antigen-binding fragment of the antibody; a method for inhibiting cell migration, cell proliferation, invasion, proliferation, or angiogenesis; a method for inhibiting angiogenesis or condition associated with cor peptide multimer; an expression vector; transformed or cell proliferation of stimulating or inhibiting angiogenesis in a subject; a method of cor its cleavage product or its peptide in a biological sample; isolated nucleic acids encoding the polypeptide, or peptide cor peptide multimer; an expression vector; transformed or transfected cells; an expression vector; transformed or transfected cells; an expression vector; transformed cor its peptide multimer; an application or cell provise; an expression or claim or its period or its constant or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pentapeptide, or the peptide multimer; an affinity ligand useful for pentapeptide, or the peptide multimer; an affinity ligand useful for binding to, or isolating, an HPRG-binding molecule or cells expressing the binding molecule, comprising the polypeptide, peptide or peptide multimer, immobilised to a solid support or carrier; and a method of isolating HPRG-binding molecule, or isolating or enriching cells expressing HPRG-binding site or receptor, from a complex mixture. The compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's or Parkinson's disease. The antibodies are stimulators of angiogenesis and are useful for promoting neurodegenesis and eare useful for promoting neurodegenesis and are useful for promoting neurodegenesis and are useful for promoting
                                                                                                                                                                                                                                                                                                                                                                                                         ine rich glycoprotein (HPRG) polypeptide, useful for ting diseases associated with undesired cell migration,
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invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                              Mazar AP;
                                                                                                                                                                                                                                                            Plunkett ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82pp; English
                                                                                 14-FEB-2002; 2002WO-US004336.
                                                                                                                                        14-FEB-2001; 2001US-0268370P
                                                                                                                                                                                                 (ATTE-) ATTENUON LLC.
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                                                                                                                                                                                                                                                                                                                                                                                                       New histidine-prol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 67;
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Histidine proline rich glycoprotein; HPRG; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian. Histidine proline rich glycoprotein pentapeptide. Mazar AP; Plunkett ML, ABB79809 standard; peptide; 5 AA. 14-FEB-2002; 2002WO-US004336. 14-FEB-2001; 2001US-0268370P. (first entry) (ATTE-) ATTENUON LLC Donate F, Harris S, WPI; 2002-666989/71. P-PSDB; ABN84910 WO200264621-A2. 25-NOV-2002 22-AUG-2002 Synthetic. ABB79809; 

New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.

English. Claim 2; Page 67; 82pp; The present sequence is a specific example of claimed anti-angiogenic polygeptides or pentapeptides of the invention. Claimed anti-angiogenic polygeptides or peptides comprise: the histidine-proline-rich (H/P) domain of human of the stability of the pentapeptide proline rich glycoprotein (HPRG, see ABB79806); an H/P domain of the stability of the see that is capable of inhibiting angiogenesis, endothelal cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808, such as the present peptide, or its variant sequence given in ABB79808, such as the present peptide or the variant of the adving an additional 1 to 4 amino acids comprising His, Pro or Gly at its recombinantly produced peptide multimers is a diagnostically labeled anti-angiogenic polypeptide, peptide or peptide multimer; a diagnostically labeled anti-angiogenic polypeptide, peptide or peptide comprising the diagnostically labeled bolypeptide, peptide or peptide or the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any without the propertied or peptide or the domains in a way which inhibits the anti-angiogenic activity of the H/P domains in a way which inhibits the anti-angiogeneis cell invasion, cell proliferation or the domains in a way which inhibits the anti-angiogeneis a method for treating a method for inhibiting cell migration, cell invasion, cell proliferation angiogenesis, or for inhibiting angiogenesis a method for treating a disease or condition associated with undesired cell migration, proliferation, or angiogenesis, a method of stransferted cells; a method of providing to a cell, tissue or organ and angiogenesis -inhibitory amount of HPRG, an H/P domain of HPRG or its peptide multimer; and propered or cells; and the proliferation; or the peptide multimer; and pelved or peptide multimer; and

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expressing HPRG-binding site or receptor, from a complex mixture. The compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative diseases like Alzheimer's or Parkinson's disease. The antibodies are stimulators of angiogenesis and are useful for promoting neurodesis and are useful for promoting neurous in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is a specific example of claimed anti-angiogenic pentapeptides of the invention. Claimed anti-angiogenic polypeptides or pentabetides comprise: the histidine-proline-rich (H/P) domain of human histidine proline rich glycoprotein (HPRG, see ABB79806); an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808, such as the present peptide, or its variant having an additional 1 to 4 amino acids comprising His, Pro or Gly at its N- or C-terminus. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or therapeutically labeled anti-angiogenic polypeptide, peptide or peptide multimer; a diagnostically useful HPRG-related composition, comprising
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invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Histidine proline rich glycoprotein; HPRG; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ine rich glycoprotein (HPRG) polypeptide, useful for
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100.0%; Pred. No. 1.8e+0
ive 0; Mismatches
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the diagnostically labeled polypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the HPP domain of human or tabbit HPRG, and which binds to HPRG or to any of the domain of human or tabbit HPRG, and which binds to HPRG or to any of the domain, or an antigen-binding fragment of the antibody: a method for inhibiting cell migration, cell profileration or angiogenesis, a method for treating a confidence of inducing apoptosis; a method for treating a subject having a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis a method of a biological sample; isolated nucleic acids encoding the polypeptide, confidence of HPRG or its cleavage product or its peptide in a beptide multimer; an expression vector; transformed or transfected cells; an method of providing to a cell, tissue or organ an angiogenesia-inhibitory amount of HPRG, an H/P domain of HPRG or its peptide or peptide multimer; an affinity ligand useful for binding to, or isolating, an HPRG-binding molecule or isolating, an HPRG-binding molecule or isolating is method of solating or carrier; and a method of isolating HPRG-binding molecule, or isolating or carrier; and a method of solating such a complex mixture. The compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, invasion, or angiogenesis, such as cancer; atherosaclerosis, diabetic retinopathy inflammation, endometriosis, architics, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative function in pertinent disease trates, and in various in metastation in pertinent disease. The antibodies are immunoassava
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/note= "Residue is conjugated to Dox, where Dox is the anthracycline doxorubicin"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAG80338 standard; peptide; 5 AA.
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AAG80338
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                                                                                                                                                                       This invention relates to novel compounds (I) comprising antineoplastic agents conjugated to enzyme cleavable peptides comprising the amino acid recognition sequence of a membrane bound and/or cell-secreted peptidase. The compounds of the invention have cytostatic activity. The products of the invention can be used as chemotherapeutic agents, preferably in the presence of a matrixin, used for targeted treatment of cancers, particularly leukaemia, lymphoma, carcinoma, sarcoma and melanoma. (I) are stable to non-specific enzymatic degradation in the blood stream and reduce damage to healthy, non-target tissue, so that the toxicity of (I) is reduced, compared to its non-conjugated form. This sequence represents an enzyme cleavable peptide described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obtaining specific binding pair member (I) that binds a complementary specific binding pair member of encapsidating specific binding pair member/ribosome complexes in a viral coat, comprises the use of a
                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                              New compounds comprising enzyme cleavable peptide conjugated to antineoplastic agent used as chemotherapeutic agents in targeted treatment of cancers.
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
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                                                                       Huang PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide; 5
15-MAR-2001; 2001WO-US008589
                  15-MAR-2000; 2000US-0189387P
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Best Local Similarity 100.
Matches 3; Conservative
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Han W, Higley CA, Hua
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Synthetic.
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                                                                                                                       The invention comprises a method (ribosome display system) for obtaining a specific binding pair (sbp) member that binds a complementary sbp member of interest. The method involves incubating mRNA molecules encoding an sbp and lacking an in-frame stop codon, allowing ribosome translation of the mRNA to produce the encoded sbp member, forming complexes comprising ribosome, mRNA, and encoded sbp member displayed on the ribosome. The ribosome display system is useful for the selection of an sbp member able to bind a complementary sbp member. The present amino acid sequence represents a mutant VL CDR3 peptide
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Pred. No. 1.8e+06;
0; Mismatches 0;
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                                                      English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Scc.
100.0%; Pre
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                                                         49; 61pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
ribosome display system.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 3; Conservatery
                                                              Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5 AA;
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us-10-074-225a-7.rag

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binds to the isolated polypeptide or peptide is human histidine-proline rich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain or fragment of human or rabbit HPRG, two chain human kininogen (HK), the D5 domain of HK, or a Tpm-binding, two chain human kininogen (HK), the D5 domain of HK, or a Tpm-binding, antiangiogenic homologue, variant, domain or fragment of the HK or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antibodies and compositions are useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease or protein His-Pro (H/P) rich domain repeat fragment.
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Sequence 5 AA;

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Gaps
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                      Indels
       Length 5;
      DB 8; Le
1.8e+06;
                      ö
      Score 21; DB 8; Pred. No. 1.860; Mismatches
91.3%; Scc.
100.0%; Pre
                      Conservative
    Query Match
Best Local Similarity
Matches 3; Conser
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2 2 m g

ADH10422 standard ADH10422 RESULT 16 ADH10422

peptide; 5 AA

(first entry) 11-MAR-2004

HPRG protein H/P rich domain mutated repeat fragment

Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit.

Synthetic

WO2003077872-A2

25-SEP-2003.

17-MAR-2003; 2003WO-US008060

5-MAR-2002; 2002US-0364047P

(ATTE-) ATTENUON LLC.

WPI; 2004-090604/09.

Mazar AP

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Juarez

F,

Donate

저,

Mccrae

New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or

NO 36; 117pp; English. Example 5; SEQ ID

The invention relates to an isolated tropomyosin (Tpm)-related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, 

an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that native Tpm internal fragment. The antiangiogenic polypeptide agent that binds to the isolated polypeptide or peptide is human histidine-proline rich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain or fragment of human or rabbit HPRG, two chain human kininogen (HK), the D5 domain of HK, or a Tpm-binding, antiangiogenic homologue, variant, domain of HK, or a Tpm-binding, antiangiogenic homologue, variant, domain or fragment of the HK or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antibodies and compositions are useful for inhibiting endothelial cell antibodies and compositions are useful for inhibiting endothelial cell apoptosis, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease or peripheral artery disease. The present sequence represents a mutated HPRG protein His-Pro (H/P) rich domain repeat fragment. 

Sequence 5 AA;

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Gaps .; 0 Indels Length 5; Score 21; DB 8; Le Pred. No. 1.8e+06; 0; Mismatches 0; 91.3%; Sc. 100.0%; Pre Query Match Best Local Similarity 100. Matches 3; Conservative

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3 PHG 5

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RESULT 17 ADH10417

ADH10417 standard, peptide; 5 AA.

ADH10417;

(first entry) 11-MAR-2004 Rabbit HPRG protein H/P rich domain repeat fragment.

Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit. 

Oryctolagus cuniculus

WO2003077872-A2

25-SEP-2003.

17-MAR-2003; 2003WO-US008060

2002US-0364047P 15-MAR-2002;

Juarez J, (ATTE-) ATTENUON LLC Donate F, Mccrae K,

Mazar AP

WPI; 2004-090604/09

New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or

Example 5; SEQ ID NO 31; 117pp; English.

The invention relates to an isolated tropomyosin (Tpm)-related

RESULT 19 ADH10416 ð of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for an internal fragment of a native Tpm isoform which is a binding site for cartianglogenic polypeptide agents; The isolated antianglogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antianglogenic polypeptide agents, as does the native Tpm internal fragment. The antianglogenic polypeptide agent that contains to the isolated polypeptide or peptide or peptide agents, as does the native Tpm internal fragment. The antianglogenic polypeptide agents, a Tpm-binding, antianglogenic citch glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antianglogenic rich glycoprotein (HRPG), rabbit HPRG, a Tpm-binding, antianglogenic homologue, variant, domain or fragment of human or rabbit HPRG, two chain commain. The Tpm-related antianglogenic receptor polypeptide or peptide, antianglogenic homologue, variant, domain or fragment of the HK or its DS domain. The Tpm-related antianglogenic receptor polypeptide or peptide, antibodies and compositions are useful for inhibiting endothelial cell apoptosis, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, prosence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased anglogenesis is desired, e.g. coronary artery disease or promoting wound healing, or for treating desease or conditions in which increased anglogenesis is desired, e.g. coronary artery disease. The present sequence represents a repeat fragment present in the rabbit HPRG protein His-Pro (H/P) rich domain. which is a is a fragment New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer. Gaps Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit. ; 0 0; Indels 91.3%; Score 21; DB 8; Length 5; 100.0%; Pred. No. 1.8e+06; protein H/P rich domain repeat fragment Mismatches Mazar AP; receptor polypeptide peptide; 5 AA ; F, Juarez J, 17-MAR-2003; 2003WO-US008060. .5-MAR-2002; 2002US-0364047P (first entry) Conservative Oryctolagus cuniculus. (ATTE-) ATTENUON LLC. WPI; 2004-090604/09. Query Match Best Local Similarity Matches 3; Conserv ADH10415 standard; WO2003077872-A2 S S Sequence 5 AA; 25-SEP-2003 Rabbit HPRG 11-MAR-2004 쏫 ADH10415; m Mccrae ઠે g

The invention relates to an isolated tropomyosin (Tpm)-related
antiangiogenic receptor polypeptide or peptide, which is a is a fragment
of a full-length native Tpm protein expressed on the surface of
endothelial cells, or a variant of the fragment. It has a molecular mass
of about 17 kDa and corresponds in its sequence to, or is a variant of,
an internal fragment of a native Tpm isolated antianglogenic receptor
contianglogenic polypeptide agents; The isolated antianglogenic receptor
continuty of binding to the antianglogenic polypeptide agent is as does the
cotivity of binding to the antianglogenic polypeptide agent that
contive Tpm internal fragment. The antianglogenic polypeptide agent that
continuty Tpm internal fragment. The antianglogenic polypeptide agent that
continue to the isolated polypeptide or peptide is human histidine-proline
continue to the isolated polypeptide or peptide is human histidine-proline
continue to the isolated polypeptide or peptide is human histidine-proline
continue the isolated polypeptide or peptide is human histidine-proline
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continue the DS domain of the Treating domesis, or concer, diabetic
continue the DS domain of the Treating disease or conditions
continue the DS domain of the PS domain His-Pro (H/P) rich domain.

Continue the DS domain of the HE addit ö Tpm; tropomyosin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit. . 0 Indels Length 5; Rabbit HPRG protein H/P rich domain repeat fragment. 91.3%; Score 21; DB 8; Le 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Mazar AP; Example 5; SEQ ID NO 29; 117pp; English ADH10416 standard; peptide; 5 AA. Juarez J, 17-MAR-2003; 2003WO-US008060 15-MAR-2002; 2002US-0364047P (first entry) Query Match Best Local Similarity 10u. Oryctolagus cuniculus. (ATTE-) ATTENUON LLC Donate F, WPI; 2004-090604/09. WO2003077872-A2. 3 PHG 5 S Sequence 5 AA; 11-MAR-2004 25-SEP-2003 Accrae K, ADH10416;

17-MAR-2003; 2003WO-US008060 15-MAR-2002; 2002US-0364047P

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The invention relates to an isolated tropomyosin (Tpm) related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that binds to the isolated polypeptide or peptide is human histidine-proline crich glycoprotein (HRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain or fragment of human or rabbit HPRG, two chain the Tpm related antiangiogenic receptor polypeptide or peptide or peptide antiangiogenic homologue, variant, domain or fragment of the HR or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antiangiogenic homologue, variant, domain or fragment of the HR or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antiangiogenic homologue, variant, domain or for inducing antiangiogenic receptor polypeptide or peptide, antibodies and compositions are useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, for inducing endothelial cell apoptosis, or for treating tumours or cancer, diabetic rethopathy, neovascular glaucoma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease or peripheral artery disease. The present sequence represents a repeat fragment present in the rabbit HBRG protein His-Produced angiogenesis is desired e.g. coronary artery disease.
New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer.
                                                                                                                                                                        NO 30; 117pp; English
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ö Gaps ; 0 0; Indels 91.3%; Score 21; DB 8; Length 5; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels peptide; 5 AA Conservative Similarity 3; Conserv RESULT 20 ADH10418 ID ADH10418 standard; PHG \_H \_\_ Query Match Best Local S: Matches 3, ADH10418; ന ന 셤 ઠે

Tpm; tropomyogin; antiangiogenic receptor; histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic; ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit. ich domain consensus repeat fragment Key Location/Qualifiers Misc-difference 1 /label= His or Pro Misc-difference 2 /label= His or Pro entry) cuniculus. protein H/P WO2003077872-A2 Oryctolagus con Homo sapiens. 11-MAR-2004 Synthetic HPRG 

gene typing; polymorphic microsatellite loci; PML; disease; disease predisposition; microsatellite marker; prion disease; cystic fibrosis; malignant hyperthermia syndrome; metabolic disease; milk protein; hormone; transcription factor; pT7-blue-vector; sheep; microsatellite.

Sheep prion protein motif #3.

29-JUL-2004

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The invention relates to an isolated tropomyosin (Tpm)-related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of adouthelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that binds to the isolated polypeptide or peptide is human histidine-prollne rich glycoprotein (HRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain of fragment of the HR or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antiangiogenic homologue, variant, domain of fragment of the HR or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antiangiogenic homologue, variant, domain or for inhibiting endothelial cell apoptosis, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, proper peripheral artery disease. The present sequence represents a consensus repart fragment in the rabbit and human HPRG protein His-Pro
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                                                                                                                                                                                                            New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
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                                                                                                                                           Mazar AP
                                                                                                                                                                                                                                                                                                   Example 5; SEQ ID NO 32; 117pp; English.
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100.0%; Pre
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                                                                                                                                          Juarez J,
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Matches
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                                                                                                                                                                                                                                              The invention describes a method of typing (M1) a gene (I) that has one or more polymorphic microsatellite loci (PML). The method comprises: PCR amplification of at least one DNA region of (I) that includes PML, using as template a DNA sample containing at least one segment of (I); and determining the length of the resulting amplicon(8). Also described are: a method of determining (M2) microsatellite markers (MM) for predisposition to a disease, associated with a gene that includes one or more PML; and prediagnosis (M3) of diseases associated with gene that include PML. The method is used to identify microsatellite markers, in a disease-related gene, that are associated with a predisposition to diseases and for prediagnosis of such diseases, especially prion diseases but also cystic fibrosis, malignant hyperthermia syndrome in pigs and metabolic diseases; also to type genes that encode milk proteins, hormones or transcription factors. The method is simpler, quicker and
                                                                                                                                                                                                                                                                                                                                                                                                     expensive than known methods based on sequencing. This sequence of a sheep prion protein motif.
                                                                                                                                                                                  microsatellite loci, useful for , by amplification and determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ligand; identification; drug target; cancer; cardiovascular disease; autoimmune disease; infection; inflammatory disease; central nervous system disorder; metabolic disease; endocrine disease; membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                 Typing genes that contain polymorphic n identifying predisposition to disease, length of amplicons.
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                                                                                                                                                                                                                             Disclosure; Page 9; 64pp; German
                                                                                                                                         Han Y;
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                                                                         09-AUG-2002; 2002DE-01036711.
                                                                                              2002DE-01036711
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                                                                                                                  (UYHO-) UNIV HOHENHEIM
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                                                                                                                                                              WPI; 2004-215730/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADR03627 standard;
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Modified-site
                              DE10236711-A1
                                                                                             09-AUG-2002;
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                                                   26-FEB-2004
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ADR03627
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The present invention relates to a method (M1) for identifying specific members of an unknown protein-ligand binding pair. The method involves synthesizing an immobilized ligand library, incubating the library with differentially labelled protein mixtures, detecting the immobilized ligand-protein pair and identifying the protein and ligand of the pair. The identified ligand and protein are specific members of an unknown differential ligand-protein binding pair. (M1) is rapid and efficient, highly accurate and is able to take a large number of unknown ligands and/or unknown proteins. (M1) is used for identifying proteins suitable as drug targets, to identify one or more drugs for treating clinical conditions such as cancer, cardiovascular diseases, autoimmune diseases, inflammatory diseases, central nervous system disorders, metabolic disease and endocrine diseases. The present sequence is a peptide ligand used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying members of protein-ligand binding pair useful as drug target, by incubating immobilized ligand library with differentially labeled protein, detecting ligand-protein pair, identifying protein and ligand of
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                                                                                                                                                                                                                                                                                                        Wenckens M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 33; SEQ ID NO 64; 172pp; English.
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2003DK-00000749
                                                                  16-JAN-2004; 2004WO-DK000023
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                                                                                                                              16-JAN-2003;
19-MAY-2003;
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29-JUL-2004.
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The invention relates to methods for selecting and identifying a cellular receptor for a virus, by immobilising, on a support, a monoclonal antibody targeted to a viral surface protein that determines attachment of the virus to the receptor. The immobilised antibody is incubated with a hexapeptide expression library and peptides bound to the immobilised antibody are eluted by competitive binding with recombinant fragments of the viral surface protein. In a reverse method, the viral surface protein is immobilised and incubated with the peptide library. In this case, the bound peptides are eluted by competitive binding with the monoclonal antibody. The hexapeptides AAW75361-W75375 represent peptides isolated by biopanning the library with an immobilised adenovirus type 5 fibre head protein and eluted using a monoclonal antibody (MAb) 7A2.7. The methods are used to identify peptides from MHC Class I and/or type III

Chibronectin proteins that allow or facilitate attachment by adenovirus that modulate Ad infection mediated by these peptides, e.g. to treat or prevent Ad infections or to facilitate infection by Ad gene therapy vertures used to treat genetic diseases, acquired immune deficiency
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                                                                           Use of peptide(s) for facilitating or modulating attachment of adenovirus to cells - useful for, e.g. treating or preventing infection and improving uptake of gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellular receptor; virus; immobilisation; monoclonal antibody; fibre; viral surface protein; hexapeptide expression library; adenovirus; major histocompatibility complex; MHC; fibronectin; gene therapy; genetic disease; acquired immune deficiency syndrome; AIDS; cancer.
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                                                                                                                                                    Example 3; Fig 2(a); 48pp; French
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                  Karayan
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(first entry)
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                 SS,
                                                WPI; 1998-416458/36.
                 Hong
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                 Boulanger P,
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02-FEB-1999
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AAW75302
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The invention relates to methods for selecting and identifying a cellular receptor for a virus, by immobilising, on a support, a monoclonal antibody targeted to a viral surface protein that determines attachment of the virus to the receptor. The immobilised antibody is incubated with a hexapeptide expression library and peptides bound to the immobilised antibody are eluted by competitive binding with recombinant fragments of the viral surface protein. In a reverse method, the viral surface protein is immobilised and incubated with the peptide library. In this case, the bound peptides are eluted by competitive binding with the monoclonal antibody. The hexapeptides AAW75293-W75307 represent peptides isolated by biopanning the library with an immobilised adenovirus type 5 fibre head protein and eluted using a monoclonal antibody (MAb) 7A2.7. The methods are used to identify peptides from MHC Class I and/or type III

Can induste Ad infection mediated by these peptides, e.g. to treat or prevent Ad infections or to facilitate infection by Ad gene therapy vectors used to treat genetic diseases, acquired immune deficiency syndrome or cancer. (Updated on 25-MAR-2003 to correct PF field.)
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                on and identification of cellular receptors for viruses - used to attachment and entry of adenovirus into cells, e.g. for treating
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                                                                                      Example 3; Fig 2(a); 43pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%; SC.
100.0%; Pre
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                                                  infection or in gene therapy
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Best Local Similarity 100.
Matches 3; Conservative
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The present invention describes a purified elastase variant (I) with an amino acid sequence different from that of a precursor elastase, the difference comprising a substitution of an active site histidine residue corresponding to residue 43 in human neutrophil elastase with a different amino acid residue so that (I) has substrate specificity substantially different from the precursor elastase. (I) has cytostatic activity, and can be used in antibody-directed enzyme activated prodrug therapy. The elastase variant can be used to cleave a particular substrate, especially those containing histidine residues at the substrate site. Site-specific proteolysis is useful in therapeutic applications, e.g. for antibodydirected enzyme activated prodrug therapy (ADEPT). AAC88022, AAC88023 and AABS5543 to AABS5526 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to conjugates of integrin receptor antagonist and a cytostatic agent with cleavable linking unit that are selectively cleaved by tumour cell metallo matrix proteases (MMPs). The conjugates of the invention may have cytostatic activity and may be used as an integrin alpha_vbeta_3 receptor antagonist or a tumour growth inhibitor. The conjugates of the invention may be used in the production of a medicament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New conjugates of integrin receptor antagonist and a cytostatic agent with specific cleavable linking unit useful in the treatment of cancer
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                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                        Score 21; DB 4; Le Pred. No. 1.8e+06; 0; Mismatches 0;
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6
/label= OTHER
/note= "Bound to Camp
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                                                                                                                                                                                                                                                                                                      Similarity
3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG31535 standard;
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Modified-site
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             containing the conjugates of the invention exhibit a selective and tumour specific action as a result of linkage to alpha vbeta 3 integrin antagonists via linking units which can be selectively cleaved by enzymes such as metallo matrix proteases, i.e. enzymes found in tumour tissue. The linking units can also maintain the serum stability of the conjugate of cytostatic and alpha vbeta 3 integrin antagonist, and at the same time, show the desired intracellular action within tumour cells as a result of its specific enzymatic and hydrolytic cleavability with release of the cytostatic. The present sequence represents a camptothecin-bistrifluoroacetate conjugated peptide used in an example of the method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of screening for compounds for promoting wakefulness or sleep in a mammal. The method involves administering a prolactin releasing peptide (PrRP) receptor (GPR10) agonist or antagonist respectively and determining the ability of the compound to promote wakefulness or sleep. The compounds identified from the method are used in the therapy of epilepsy and other diseases associated with absence seizures and in promoting wakefulness and sleep in individuals having sleep disorders such as insomnia and narcolepsy. PrRP receptor agonists may be used to treat common disorders which lead
Compounds of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Screening for compounds useful for promoting wakefulness or sleep, and for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep apnea, comprises administering a prolactin releasing peptide agonist or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; wakefulness; sleep disorder; prolactin releasing peptide recept PrRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea; insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure; anticonvulsant; mutant; mutein.
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100.0%; Pred. No. 1.8e+06;
ive 0; Mismatches 0;
   treatment of carcinomatous disorders.
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Matches 3; Conserv
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                                                                                                                                                                                                                                                        Sequence 6 AA;
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Sequence 6 AA;

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to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and psychogenic hypersomnia. PrRP receptor antagonists are useful for promoting sleep and for treating insomnia such as adjustment sleep disorder and psychophysiologic insomnia. The present sequence is human GPR10 mutant C-terminal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therefore reducing the side-effects associated with the use of such drugs. The present sequence represents a camptothecin peptide conjugate, which is used in an example from the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "N-terminally modified with 20-0-" 6
//note= "C-terminally modified with -camptothecin TFA"
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  peptide conjugate; cytostatic; glycoconjugate; tumour; cleavable peptidic linking unit; cancer.
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                                                                                                                                               Indels
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                                                                                                                 Score 21; DB ;; Pred. No. 1.8 0; Mismatches
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linking units so as
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100.0%; Pr
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                                                                                                                                                                                                                                                                               ABP53526 standard;
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cleavable peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                             Brain-occurring ubiquitin-specific protease and encoded DNA, applicable in studying molecular mechanism of expression neuroplasticity and pathosis of neurodegeneration.
                        Gaps
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100.0%; Pred. No. 1.8e+06;
:ive 0; Mismatches 0;
 91.3%; Score 21; DB 100.0%; Pred. No. 1.8 ive 0; Mismatches
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                        Conservative
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polypeptide-tagged collecti
pharmaceutical; diagnostic
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  WPI; 2004-376185/35
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                                                                                                                                                                   Evenly distributing tags among members of a starting library, useful developing pharmaceuticals and diagnostics, comprises dividing the starting library into sub libraries and attaching a tag to members of each sub library.
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 collection; capture system; tagged polypeptide
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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Best Local Similarity
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   useful in
Evenly distributing tags among members of a starting library, useful developing pharmaceuticals and diagnostics, comprises dividing the starting library into sub libraries and attaching a tag to members of
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
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                                                                                                                                                                   collection; capture system; tagged polypeptide;
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                                                                                                                                                   the invention SEQ ID NO:240
          Length 6;
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                  red. No. 1.8e+06;
Mismatches 0;
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          DB 8;
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         Score 21;
Pred. No.
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                                                                                                                                                                                                                                            30-OCT-2003; 2003WO-US034821
                                                                                                  peptide;
Query Match
Best Local Similarity 100.v
~ hes 3; Conservative
                                                                                                                                                                           agnostic
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                  polypeptide-tagged
pharmaceutical; di
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                                                                                                  ADO37180 standard;
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                                         3 PHG 5
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                                                                                                                                                                                            Synthetic
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ADO37698
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The invention relates to novel methods for producing polypeptide-tagged collections and capture systems containing the tagged polypeptides. The method is useful for evenly distributing tags among members of a starting library. The system, collection, kits and methods are useful in developing pharmaceuticals and diagnostics. The present sequence is used in the exemplification of the invention.
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pharmaceutical; diagnostic.
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100.0%; Pred. No. 1.8e+06;
tive 0; Mismatches 0;
    capture system;
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polypeptide-tagged collect:
pharmaceutical; diagnostic
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The biological particles are

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acid, liposomes and other micellar agents.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Capturing biological particles, by contacting biological particles with capture system comprising addressed loci, addressed collection of polypeptide tagged molecules, capture agents, and polypeptide tag to which capture agent binds.
                                             developing pharmaceuticals among members of a starting library, useful state oping pharmaceuticals and diagnostics, comprises dividing the starting library into sub libraries and attaching a tag to members of each sub library.
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                    WPI; 2004-376185/35.
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cells chosen from immune cells, neurons, cancer cells, bacterial cells and infected cells, subcellular compartment, organelles, viral particles or pathogens. The cells are dendritic cells, T cells, or B cells. The method is also useful for identifying molecules that interact with infectious agents, for profiling the surface of a biological particle, for identifying molecules that modulates the biological particle, for identifying molecules that modulates the considerable in the biological particle, and for mapping epitopes of molecules displayed on the surface of a biological particles. The method is also useful for sorting biological particles, for identifying a receptor on the surface of biological particle that transduces a signal from a polypeptide, and for molecule that interacts with an apically-localized molecule on a biological particle. The present sequence was used to illustrate the invention.
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100.0%; Pred. No. 1.8e+06;
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cells chosen from immune cells, neurons, cancer cells, bacterial cells and infected cells, subcellular compartment, organelles, viral particles cor pathogens. The cells are dendritic cells, T cells, or B cells. The cethod is also useful for identifying molecules that interact with infectious agents, for profiling the surface of a biological particles, for identifying molecules that modulates the corresponding in the biological particle, for identifying molecules that modulates the cafficking, activity or functional or structural property in the biological particle, and for mapping epitopes of molecules displayed on the surface of a biological particles. The method is also useful for sorting biological particles, for identifying a receptor on the surface of biological particles, for identifying a receptor on the surface of biological particles. The method is also useful for sorting biological particles, for identifying a receptor on the surface of biological particle that transduces a signal from a polypeptide, and molecule on a biological particle. The present sequence was used to illustrate the invention.
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Ä Sequence 6

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                   Indels
  Length 6;
 Score 21; DB 8; Le; Pred. No. 1.8e+06; 0; Mismatches 0;
91.3%; SCO
y 100.0%; P:
rvative 0;
Query Match
Best Local Similarity
Matches 3; Conser
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peptide; 6 AA ADO28426 standard; 12-AUG-2004 AD028426 AD028426

system related peptide, SEQ ID 964 (first entry) Capture 

Capture system

Synthetic

WO2004042019-A2

30-OCT-2003; 2003WO-US034693 21-MAY-2004

30-OCT-2002; 2002US-0422923P.

(POIN-) POINTILLISTE INC.

Jesaitis L, Atkinson B, Ault-Riche D,

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Sperinde

Kumble KD,

WPI; 2004-431543/40.

particles with 50 Capturing biological particles, by contacting biological particles capture system comprising addressed loci, addressed collection of polypeptide tagged molecules, capture agents, and polypeptide tag which capture agent binds.

NO 964; SOSpp; English Disclosure; SEQ ID The present invention relates to a method for the capture and analysis of biological particle using a capture system. The method is useful for capturing biological particles such as cells, portions of cells, cell membranes, viruses, viral capsids, viral particles, bacterial cells, subcellular compartments, organelles and micelles, prokaryotic cells, eukaryotic cells, intracellular particles, nuclei, cell membranes, cell membrane fragments, nuclear membranes fragments, viral vectors or viral capsids with or without packaged nucleic acid, phage, phage vectors, phage capsids with or without encapsulated nucleotide

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cells chosen from immune cells, neurons, cancer cells, bacterial cells and infected cells, subcellular compartment, cancer cells, bacterial cells or pathogens. The cells are dendritic cells, T cells, or B cells. The interact with infectious agents, for identifying molecules that interact with infectious agents, for profiling the surface of a biological particle, for identifying molecules that modulates the biological particle, for identifying molecules that modulates the trafficking, activity or functional or structural property in the biological particle, and for mapping epitopes of molecules displayed on the surface of a biological particles. The method is also useful for sorting biological particles, for identifying a receptor on the surface of biological particles, for identifying a receptor on the surface of biological particle that transduces a signal from a polypeptide, and for identifying the molecule that interacts with an apically-localized molecule on a biological particle. The present sequence was used to
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The biological particles
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llarity 100.0%; Pred. No. 1.8e+06;
Conservative 0; Mismatches 0;
   agenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     system related peptide, SEQ ID 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 232; 505pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jesaitis L,
 liposomes and other micellar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO27694 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-OCT-2003; 2003WO-US034693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-2002; 2002US-0422923P. 30-OCT-2002; 2002US-0423018P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atkinson B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POIN-) POINTILLISTE INC.
                                                                                                                                                                                                                                                                                               illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-431543/40.
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004042019-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capture system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-AUG-2004
                                                                                                                                                                                                                                                                                                                                        Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADO27694;
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acid, liposomes and other micellar agents. The biological particles are cells chosen from immune cells, neurons, cancer cells, bacterial cells and infected cells, subcellular compartment, organelles, viral particles or pathogens. The cells are dendritic cells, T cells, or B cells. The method is also useful for identifying molecules that interact with infectious agents, for profiling the surface of a biological particles, for identifying molecules that modulates the biological particle, for identifying molecules that modulates the trafficking, activity or functional or structural property in the biological particle, for identifying a receptor on the surface of a biological particles. The method is also useful for sorting biological particles, for identifying a receptor on the surface of biological particles, for identifying a receptor on the surface of biological particle that transduces a signal from a polypeptide, and for identifying the molecule that interacts with an apically-localized molecule on a biological particle. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             illustrate the invention
          $$$$$$$$$$$$$$$$$$$$$$$$$
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Sequence 6 AA;

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0
                0; Indels
 Length 6;
 Score 21; DB 8; I
Pred. No. 1.8e+06;
                Mismatches
                ö
                 Conservative
Query Match
Best Local Similarity
Matches 3; Conser
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Gaps

standard; ADO27702; AD027702 RESULT 40 AD027702 

peptide; 6 AA.

Capture system related peptide, entry (first 12-AUG-2004

SEQ ID 240

Capture

Synthetic

21-MAY-2004

WO2004042019-A2

30-OCT-2003; 2003WO-US034693 30-OCT-2002; 2002US-0422923P.

(POIN-) POINTILLISTE INC.

Sperinde Kumble KD, Jesaitis L, Ault-Riche D, Atkinson B,

WPI; 2004-431543/40.

Capturing biological particles, by contacting biological particles with capture system comprising addressed loci, addressed collection of polypeptide tagged molecules, capture agents, and polypeptide tag to which capture agent binds.

NO 240; 505pp; English Disclosure; SEQ ID

The present invention relates to a method for the capture and analysis of biological particle using a capture system. The method is useful for capturing biological particles such as cells, portions of cells, cell membranes, viruses, viral capsids, viral particles, bacterial cells, subcellular compartments, organelles and micelles, prokaryotic cells, eukaryotic cells, intracellular particles, nuclei, cell membranes, cell membrane fragments, nuclear membranes fragments, viral vectors or viral capsids with or without packaged nucleic acid, phage, phage vectors, phage capsids with or without encapsulated nucleotide

acid, liposomes and other micellar agents. The biological particles are cells chosen from immune cells, neurons, cancer cells, bacterial cells and infected cells, subcellular compartment, organelles, viral particles or pathogens. The cells are dendritic cells, T cells, or B cells. The method is also useful for identifying molecules that interact with infectious agents, for profiling the surface of a biological particle, for identifying molecules that modulates the biological particle, for identifying molecules that modulates the crafficking, activity or functional or structural property in the biological particle, and for mapping epitopes of molecules displayed on the surface of a biological particles. The method is also useful for sorting biological particles, for identifying a receptor on the surface of biological particles, for identifying a receptor on the surface of biological particle that transduces a signal from a polypeptide, and confidentifying the molecule that interacts with an apically-localized molecule on a biological particle. The present sequence was used to illustrate the confidential particle. The present sequence was used to also a signal from a biological particle. The present sequence was used to also and also an illustrate the invention 

Sequence 6 AA;

. 0 Length 6; Score 21; DB 8; I Pred. No. 1.8e+06; 0; Mismatches 0; ; 0 91.3%; Similarity 100 3; Conservative Query Match Best Local S Matches 3

PHG 5 ઠ Search completed: June 15, 2005, 14:15:45 Job time : 94 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

June 15 Run on:

, 2005, 14:06:20 ; Search time 23.5 Seconds (without alignments) 15.883 Million cell updates/sec

US-10-074-225A-7 23 1 XXPHG 5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

513545 segs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Patents AA:\* Issued Database :

1: /cgn2 6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2 6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	12,	12,	12,	Sequence 64, Appl Darent No. 5217869		'n	Sequence 5, Appli	7	Sequence 11, Appl	12,	12,	13,	13,	2, 4		12	Sequence 1, Appli	13	10	124,	125, 7	140,	144,	102,	124,	125,
ID	US-07-729-099-12	US-08-257-392-12	US-U8-770-035-12	US-10-122-246A-64 4217869-49	5217869-59	US-09-095-407-3	US-09-560-915-5	US-09-155-613A-71	PCT-US95-04567-11	US-08-776-265-12	US-09-398-184-12	US-08-405-647B-13	US-08-985-499-13	US-09-125-099-2	US-09-239-043D-1149	US-09-239-043D-1209	US-09-112-956-1	PCT-US96-03180-13	US-09-510-738A-102	US-09-510-738A-124	US-09-510-738A-125	US-09-510-738A-140	US-09-510-738A-144	US-09-861-966-102	US-09-861-966-124	US-09-861-966-125
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Sequence 140, App	Sequence 144, App	Sequence 1128, Ap	Sequence 1667, Ap	Sequence 13, Appl	Sequence 102, App	Sequence 124, App	Sequence 125, App		Sequence 144, App	Sequence 10, Appl	Sequence 11, Appl	Sequence 13, Appl	Seguence 92, Appl	Sequence 56, Appl	14,	3, 8	e,	
US-09-861-966-140	US-09-861-966-144	US-09-239-043D-1128	US-09-239-043D-1667	US-09-870-089B-13	US-09-919-048-102	US-09-919-048-124	US-09-919-048-125	US-09-919-048-140	US-09-919-048-144	US-08-049-511-10	US-08-049-511-11	US-08-049-511-13	US-08-556-597-92	US-08-318-856A-56	US-09-043-930-14	US-09-258-689-3	US-09-195-379-3	
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91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	
21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	
28	29	30	31	32	33	34	35	36		38	39	40	41	42	43	44	45	

### ALIGNMENTS

```
Length 5;
       US-07-729-099-12

Sequence 12, Application US/07729099

Patent No. 5403581

GENERAL INFORMATION:

APPLICANT: Binger, Mary-Helen

APPLICANT: Basamontes, Luis

TITLE OF INVENTION: Coccidiosis Vaccines

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSE: Hoffmann-La Roche Inc.

STREET: 340 Kingsland Street

CITY: Nutley

STATE: New Jersey

COUNTRY: U.S.

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM PC Compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/729,099

FILING DATE: 19910712

CLASSIFCATION: 424

FILING DATE: TUDDAMATION: ACTANT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.3%; Score 21; DB 1; Le Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATORNEY/AGENT TEATON:
ATTORNEY/AGENT TEACHERINE ROBEMAN, CACHERINE REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eimeria tenella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
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US-07-729-099-12
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RESULT 1
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S-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-249A-94

US-10-122-246A

US-10-122-246A

US-10-12-246A

US-10-12-2
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                       ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,035
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/729,099
FILING DATE:
APPLICATION NUMBER: 34,240
FILING DATE:
NAME: ROSEMAN INFORMATION:
NAME: ROSEMAN (Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8514
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1335-6208
TELEFRAX: (201) 235-6208
TELEFRAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 91.3%; Score 21; DB 3; Louset Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eimeria tenella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
HYPOTHETICAL: YES
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Eimeria tenel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHG 5
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                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Binger, Mary-Helen
APPLICANT: Binger, Mary-Helen
APPLICANT: Binger, Luis
TITLE OF INVENTION: Coccidiosis Vaccines
CORRESPONDENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Hoffmann-La Roche Inc.
CITY: Nutley
STREET: 340 Kingsland Street
CITY: Nutley
STREET: Bow Jersey
COUNTRY: U.S.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREST APPLICATION DATA:
APPLICATION NUMBER: US/08/257,392
FILING DATE: 09-JUN-1994
CLASSIFICATION ATA:
APPLICATION NUMBER: US 07/729,099
FILING DATE: 12-JUL-1991
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,240
FILING DATE: 12-JUL-1991
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (201) 235-6208
TELEPHONE: (201) 235-6208
TELEPHONE: (201) 235-6208
TELEPHONE: (201) 235-6208
TELEPHONE: CANARICERISTICS:
LENGTH: 5 amino acid
TOPPLOCY: Innear

WANTER WANTER TYPE: neoctide
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US-08-770-035-12
; Sequence 12, Application US/08770035
; Patent No. 6008342
; GENERAL INFORMATION:
; APPLICANT: Binger, Mary-Helen
APPLICANT: Pasamontes, Luis
; TILLE OF INVENTION: Coccidiosis Vaccines
NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
                                                                                     RESULT 2
US-08-257-392-12
; Sequence 12, Application US/08257392
; Patent No. 5688513
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eimeria tenella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: YES FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
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US-08-257-392-12
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7. 4.1e+05;
0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
5217869-59
;Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
                                                                                                                                                                                                                                 RESULT 5
5217869-59
;Patent No. 5217869
; APPLICANT: KAUVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
                                                                                                                             DB 4; Le
4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
4-fluorophenylalanine
                                                                                                                             Score 21; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-09-095-407-3
; Sequence 3, Application US/09095407
; Patent No. 6124137
; GENERAL INFORMATION:
; APPLICANT: Hutchens, T. William
Yip, Tai-Tung
                                                                                                                                                                                                                                                                                                      | NUMBER OF SEQUENCES: 121
| CURRENT APPLICATION DATA:
| APPLICATION NUMBER: US/07/255,906
| FILING DATE: 11-OCT-1988
| SEQ ID NO:59:
| LENGTH: 5
| 5217869-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 121
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/255,906
FILING DATE: 11-OCT-1988
                                                                                          AMIDATION
                                                                                                                          Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
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       FEATURE:
NAME/KEY: MOD RES
LOCATION: (2)...(2)
OTHER INFORMATION: 4
FEATURE:
NAME/KEY: MOD RES
LOCATION: (5)...(5)
OTHER INFORMATION: A
US-10-122-246A-64
OTHER INFORMATION:
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Use of a Polypeptide as Cell Receptor for Adenoviruses
51-036
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    DB 3; Length 6;
4.1e+05;
hes 0; Indels
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GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: DIHYDROPYRIMIDINE DEHYDROGENASE

TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Housen

STATE: Texas

COUNTRY: United States of America

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Date of America

ZIP: 77210

COMPUTER: BM PC compatible

SOFTWARE: PatentIn Release #1.0, Version
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100.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 0;
  Score 21; DB:
Pred. No. 4.10; Mismatches
                                                                                                                                                                                                                                                                               RESULT 9
US-09-155-613A-71
Sequence 71, Application US/09155613A
Patent No. 6420120
GENERAL INFORMATION:
APPLICANT: Boulanger, Pierre
APPLICANT: Hong, Saw See
TITLE OF INVENTION: Use of a Polypeptide as Contract of INVENTION OF STATION NUMBER: PRIOR FILING DATE: 1998-09-09
PRIOR FILING DATE: 1997-09-09
PRIOR FILING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 71
LENGTH: 6
THENGTH: 
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04567
TOTAL NATE: CONCURRENTLY HEREWITH
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Query Match
Best Local Similarity 100.
Matches 3; Conservative
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3; Conservative
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CLASSIFICATION:
PRIOR APPLICATION
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PCT-US95-04567-11
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Matches 3
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APPLICATION NUMBER: US 08/27/357

APPLICATION NUMBER: US 08/27/357

APPLICATION NUMBER: US 08/27/357

APPLICATION NUMBER: US 08/27/357

FREEFRONG NUMBER: US 08/27/357

FREEFRONG NUMBER: US 08/27/37

FREEFRONG NUMBER:
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FERRERO, Lucia
TITLE OF INVENTION: No. 6649394el Topoisomerase IV, Corre
                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett Dunner, L.L.P.
STREET: 1300 I. Street, N.W., Suite 700
CITY: Washington
                                                   0; Indels
                          Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 03806.0394-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                          DB 3; Le
4.1e+05;
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100.0%; Pred. No. 4.1e+05;
iive 0; Mismatches 0;
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Pred. No. 4.16
0; Mismatches
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IPTION: SEQ ID NO: 12:
                                                                                                                              RESULT 12
US-09-398-184-12
; Sequence 12, Application US/09398184
; Patent No. 6649394
; GENERAL INFORMATION:
; APPLICANT: BLANCHE, Francis
; APPLICANT: CAMERON, Beatrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on US/08405647B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 408-4444
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acru
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTERISTICS
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                      Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
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JULE TYPE:
SNCE DESCRI
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US-08-405-647B-13
; Sequence 13, Applicati
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SEQUENCE
US-09-398-184-12
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US-08-776-265-12
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GENERAL INFORMATION:
APPLICANT: Sherman, Irwin W.
APPLICANT: Crandall, Ian E.
APPLICANT: Sholet, Stephen B.
APPLICANT: Thevenin, Bernard Jean-Marie
TITLE OF INVENTION: Compositions and Methods for Reducing
TITLE OF INVENTION: Adhesiveness of Defective Red Blood Cells
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/08985499;
Patent No. 6191103;
GENERAL INFORMATION:
APPLICANT: Shohet, Stephen B.
APPLICANT: Sherman, Irwin
TITLE OF INVENTION: Mammal
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OOPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,647B
FILING DATE: 17-MAR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 02307E-068700US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
TENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.1e+05;
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Mismatches
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ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

"MOTTER: IBM PC compatible

"""TEM: PC-DOS/MS-DOS
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-405-6478-13
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Best Local Similarity
Matches 3; Conserv
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US-08-985-499-13
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VARIANTS OF THYMIDINE KINASE, RELATED NUCLEIC ACIDS
SEQUENCES AND THEIR USE IN GENIC THERAPY
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нея 0; Indels
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100.0%; Pred. No. 4.1e+05
iive 0; Mismatches (
                                                                ATTORNEY AGENT INFORMATION:

NAME: Hyman, Laurence J.

REGISTRATION NUMBER: 35,551

REFERENCE/DOCKET NUMBER: 02307E-084500US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09125099A; Sequence 2, Application US/09125099A; Batent No. 6207150; GENERAL INFORMATION: APPLICANT: CROUZET, Joel APPLICANT: CROUZET, Michel APPLICANT: COUDER, Michel APPLICANT: COUDER, Michel APPLICANT: CAMERON, Beatrice TITLE OF INVENTION: VARIANTS OF THYMIDINE KIN. TITLE OF INVENTION: VARIANTS OF THYMIDINE KIN. FILLE REFERENCE: ST96010-US; CURRENT APPLICATION NUMBER: US/09/125,099A; CURRENT APPLICATION NUMBER: PCT/FR97/00193; EARLIER FILING DATE: 1996-02-09; EARLIER FILING DATE: 1996-02-09; EARLIER FILING DATE: 1996-08-01; NUMBER OF SEQ ID NOS: 12. SOFTWARE: Patentin Ver. 2.0
            APPLICATION NUMBER: US/08/985,499
FILING DATE: 05-DEC-1997
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1149, Application US/09239043D; Patent No. 6689363; GENERAL INFORMATION: APPLICANT: Sette, Alessandro; APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: herpes simplex virus 7 US-09-125-099-2
                                                                                                                                                                                                                                                                                                                                                                   91.3%;
100.0%;
CURRENT APPLICATION DATA:
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Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                ptide
                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity
Matches 3; Conser
                                                                                                                                                                                                                                                        TYPE: amino & STRANDEDNESS:
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US-09-239-043D-1149
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US-09-125-099-2
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APPLICANT: Cells, Esteu...
APPLICANT: Kibo, Ralph T.
APPLICANT: Kibo, Ralph T.
APPLICANT: Grey, Moward M.
APPLICANT: Grey, Moward M.
APPLICANT: Grey, Moward M.
APPLICANT: Orey, Moward M.
APPLICANT: Chemin to Bindunch Inc.
ITILE OF INVERTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCS: 2060.006007
CURRENT FILING DATE: 1990-10-127
PRIOR PILING DATE: 1990-10-127
PRIOR PILING DATE: 1990-10-127
PRIOR PILING DATE: 1997-00-127
PRIOR PILING DATE: 1997-00-127
PRIOR PILING DATE: 1997-00-136
PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR PILING DATE: 1997-00-1360
PRIOR APPLICATION NUMBER: US 08/461,603
PRIOR APPLICATION NUMBER: US 08/44,610
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR PRIOR DATE: 1994-03-04
PRIOR PRIOR PRIOR DATE: 1994-03-04
PRIOR PRIOR DATE: 1994-03-04
PRIOR PRIOR DATE: 1994-03-04
PRIOR PRIOR DATE: 1994-03-04
PRIOR P
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US-09-239-043D-1209

Sequence 1209, Application US/09239043D

Sequence 1209, Application US/09239043D

Sequence 1209, Application US/09239043D

BENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Southwood, Scott
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph T.
APPLICANT: Chesnut, Robert
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
APPLICANT: TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
CURRENT FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-11-10
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Best Local Similarity
Matches 3; Conserv
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US-09-112-956-1
; Sequence 1, Application US/09112956
; Patent No. 6750025
; GENERAL INFORMATION:
; APPLICANT: Hammond, David
; APPLICANT: Medina, Emma
; TITLE OF INVENTION: A NOVEL METHOD OF DETECTING AND ISOLATING PRION
; TITLE OF INVENTION: DIAGNOSING AND TREATING PRION DISEASES
; FILE REFERENCE: 92053/26
; CURRENT APPLICATION NUMBER: US/09/112,956
; CURRENT FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PATENTIN Version 3.0
; SEQ ID NO 1
; LENGTH: 8
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PRIOR APPLICATION NUMBER: US 08/978,291
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-11-25
PRIOR APPLICATION NUMBER: US 08/820,360
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1996-05
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-11-23
PRIOR FILING DATE: 1994-11-23
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-02-16
PRIOR FILING DATE: 1994-02-16
PRIOR FILING DATE: 1994-02-16
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-02-16
PRIOR FILING DATE: 1994-03-04
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GENERAL INFORMATION:
APPLICANT: The Regents of the University
APPLICANT: of California
TITLE OF INVENTION: COMPOSITIONS AND METR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-112-956-1
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Best Local Similarity
Matches 3; Conser
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PCT-US96-03180-13
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TYPE: PRT
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Best Local S
Matches 3
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RESULT 20
US-09-510-738A-102
; Sequence 102, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,738A
; CURRENT FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 09/039,211
; PRIOR FILING DATE: 03-14-1998
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 102
; LENGTH: 9
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TITLE OF INVENTION: ADHESIVENESS OF DEFECTIVE RED BLOOD CELLS
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 North Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/03180
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 3; L4
Pred. No. 4.1e+05;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berliner, Robert
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-370
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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ilarity 100.0%;
Conservative 0
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Matches 3; Conservative
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MOLECULE TYPE: peptide
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE REFERENCE: D6223CIP-A CURRENT APPLICATION NUMBER: US/09/510,738A CURRENT FILING DATE: 2000-02-22 PRIOR PILING DATE: 03-14-1998 NUMBER OF SEQ ID NOS: 188 SEQ ID NO 124 LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'Brien, Timothy J.
ENTION: Compositions and Methods for the Early Diagnosis of
ENTION: Ovarian Cancer
CE: D6223CIP-A
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ENTION: Compositions and Methods for the Early Diagnosis of
ENTION: Ovarian Cancer
CE: D6223CIP-A
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TITLE OF INVENTION: Compositions and Methodi

TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP-A

CURRENT APPLICATION NUMBER: US/09/510,738A

CURRENT FILING DATE: 09/039,211

PRIOR FILING DATE: 03-14-1998

NUMBER OF SEQ ID NOS: 188

SEQ ID NO 125

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Residues 224-232 of the huge-
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2000-02-22
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US-09-510-738A-140
; Sequence 140, Application US/09510738A
; Patent No. 6268165
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and M.
; TITLE OF INVENTION: Ovarian Cancer
; FILE REFERENCE: D6223CIP-A
; CURRENT APPLICATION NUMBER: US/09/510,73
; CURRENT FILING DATE: 2000-02-22
                   Sequence 124, Application US/09510738A Patent No. 6268165
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 125, Application US/09510738A; Patent No. 6268165; GENERAL INFORMATION: ; APPLICANT: O'Brien, Timothy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                COTHER INFORMATION:
US-09-510-738A-124
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US-09-510-738A-125
US-09-510-738A-124
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US-09-861-966-102
US-09-861-966-102

Sequence 102, Application US/09861966

Patent No. 6518028

GENERAL INFORMATION:

TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer

FILE REFERENCE: D6223CIP-A/Div

CURRENT PFLING DATE: 2001-05-21

PRIOR FILING DATE: 2000-02-22

NUMBER OF SEQ ID NOS: 188

SEQ ID NO 102

LENGTH: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 144, Application US/09510738A
Sequence 144, Application US/09510738A
Patent No. 6268165
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE REFERENCE: D6223CIP-A
CURRENT APPLICATION NUMBER: US/09/510,738A
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: 09/039,211
PRIOR FILING DATE: 03-14-1998
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 144
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CORGANISM: Homo sapiens
FEATURE:
COTHER INFORMATION: Residues 222-230 of the hepsin protein
US-09-861-966-102
                                                                                                                                                                                                                               ; OTHER INFORMATION: Residues 222-230 of the hepsin protein US-09-510-738A-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Residues 224-232 of the hepsin protein US-09-510-738A-144
                                                                                                                                                                                                                                                                                                                 Query Match 91.3%; Score 21; DB 3; Length 9; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.3%; Score 21; DB 3; Le Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 03-14-
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 140
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-09-510-738A-144
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PHG 6
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US-09-239-043D-1128
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US-09-861-966-144
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; Sequence 125, Application US/09861966
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer; FILE REFERENCE: D6223CIP-A/Div CURRENT APPLICATION NUMBER: US/09/861,966
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 09/510,738
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 125
; LENGTH: 9
                                                                                                                                                                                                     Sequence 124, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer FILE REFERENCE: D6223CIP-A/Div CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: 09/510,738
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 124
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.3%; Score 21; DB 4; Length 9; larity 100.0%; Pred. No. 4.1e+05; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Residues 222-230 of the hepsin protein
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                     Length 9;
                 91.3%; Score 21; DB 4; Le
100.0%; Pred. No. 4.1e+05;
ive 0; Mismatches 0;
Query Match
Best Local Similarity 100.0.
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 3; Conser
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; OTHER INFORMATION:
US-09-861-966-125
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; OTHER INFORMATION:
US-09-861-966-124
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US-09-861-966-124
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US-09-861-966-125
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US-09-861-966-140
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; Patent No. 6518028
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of
; TITLE OF INVENTION: Ovarian Cancer;
; TITLE OF INVENTION: Ovarian Cancer;
; FILE REFERENCE: D6223CIP-A/Div
; CURRENT APPLICATION NUMBER: US/09/861,966
; CURRENT FILING DATE: 2001-05-21
; PRIOR FILING DATE: 2000-02-22
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 144
; LENGTH: 9
Sequence 140, Application US/09861966
Patent No. 6518028
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: Compositions and Methods for the Early Diagnosis of TITLE OF INVENTION: Ovarian Cancer TITLE OF INVENTION: Ovarian Cancer FILLE REFERENCE: D6223CIP-A/Div CURRENT APPLICATION NUMBER: US/09/861,966
CURRENT FILING DATE: 2001-05-21
PRIOR FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 140
LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Residues 224-232 of the hepsin protein US-09-861-966-144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Vitiello, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Rubo, Ralph T.
APPLICANT: Grey, Howard M.
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 3; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
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Query Match
Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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US-09-919-048-102
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Southwood, Scott
APPLICANT: Vitiello, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard M.
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0060007
CURRENT APPLICATION NUMBER: US/09/239,043D
CURRENT FILING DATE: 1999-01-27
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: US 08/978,291
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                               E OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus E OF INVENTION: Using Peptide and Nucleic Acid Compositions PREFERENCE: 2060.0060007
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            APPLICANT: EDIMMUNE INC.

TITLE OF INVENTION: Using Peptide and Nucleic FILE REFERENCE: 2060.0060007

CURRENT APPLICATION NUMBER: US/09/239,043D

CURRENT APPLICATION NUMBER: US 09/189,702

PRIOR APPLICATION NUMBER: US 08/978,291

PRIOR PILING DATE: 1998-11-10

PRIOR PILING DATE: 1997-11-25

PRIOR PILING DATE: 1997-03-12

PRIOR PILING DATE: 1997-03-13

PRIOR FILING DATE: 1997-03-13

PRIOR PILING DATE: 1997-03-13

PRIOR PILING DATE: 1996-03-13

PRIOR PILING DATE: 1997-03-12

PRIOR PILING DATE: 1996-03-13

PRIOR PILING DATE: 1994-12-01

PRIOR PILING DATE: 1994-12-01

PRIOR PILING DATE: 1994-12-01

PRIOR PILING DATE: 1994-12-01

PRIOR PILING DATE: 1994-03-03

PRIOR PILING DATE: 1994-03-04

PRIOR PILING DATE:
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APPLICATION NUMBER: US 08/820,360
FILING DATE: 1997-03-12
APPLICATION NUMBER: US 60/013,363
FILING DATE: 1996-03-13
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Sidney, John
Southwood, Scott
Vitiello, Maria A.
Livingston, Brian D.
Celis, Esteban
Kubo, Ralph T.
Grey, Howard M.
Chesnut, Robert
Epimmune Inc.
Robert
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Best Local Similarity 100.
Matches 3; Conservative
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, ORGANISM: Orthol
US-09-239-043D-1128
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US-09-239-043D-1667
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Query Match
Best Local Similarity 100.
Matches 3; Conservative
    Query Match
Best Local Similarity 100.
Matches 3; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 3; Conserv
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US-09-919-048-140
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US-09-919-048-144
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Sequence 124, Application US/09919048

GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Cannon, Martin J.
APPLICANT: Santin, Alessandro
TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
FILE REFERENCE: D6223CIP/A/D/CIP
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 09/861,966
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 188
SEQ ID NO 124

LENGTH: 9
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; Sequence 125, Application US/09919048
; Fatent No. 6787354
; GENERAL INFORMATION:
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
; FILE REFERENCE: D6223CIP/A/D/CIP
; CURRENT APPLICATION NUMBER: US/09/919,048
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/861,966
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 125
; LENGTH: 9
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                                                                                                                                                               Query Match
Best Local Similarity 100.0%; P. Matches 3; Conservative 0;
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residue
US-09-919-048-102
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ORGANISM: Homo sapiens
FEATURE:
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ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 3; Conser
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US-09-919-048-124
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US-09-919-048-125
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Sequence 144, Application US/09919048

Batent No. 6787354

GENERAL INFORMATION:

APPLICANT: Cannon, Martin J.

APPLICANT: Santin, Alessandro

TILLE REFERENCE: D6223CIP/A/D/CIP

CURRENT APPLICATION NUMBER: US/09/919,048

CURRENT FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 188

SEQ ID NO 144

LENGTH: 9
                                                                                                                                                                                                                                                            Sequence 140, Application US/09919048
; Sequence 140, Application US/09919048
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Cannon, Martin J.
; APPLICANT: Santin, Alessandro
; TITLE OF INVENTION: Methods for the early diagnosis of ovarian cancer;
; FILE REFERENCE: D6223CIP/A/D/CIP
; CURRENT APPLICATION NUMBER: US/09/919,048
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/861,966
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 188
; SEQ ID NO 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Residues 222-230 of the hepsin protein US-09-919-048-140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.3%; Score 21; DB 4; Length 9; 100.0%; Pred. No. 4.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Residues 224-232 of the hepsin protein US-09-919-048-144
                   Length
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              Score 21; DB 4; Le
Pred. No. 4.1e+05;
0; Mismatches 0;
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100.0%; Pred. No. 4.1e+05;
tive 0; Mismatches 0;
91.3%; Scc.
100.0%; Prf
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APPLICANT: HERMANN, WILLIAM J
APPLICANT: GAWISH, ALI ABDEL SALAM
TITLE OF INVENTION: METHOD OF TREATING
TITLE OF INVENTION: HERPATITIS B INFECTION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSES: TILTON, FALLON, LUNGMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE, SUITE 960
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: 19930419
CLASSIFICATION NUMBER: US/09/780,084
FILING DATE: 19330419
CLASSIFICATION NUMBER: US/07/780,084
FILING DATE: 195071
PRIOR APPLICATION NUMBER: US/07/780,267
FILING DATE: 11-UJL-1991
PRIOR APPLICATION NUMBER: US/07/228,364
FILING DATE: 11-UJL-1991
PRIOR APPLICATION NUMBER: US/07/228,364
FILING DATE: 11-UJL-1991
PRIOR APPLICATION NUMBER: US/07/228,364
FILING DATE: 11-UJL-1991
PRIOR APPLICATION NUMBER: 31,327
REFERENCE/DOCKET INFORMATION:
NAME: FENTRESS, SUSAN B
FILING DATE: 11-UJL-1991
PRIOR APPLICATION NUMBER: 92008A
TELECOMMUNICATION NUMBER: 92008A
TELEDROME: FENTRESS, SUSAN B
REGESTRATION NUMBER: 31,456-8000
INPORMATION FOR SEQ ID NO: 11:
CROMITER OF THE SET OF 
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Sequence 13, Application US/08049511;
Batent No. 5316775;
GENERAL INFORMATION:
APPLICANT: WAGLE, SUDHAKAR S
APPLICANT: STEINBACH, THOMAS
APPLICANT: LAWYER, CARL H
APPLICANT: HERMANN, WILLIAM J
APPLICANT: HERMANN, WILLIAM J
TITLE OF INVENTION: METHOD OF TREATING
TITLE OF INVENTION: HEPATITIS B INFECTION
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: TILTON, FALLOW.
STREET: 100 come
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
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Best Local Similarity 100.
Matches 3; Conservative
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US-08-049-511-13
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                                     US-08-049-511-10

Sequence 10, Application US/08049511

Patent No. 5316770:

APPLICANT: WAGIE, SUDHAKAR S
APPLICANT: LAFEINBAH, THOMAS
APPLICANT: LAFER CARL H
APPLICANT: LAFER CARL H
APPLICANT: LAFER CARL H
APPLICANT: HARMANN, WILLIAM J
APPLICANT: HARMANN, WILLIAM J
APPLICANT: HARMANN, WILLIAM J
APPLICANT: HARMANN, WILLIAM J
APPLICANT: CAMISH, ALI ABBEL SALAM
TITLE OF INVENTION: HEPATITIS B INFECTION
NUMBER OF SEQUENCES: 14
CONTRESPONDENCE ADDRESS:
ADDRESSEE: TLLTON, FALLON, LUNGMUS & CHESTNUT
STREET: 100 SOUTH WACKER DRIVE, SUITE 960
CITY: CHICAGO
CITY: CHICAGO
COUNTRY: USS SYSTEM: PC-DOS/MS-DOS
COUNTRY: LEM PC COMPATIBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BAFC COMPATION DATA:
APPLICATION NUMBER: US/01/804,844
FILING DATE: 19930419
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/728,267
FILING DATE: 10-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/228,364
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/228,364
FILING DATE: 11-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/228,364
FILING DATE: 10-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/228,364
FILING DATE: 11-OCT-1991
PRIOR APPLICATION NUMBER: US/07/228,364
FILING DATE: 10-OCT-1991
PRIOR APPLICATION NUMBER: US/07/228,364
FILING DATE: US-OCT-1991
PRIOR APPLICATION NUMBER: US/07/228,364
FILING DATE: US-OCT-1991
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US-08-049-511-11
; Sequence 11, Application US/08049511
; Patent No. 5316775
; GENERAL INFORMATION:
; APPLICANT: WAGLE, SUDHAKAR S
; APPLICANT: STEINBACH, THOMAS
; APPLICANT: LAWYER, CARL H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FENTRESS, SUSAN B
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: 92001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/456-8000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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TYPE: AMINO ACID
STRANDEDNESS: un
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                           RESULT 38
US-08-049-511-10
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CITY: CHICAGO
STATE: LLILINOIS
COUNTRY: USA
ZIP: 60664-4002
COMPUTER: TEMPOR COMPATIBLE
COMPUTER: TEMPOR COMPATION NUMBER: US/08/049,511
FILING DATE: 19930419
CLASSIFICATION NUMBER: US/07/780,084
FILING DATE: 15-0CT-1991
PRIOR APPLICATION NUMBER: US/07/780,844
FILING DATE: US-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/28,267
FILING DATE: US-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/228,364
FILING DATE: US-0CT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/228,364
FILING DATE: US-0CT-1991
APPLICATION NUMBER: US/07/228,364
FILING DATE: US-0CT-1991
APPLICATION NUMBER: US/07/228,364
FILING DATE: US/07/228,364
FILING DATE
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15, 2005, 14:24:18 Search completed: June Job time: 24.5 secs

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Sequence 31, Appl
Sequence 25, Appl
Sequence 32, Appl
Sequence 7, Appli
Sequence 9, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 21, Appl
                                                                                                                ; Search time 79.75 Seconds (without alignments) 24.034 Million cell updates/sec
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2: \( \cgn2 = \begin{align*} \properties \text{AB:} \\
3: \( \cgn2 = \begin{align*} \properties \text{AB:} \\
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5: \( \cgn2 = \begin{align*} \properties \text{AB:} \\
6: \( \cgn2 = \begin{align*} \properties \text{AB:} \\ \properties \text
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7 US-10-923-940-25

US-09-817-661-32

1 US-10-074-225A-7

1 US-10-074-225A-9

1 US-10-074-225A-9

1 US-10-074-225A-10

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 version - 2005 (
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Maximum Match 100%
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GenCore
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Match
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Maximum DB
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Perfect sc
Sequence:
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No.
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12 21 91.3 6 14 US-10-153-312A-1 Sequence 1, Appli 21 91.3 6 14 US-10-096-77-5 Sequence 5, Appli 22 91.3 6 16 US-10-699-088-232 Sequence 212, Appli 15 21 91.3 6 16 US-10-699-088-758 Sequence 220, Appli 21 91.3 6 16 US-10-699-088-758 Sequence 240, Appli 21 91.3 6 16 US-10-699-088-955 Sequence 957, Appli 22 91.3 6 16 US-10-699-088-955 Sequence 957, Appli 22 91.3 6 16 US-10-699-18-53 Sequence 957, Appli 22 2 191.3 6 16 US-10-699-18-964 Sequence 957, Appli 22 2 191.3 6 16 US-10-699-113-240 Sequence 957, Appli 22 2 191.3 6 16 US-10-699-113-240 Sequence 240, Appli 22 2 191.3 6 16 US-10-699-113-240 Sequence 758, Appli 22 2 191.3 6 16 US-10-699-113-240 Sequence 758, Appli 22 2 191.3 6 17 US-10-699-113-240 Sequence 758, Appli 22 2 191.3 6 17 US-10-699-114-758 Sequence 758, Appli 22 2 191.3 6 17 US-10-699-114-759 Sequence 758, Appli 22 2 191.3 6 17 US-10-699-114-759 Sequence 957, Appli 22 2 191.3 6 17 US-10-699-114-759 Sequence 967, Appli 21 91.3 6 17 US-10-699-114-964 Sequence 970, Appli 21 91.3 6 17 US-10-699-114-964 Sequence 970, Appli 21 91.3 6 17 US-10-699-114-964 Sequence 970, Appli 21 91.3 7 17 US-10-806-924-10 Sequence 70, Appli 21 91.3 7 17 US-10-806-924-10 Sequence 70, Appli 21 91.3 7 17 US-10-806-924-10 Sequence 970, Appli 91.3 7 17 US-10-912-512-70 Sequence 97
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### ALIGNMENTS

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ΠD
                           Sequence 31, Application US/10476861A
Sequence 31, Application US/10476861A
Publication No. US20050084902A1
GENERAL INFORMATION:
APPLICANT: NOKIHARA, Kiyoshi et al.
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 0760-0325P
CURRENT APPLICATION NUMBER: US/10/476,861A
CURRENT FILING DATE: 2003-11-06
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.2
SEQ ID NO 31
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%; Pred. No. 1.5e+06; 
0; Mismatches 0; Indels
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TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: NO: 7 and example 3

US-10-476-861A-31
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RESULT 1
US-10-476-861A-31
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Matches 3
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RESULT 2 US-10-923-940-25 ; Sequence 25, Application US/10923940

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APPLICANT: PUNKETT, Marian L
APPLICANT: PUNKETT, Marian L
APPLICANT: PUNKETT, Marian L
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: HARRIS, Scott
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC /
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFERENCE: 38342-178463
CURRENT PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 5
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Publication No. US20030082740A1
GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: PLUNKETT, Marian L
APPLICANT: HARRIS, Scott
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC I
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFERENCE: 38342-178463
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                                                                                                                                                                                         FEATURE:
CTHEN INFORMATION: Synthetic Peptide
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(2)
COTHER INFORMATION: Xaa at positions 1 and 2 can be either His or Pro US-10-074-225A-7
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CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/268,370
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Synthetic Peptide US-10-074-225A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/10074225A Publication No. US20030082740A1 GENERAL INFORMATION:
                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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US-10-074-225A-9
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US-10-074-225A-7

i Sequence 7, Application US/10074225A

j Sequence 7, Application US/10074225A

j Publication No. US20030082740A1

j GENERAL INFORMATION:
    APPLICANT: DONATE, Fernando
    APPLICANT: PLUNKETT, Marian L
    APPLICANT: HARRIS, Scott
    APPLICANT: MAZAR, Andrew P
    TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC
    TITLE OF INVENTION: ANTI-TUMOR AGENT
    TITLE OF INVENTION: ANTI-TUMOR AGENT
    FILE REFERENCE: 38342-178463

; CURRENT APPLICATION NUMBER: US/10/074,225A
                 GENERAL TOTAL STATE OF TOTAL STATE OF TITLE OF INVENTION:

TITLE OF INVENTION: Activity

TITLE OF INVENTION: Activity

FILE REFERENCE: 2005284-0010

CURRENT APPLICATION NUMBER: US/10/923,940

CURRENT APPLICATION NUMBER: US/10/923,940

CURRENT PILING DATE: 2004-08-23

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.2

SEQ ID NO 25

LENGTH: 4

TYPE: PRT

ORGANISM: Artificial

FEATURE:

COTHER INFORMATION: Identified by phage display. Not from any organim

US-10-923-940-25
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sequence
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llarity 100.0%; Pred. No. 1.5e+06;
Conservative 0; Mismatches 0;
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US-09-817-661-32
; Sequence 32, Application US/09817661
; Patent No. US20020076692A1
; GENERAL INFORMATION:
; APPLICANT: Osbourn, Jane
; TITLE OF INVENTION: Improvements to ribosome
; TILE REFERENCE: 84633
; CURRENT APPLICATION NUMBER: US/09/817,661
; CURRENT FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
   US20050113297A1
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Best Local Similarity 100.
Matches 3; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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us-10-074-225a-7.rapb

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gequence 71, Application US/10156820

Publication No. US20020150558A1

GENERAL INFORMATION:

APPLICANT: Boulanger, Pierre

APPLICANT: Hong, Saw See

APPLICANT: Karayan, Lucie

APPLICANT: Karayan, Lucie

TITLE OF INVENTION: Use of a Polypeptide as Cell Receptor for Adenoviruses

TITLE REFERENCE: 032751-036

CURRENT FILING DATE: 2002-06-30

PRIOR APPLICATION NUMBER: PCT/FR98/00184

PRIOR FILING DATE: 1998-01-30

PRIOR FILING DATE: 1997-09-09

PRIOR FILING DATE: 1997-09-09

NUMBER OF SEQ ID NOS: 98

SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020037533A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Promoting Wakefulness and Sleep

FILE REFERENCE: P-UC 4679

CURRENT APPLICATION NUMBER: US/09/932,161

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 6
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100.0%; Pred. No. 1.5e+06;
tive 0; Mismatches 0;
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; OTHER INFORMATION: human GPR10 variant
US-09-932-161-5
                                                                                                                                                                                          OTHER INFORMATION: Synthetic Peptide
   PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 3; Conservative
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US-10-156-820-71
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US-09-932-161-5
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Publication No. US20030082740A1

GENERAL INFORMATION:

APPLICANT: PLUNKETT, Marian L

APPLICANT: PLUNKETT, Marian L

APPLICANT: MAZAR, Andrew P

TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC

TITLE OF INVENTION: ANTI-TUMOR AGENT

TITLE OF INVENTION: ANTI-TUMOR AGENT

TITLE OF INVENTION: ANTI-TOWN AGENT

STORRENT FILING DATE: 2002-02-14

NUMBER: PATE: 2001-02-14

NUMBER: PATE: 2001-02-14

NUMBER: PATE: DOIL OS: 11

SOFTWARE: PATE: DOIL OS: 11

SEQ ID NO 10

LENGTH: S
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US-10-074-225A-11

US-10-074-225A-11

Sequence 11, Application US/10074225A

Publication No. US20030082740A1

GENERAL INFORMATION:

APPLICANT: DONATE, Fernando

APPLICANT: PLUNKETT, Marian L

APPLICANT: HARRIS, Scott

APPLICANT: MAZAR, Andrew P

TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC

TITLE OF INVENTION: ANTI-TUMOR AGENT

FILE REFERENCE: 38342-178463

CURRENT APPLICATION NUMBER: US/10/074,225A

CURRENT PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/268,370
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100.0%; Pred. No. 1.5e+06;
ive 0; Mismatches 0;
       NUMBER: US/10/074,225A
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2002-02-14
FRIOR APPLICATION NUMBER: US 60/268,370
FRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 5
TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Synthetic Peptide
US-10-074-225A-9
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Best Local Similarity
Matches 3; Conser
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; OTHER INFORMATION:
US-10-074-225A-10
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US-10-074-225A-10
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RESULT 14
US-10-699-088-232

J. Sequence 232, Application US/10699088

j. Bublication No. US20040209282A1

j. Sequence 232, Application US/20040209282A1

j. Publication No. US20040209282A1

j. Publication No. US20040209282A1

j. APPLICANT: Dana Ault-Riche

j. APPLICANT: Dana Ault-Riche

j. APPLICANT: Dana Ault-Riche

j. TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE

j. TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDES

j. FILE REPERENCE: 25885-1754

j. CURRENT APPLICATION NUMBER: US/10/699,088

j. CURRENT PILING DATE: 2003-10-30

j. PRIOR PILING DATE: 2002-10-30

j. PRIOR FILING DATE: 2002-10-30

j. PRIOR FILING DATE: 2002-10-30

j. PRIOR FILING DATE: 2002-10-30

j. NUMBER OF SEQ ID NOS: 1094

j. SOFTWARE: FastSEQ for Windows Version 4.0

j. SEQ ID NO 232

LENGTH: 6

LENGTH: 6
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                                                                                                                                                                                                                                                                        Sequence 5, Application US/10096777

Sequence 5, Application US/20030171270A1

GENERAL INFORMATION:

APPLICANT: Civelli, Olivier

APPLICANT: Lin, Steven

TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PrRP)

FILE REFERENCE: P-UC 3534

CURRENT APPLICATION NUMBER: US/10/096,777

CURRENT FILING DATE: 2002-03-12

PRIOR APPLICATION NUMBER: US/09/560,915

PRIOR APPLICATION NUMBER: US/09/560,915

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 6
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                         Length 6;
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                     91.3%; Score 21; DB 14; I larity 100.0%; Pred. No. 1.5e+06; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-10-699-088-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10
US-10-096-777-5
                       Query Match
Best Local Similarity
Matches 3; Conserv
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US-10-096-777-5
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# APPLICANT: Bayer AS
# TITLE OF INVENTION: Cytostatic-Glycoconjugates having specifically cleavable linking
# FILE REFERENCE: LeA 34 491
# CURRENT APPLICATION NUMBER: US/10/026,237
# CURRENT APPLICATION NUMBER: EP 00128402.5
# PRIOR APPLICATION NUMBER: EP 00128402.5
# PRIOR FILING DATE: 2000-12-27
# NUMBER OF SEQ ID NOS: 33
# SOFTWARE: Patentin version 3.1
# SOFTWARE: PATENT OF SEQ ID NOS: 33
# SOFTWARE: PRT
# ORGANISM: Artificial
# FEATURE:
# ORGANISM: Artificial
# FEATURE:
# OTHER INFORMATION: Amino Acid sequence not obtained from organism, but synthesized # US-10-026-237-25
# US-10-026-237-25
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Sequence 1, Application US/10153312A

Publication No. US20030040016A1

GENERAL INFORMATION:

APPLICANT: Singh, Sharat

APPLICANT: Zivin, Robert Allan

TILLE REFERENCE: 5025-806.US03

CURRENT APPLICATION NUMBER: US/10/153,312A

CURRENT FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: US 60/334,902

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 6

TYPE: PRT

CREANISM: Artificial Sequence
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US-10-026-237-25
; Sequence 25, Application US/10026237
; Publication No. US20020173452A1
; GENERAL INFORMATION:
                i LENGTH: 6

TYPE: PRT

CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Phagotope
US-10-156-820-71
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Best Local Similarity
Matches 3; Conser
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Best Local Similarity
Matches 3; Conser
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US-10-153-312A-1
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US-10-153-312A-1
SEQ ID NO 71
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JUNE OF THING DATE: 2002-10-30

FILE REFERENCE: 25885-1754

CURRENT FILING DATE: 2003-10-30

FRIOR FILING DATE: 2002-10-30

FRIOR FILING DATE: 2002-10-30
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Publication No. US20040209282A1

GENERAL INFORMATION:
APPLICANT: Dana Ault-Riche
APPLICANT: Bruce Atkinson
TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED COLLECTIONS AND CAPTURE
TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDES
TITLE OF INVENTION: MUMBER: US/10/699,088
CURRENT APPLICATION NUMBER: US/10/699,088
CURRENT APPLICATION NUMBER: 60/422,923
PRIOR FILING DATE: 2002-10-30
PRIOR FILING DATE: 2002-10-30
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 1094
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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LENGTH: 6
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                                                                                                              RESULT 15
US-10-699-088-240

i Sequence 240, Application US/10699088

i Publication No. US20040209282A1

i GENERAL INFORMATION:

i APPLICANT: Dana Ault-Riche

APPLICANT: Bruce Atkinson

i TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE

I TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDES

FILE REFERENCE: 25885-1754

CURRENT FILING DATE: 2003-10-30

PRIOR PLING DATE: 2003-10-30

PRIOR PLING DATE: 2002-10-30

PRIOR PLING DATE: 2002-10-30

PRIOR PLING DATE: 2002-10-30

NUMBER OF SEQ ID NOS: 1094

SOUTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 240

LENGTH: 6
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US-10-699-088-758

; Sequence 758, Application US/10699088
; Sequence 758, Application US/10699088
; Publication No. US20040209282A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Atkinson
; TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE
; TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDES
; TITLE OF INVENTION NUMBER: US/10/699,088
; CURRENT APPLICATION NUMBER: 60/422,923
; PRIOR PELING DATE: 2003-10-30
; PRIOR PELING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 758
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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CTHER INFORMATION:

US-10-699-088-240
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; Sequence 232, Application US/10699113
; Publication No. US20040241748A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Schulz, Rainer
; APPLICANT: Schulz, Renneth
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
; FILE REFERENCE: 25885-1755
; CURRENT APPLICATION NUMBER: US/10/699,113
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/446,687
; RUMBER OF SEQ ID NOS: 948
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 6
; TURENT FILING DATE: 2003-02-10
        APPLICANT: Kumble, Krishnanand
APPLICANT: Schulz, Rainer
APPLICANT: Schulz, Renneth
TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
FILE REFERENCE: 25885-1758
CURRENT APPLICATION NUMBER: US/10/699,113
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: 60/446,687
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 948
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 6
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; Sequence 240, Application US/20040241748A1
; Publication No. US20040241748A1
; GENERAL INFORMATION:
; APPLICANT: Rumble, Krishnanand
; APPLICANT: Schulz, Rainer
; APPLICANT: Schulz, Kenneth
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6;
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CTHER INFORMATION: synthetic peptide US-10-699-113-53
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CTHER INFORMATION: synthetic peptide
US-10-699-113-232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
 Ault-Riche, Dana
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Best Local Similarity
Matches 3; Conserv
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        Sequence 364, Application US/10699088

Publication No. US20040209282A1

GENERAL INFORMATION:

APPLICANT: Dana Ault-Riche

APPLICANT: Dana Ault-Riche

APPLICANT: Bruce Atkinson

TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDES

FILE REFERENCE: 25885-1754

CURRENT APPLICATION NUMBER: US/10/699,088

CURRENT APPLICATION NUMBER: 60/422,923

PRIOR FILING DATE: 2003-10-30

PRIOR FILING DATE: 2002-10-30

SOFTWARE FastSEQ for Windows Version 4.0

SEQ ID NO 964

LENGTH: 6
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; Sequence 46, Application US/10699113
; Publication No. US20040241748A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Kumble, Krishnanand
; APPLICANT: Schulz, Rainer
; APPLICANT: Schulz, Renneth
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
; FILE REFERENCE: 25885-1755
; CURRENT FILING DATE: 2003-10-30
; FRIOR APPLICATION NUMBER: 60/446,687
; RIOR APPLICATION NUMBER: 60/446,687
; RIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
: LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%; Score 21; DB 16; Length 6; ilarity 100.0%; Pred. No. 1.5e+06; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic peptide
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US-10-699-113-53
; Sequence 53, Application US/10699113
; Publication No. US20040241748A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic |
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conser
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; OTHER INFORMATION:
US-10-699-113-46
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US-10-699-088-964
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US-10-699-113-46
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US-10-699-114-240
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US-10-699-113-765
i Sequence 765, Application US/10699113
i Publication No. US20040241748A1
i GENERAL INFORMATION:
i APPLICANT: Ault-Riche, Dana
i APPLICANT: Kumble, Krishnanand
i APPLICANT: Schulz, Rainer
i APPLICANT: Schulz, Renneth
i TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
i FILE REFERENCE: 25885-1755
i CURRENT FILING DATE: 2003-10-30
i PRIOR FILING DATE: 2003-02-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kumble, Krishnanand
APPLICANT: Schulz, Rainer
APPLICANT: Schulz, Rainer
APPLICANT: Schulz, Rainer
APPLICANT: Schulz, Renneth
TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
FILE REFERENCE: 25885-1755
CURRENT APPLICATION NUMBER: US/10/699,113
CURRENT FILING DATE: 2003-10-30
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 948
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 758
LENGTH: 6
                                                                                                                                                                                                                                                                                            Length 6;
                                                                                                                                                                                                                                                                                        91.3%; Score 21; DB 16; Length 6;
100.0%; Pred. No. 1.5e+06;
ive 0; Mismatches 0; Indels
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FILE REFERENCE: 25885-1755
CURRENT APPLICATION NUMBER: US/10/699,113
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: 60/446,687
PRIOR FILING DATE: 2003-02-10
NUMBER OF SEQ ID NOS: 948
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 240
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                 synthetic peptide
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US-10-699-113-758
; Sequence 758, Application US/10699113
; Publication No. US20040241748A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ault-Riche, Dana APPLICANT: Kumble, Krishnanand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 3; Conservative
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US-10-699-113-240
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US-10-699-113-758
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Best Local S
Matches 3
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APPLICANT: Dana Ault-Riche
APPLICANT: Bruce Atkinson
APPLICANT: Bruce Atkinson
APPLICANT: Lynne Jersaitis
APPLICANT: Gizette Sperinde
TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METHC
TITLE OF INVENTION: USING THE SYSTEMS
FILE OF INVENTION NUMBER: US/10/699,114
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: 60/422,923
PRIOR APPLICATION NUMBER: 60/422,923
PRIOR APPLICATION SYSTEMS
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 1094
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 232
LENGTH: 6
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; Bublication No. US20050042623A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Atkinson
; APPLICANT: Lynne Jersaitis
; TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METHC
; TITLE OF INVENTION: USING THE SYSTEMS
; FILE REFERENCE: 25885-1759
; CURRENT APPLICATION NUMBER: US/10/699,114
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
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                                                                                                                                                                                                                                                                                                   Query Match 91.3%; Score 21; DB 16; I
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
NUMBER OF SEQ ID NOS: 948
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 765
LENGTH: 6
                                                                                                                ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-113-765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: synthetic peptide
US-10-699-114-232
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Publication No. US20050042623A1
GENERAL INFORMATION:
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RESULT 30

US-10-699-114-957

Sequence 977, Application US/10699114

Publication No. US20050042623A1

GENERAL INFORMATION:

APPLICANT: Dana Ault-Riche

APPLICANT: Lynne Jersaitis

APPLICANT: Lynne J
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CURRENT APPLICATION NUMBER: US/10/699,114
CURRENT FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: 60/423,018
PRIOR FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: 60/422,923
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 1094
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 765
LENGTH: 6
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Publication No. US20050042623A1;
GENERAL INFORMATION:
APPLICANT: Dana Ault-Riche
APPLICANT: Bruce Atkinson
APPLICANT: Krishnanand Kumble
APPLICANT: Lynne Jersaitis
APPLICANT: Gizette Sperinde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: synthetic peptide US-10-699-114-765
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 3; Conserv
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US-10-699-114-758
is Sequence 758, Application US/10699114
is Sequence 758, Application US/10699114
is Sequence 758, Application No. US20050042623A1
is Sequence 758, Application No. US20050042623A1
is APPLICANT: Dana Ault-Riche
is APPLICANT: Lynne Jersaitis
is APPLICANT: Lynne Jersaitis
is APPLICANT: Gizette Sperinde
is TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH
is TITLE OF INVENTION: USSTEMS
is TILE OF INVENTION: USSTEMS
is TILE OF INVENTION: USPERS (0/423,018
is PRIOR FILING DATE: 2002-10-30
is PRIOR FILING DATE: 2003-10-30
is PRIOR 
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APPLICANT: Dana Ault-Riche
APPLICANT: Bruce Atkinson
APPLICANT: Krishnanand Kumble
APPLICANT: Lynne Jersaitis
APPLICANT: Lynne Jersaitis
APPLICANT: Gizette Sperinde
TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH
TITLE OF INVENTION: USING THE SYSTEMS
FILE REFERENCE: 25885-1759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
      PRIOR FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: 60/422,923
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 1094
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 240
LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic peptide
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US-10-699-114-765
; Sequence 765, Application US/10699114
; Publication No. US20050042623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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CTHER INFORMATION:
US-10-699-114-240
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US-10-699-114-758
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Gaps

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Sequence 203, Application US/10806924

Sequence 203, Application US/10806924

Publication No. US20050095648A1

GENERAL INFORMATION:

APPLICANT: Geysen, H. Mario

APPLICANT: Geysen, H. Mario

APPLICANT: Ault-Riche, Dana

TITLE OF INVENTION: Method for designing linear epitopes

TITLE OF INVENTION: and polypeptide epitopes

FILE REFERENCE: 25885-1760

CURRENT APPLICATION NUMBER: US/10/806,924

CURRENT FILING DATE: 2004-03-22

NUMBER OF SEQ ID NOS: 911

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 203

LENGTH: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 195, Application US/10806924
Publication No. US20050095648A1
Publication No. US20050095648A1
Publication No. US20050095648A1
APPLICANT: Geysen, H. Mario
APPLICANT: Ault-Riche, Dana
TITLE OF INVENTION: Method for designing linear epitopes
TITLE OF INVENTION: and polypeptide epitopes
FILE REFERENCE: 25885-1760
CURRENT APPLICATION NUMBER: US/10/806,924
CURRENT FILING DATE: 2004-03-22
NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 195
LENGTH: 6
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                                                                                                                                                                                                       Length 6;
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                                                                                                                                                                                                    Query Match
91.3%; Score 21; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0;
                 ; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-806-924-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: synthetic peptide US-10-806-924-195
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US-10-806-924-203
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TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH FILE OF INVENTION: USING THE SYSTEMS FILE REPERENCE: 25885-1759 CURRENT APPLICATION NUMBER: US/10/699,114 CURRENT APPLICATION NUMBER: 60/423,018 PRIOR PILING DATE: 2002-10-30 PRIOR FILING DATE: 2002-10-30 PRIOR FILING DATE: 2002-10-30 PRIOR FILING DATE: 2002-10-30 NUMBER OF SEQ ID NOS: 1094 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 964
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i Sequence 9, Application US/10806924

j Publication No. US20050095648A1

j GENERAL INFORMATION:

APPLICANT: Geysen, H. Mario

APPLICANT: Ault-Riche, Dana

TITLE OF INVENTION: Method for designing linear epitopes

TITLE OF INVENTION: and polypeptide epitopes

FILE REFERENCE: 25885-1760

CURRENT PELLICATION NUMBER: US/10/806,924

CURRENT FILING DATE: 2004-03-22

NUMBER OF SEQ ID NOS: 911

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 6

TYPE: PRT
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US-10-806-924-16
; Sequence 16, Application US/10806924
; Publication No. US20050095648A1
; GENERAL INFORMATION:
; APPLICANT: Geysen, H. Mario
; APPLICANT: Ault-Riche, Dana
; TITLE OF INVENTION: method for designing linear epitopes
; TITLE OF INVENTION: and polypeptide epitopes
; TITLE OF INVENTION: Method for designing linear epitopes
; TITLE OF INVENTION: MUMBER: US/10/806,924
; CURRENT APPLICATION NUMBER: US/10/806,924
; CURRENT FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; L
1.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.3%; Score 21; DB 17; I 100.0%; Pred. No. 1.5e+06; vative 0; Mismatches 0;
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                           synthetic peptide
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conser
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US-10-699-114-964
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US-10-806-924-9
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Gaps

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Gaps

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APPLICANT: Baldwin, Toby L.

APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Wangsen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Winetzky, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
TITLE OF INVENTION: Complexes
FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/09/954,385
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 70
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 377, Application US/09954385;
Sequence 377, Application No. US20030100467A1;
General INFORMATION:
APPLICANT: Aehle, Wolfgang;
APPLICANT: Baldwin, Toby L.
APPLICANT: Use Giselle G.
APPLICANT: Wang, Huaming
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 91.3%; Score 21; DB 10; I Best Local Similarity 100.0%; Pred. No. 1.5e+06; Matches 3; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: binding peptide US-09-954-385-70
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US-10-646-807-12
; Sequence 12, Application US/10646807
; Publication No. US20040077005A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: binding peptide
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity
Matches 3; Conserv
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US-10-13/
US-10-13/
US-10-106-924-728

i Sequence 728, Application US/10806924

j Publication No. US20050095648A1

j GENERAL INFORMATION:

j APPLICANT: Ault-Riche, Dana

j TITLE OF INVENTION: Method foor designing linear epitopes and algorithm therefor

j TITLE OF INVENTION: and polypeptide epitopes

j TITLE OF INVENTION: and polypeptide epitopes

j FILE REFERENCE: 25885-1760

j CURRENT APPLICATION NUMBER: US/10/806,924

CURRENT APPLICATION NUMBER: US/10/806,924

CURRENT FILING DATE: 2004-03-22

j NUMBER OF SEQ ID NOS: 911

sOFTWARE: FastSEQ for Windows Version 4.0

sEQ ID NO 728

LENGTH: 6

TYPE: PRT

CURRENT ARTIFICIAL Sequence
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Geysen, H. Mario
APPLICANT: Geysen, H. Mario
APPLICANT: Ault-Riche, Dana
TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
TITLE OF INVENTION: and polypeptide epitopes
TITLE NEFERENCE: 25885-1760
CURRENT APPLICATION NUMBER: US/10/806,924
CURRENT FILING DATE: 2004-03-22
NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 721
LENGTH: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
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; Sequence 721, Application US/10806924
; Publication No. US20050095648A1
; GENERAL INFORMATION:
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US-09-954-385-70
; Sequence 70, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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US-10-806-924-728
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CAMERON, Beatrice

GROUZET, Joel

FRERERO, Lucia

TITLE OF INFRENCHON, Lucia

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESS:

CONTRYTON NOWERS: 1.L.P.

CITY: Machington

CITY: Machington

CITY: Machington

CONTRY: USA

CONTRY

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Search completed: June 15, 2005, 14:50:17 Job time : 80.75 secs

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5.1.6
Compugen Ltd
version :
GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

June 15, 2005, 14:04:57 ; Search time 17.5 Seconds (without alignments) 27.491 Million cell updates/sec Run on:

US-10-074-225A-7 23 1 XXPHG 5

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

seqs, 96216763 residues 283416 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79: \* 1: pir1: \* 2: pir2: \* 3: pir3: \* 4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	thrombopoietin rec	dihydropyrimidine	larval-specific li	ribosomal protein	hemopexin - chicke	rbpL protein - Rho	conserved hypothet	hypothetical prote	hypothetical prote		_				hypothetical prote	Ø	hypothetical prote	æ	hypothetical prote	tracheobronchial m	(p)ppGpp 3-pyropho	cre protein - Stre	pyrophosphate-fruc	protein F28J9.16 (	hypothetical prote			×	prophage pi3 prote
SUMMARIES	ID	178841	A44626	A27108	S11610	C31514	E41080	G75398	S12207	A71278	T18887	H81370	A99802	E97985	T50885	H81124	866330	B86823	S57791	T49863	A33811	C97837	A45765	T03588	A86485	D82459	A84213	G82472	ERAD64	E86800
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	Score	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
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77 hypothetical prote	hypothetical	58 conserved hypothet					probable phas		hypothetical	hypothetical	hypothetical	hypothetical	ferredoxin -	12 hypothetical prote	hypothetical	ALI GNMENTS			ment)		#sequence_revision 02-Aug-1996 #text_cnange 05-Nov-1999
PQ027	S10211	G75258	839675	B31048	T25844	AC1037	AG0927	B55855	T17586	G95330	AH1989	AG2520	B72286	T32842	C75627	AL.			mouse (fragment)		vision
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21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21		н		thrombopoietin receptor -	C;Species: Mus sp.	C;Date: 02-Aug-1996 C:Accession: 178841
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		RESULT	178841	thrombo	Cispect	C;Date: C:Acces

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Alexander, W.S.; Dunn, A.R.
R; Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995
A; Title: Structure and transcription of the genomic locus encoding murine
A; Reference number: I58350; MUID:95166571; PMID:7862460
A; Reference number: I78841
A; Ratus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-18 < RES>
A; Cross-references: GB:S76842; NID:g912990; PIDN:AAB33462.1; PID:g912991
C; Genetics:
A; Genetics:
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100.0%; Pred. No. 1.2e+02;
:ive 0; Mismatches 0;
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RESULT 2
A44626
dlydroptyrmidine dehydrogenase (NADP) (EC 1.3.1.2) - bovine (fragment)
NyAlternate names: dihydrothymine dehydrogenase; dihydrouracil dehydrogenase
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Species: Dos primigenius
N;Coression: A44626; A1066
A;Reference number: A44626; MUD::92184771; PMID::1544906
A;Retus: preliminary
A;Residues: 1-33 cpox
A;Residues: 1-33 cpox
A;Residues: 1-33 cpox
A;Reference number: A41066; MUD::92041818; PMID::1939061
A;Reference number: A41066
A;Molecule type: protein
A;Residues: 13-23 cpox
A;Residues: 13-23 cpox
C;Superfamily: unassigned ferredoxin 2[4Fe-48]-related proteins; ferredoxin 2[4Fe-48] hom
C;Keywords: NADP; oxidoreductase
F;16/Binding site: substrate (Cys) #status experimental

A; Reference number: A90148; MUID:88339942; PMID:3421961

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Query Match
Best Local Similarity 100.
Matches 3; Conservative
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E41080
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S12207
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S11610
ribosomal protein S4.eR [validated] - Halobacterium salinarum (fragment)
N;Alternate names: ribosomal protein HS5
C;Species: Halobacterium salinarum
C;Species: Halobacterium salinarum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S11610
R;Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982
A;Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaeba
A;Reference number: S11609
A;Molecule type: protein
A;Residues: 1-32 < YAG5
A;Residues: 1-32 < YAG5
A;Cross-references: UNIPROT:Q7M553
A;Note: the protein is designated as Halobacterium cutirubrum
C;Superfamily: rat ribosomal protein S4
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                        RESULT 3
A27108
larval-specific lipoprotein - honeybee (fragment)
C; Species: Apis mellifera (honeybee)
C; Species: Apis mellifera (honeybee)
C; Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C; Accession: A27108
R; Shipman, B.A.; Ryan, R.O.; Schmidt, J.O.; Law, J.H.
Biochemistry 26, 1885-1889, 1987
A; Title: Purification and properties of a very high density lipoprotein from the hemolyma; Reference number: A27108
A; Reference number: A27108
A; Molecule type: protein
A; Residues: 1-27 < SHI>
A; Cross-references: UNIPROT: P09355
C; Keywords: lipid binding; lipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
(231514
hemopexin - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: 28-Feb-1990 #text_change 09-Jul-2004
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: C31514
C;Accession: C31514
R;Wellner, D.; Cheng, K.C.; Muller-Eberhard, U.
Bjochem. Biophys. Res. Commun. 155, 622-625, 1988
A;Title: N-terminal amino acid sequences of the hemopexins from chicken, rat and rabbit.
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   Score 21; DB 2; L¢; Pred. No. 1.6e+02; 0; Mismatches 0;
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Similarity 100.0%; Pred. No. 1.9e+02;
3; Conservative 0; Mismatches 0;
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Best Local Similarity 100.
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Type protein - Rhodobacter sphaeroides (fragment)
C; Species: Rhodobacter sphaeroides
C; Species: Rhodobacter sphaeroides
C; Species: Rhodobacter sphaeroides
C; Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 09-Jul-2004
C; Accession: E41080
R; Chen, J.H.; Gibson, J.L.; McCue, L.A.; Tabita, F.R.
J. Biol. Chem. 266, 20447-20452, 1991
A; Title: Identification, expression, and deduced primary structure of transketolase and c A; Reference number: A41080; MUID: 92041881; PMID: 1939098
A; Reference number: A41080
A; Reference number: A41080
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-36 < CHE>
A; Cross-references: UNIPROT: P29278; GB: M68914; NID: g151988; PIDN: AAA26158.1; PID: g551958
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G75398
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C, Species: Deinococcus radiodurans
C; Species: Denococcus radiodurans
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C; Accession: G75398
R; White, O. O; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75398
A;Residues: 1-38 eWH.>
A;Residues: 1-38 eWH.>
A;Residues: 1-38 eWH.>
A;Residues: Las eWH.>
A;Residues: 
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100.0%; Pred. No. 2.5e+02;
ative 0; Mismatches 0;
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A; Accession: C31514
A; Molecule type: protein
A; Residues: 1-34 < WE3>
A; Cross-references: UNIPROT: P20057
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50S ribosomal protein L34 Cj0961c (imported) - Campylobacter jejuni (strain NCTC 11168)
C; Species: Campylobacter jejuni
C; Species: Campylobacter jejuni
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: H81370
R; Parkhill, J; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C; W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A; Reference number: A81250; MUID:20150912; PMID:10688204
A; Reference number: H81370
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-44 < PAR>
A; Residues: 1-44 < PAR>
A; Residues: 1-44 < PAR>
A; Cross-references: UNIPROT:Q9PNX4; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73218
A; Excherimental source: serotype O2, strain NCTC 11168
C; Genetics:
A; Genetics:
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A99802
hypothetical protein EC81385 [imported] - Escherichia coli (strain O157:H7, substrain RIN C; Species: Escherichia coli
C; Species: Bacherichia coli
C; Species: Bacherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C; Accession: A99802
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G., gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon A; Reference number: A99802
A; Accession: A99802
A; Accession: A99802
A; Accession: A99802
A; Residues: 1-46 < HAY>
A; Coss-references: UNIPROT: Q8X2G6; GB: BA000007; PIDN: BAB34808.1; PID:g13360845; GSPDB:G)
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Genetics:
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B97985
hypothetical protein spr0909 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: B97985
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Ete, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
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100.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 0;
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Best Local Similarity
Matches 3; Conser
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PHG 16
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A71278
hypothetical protein TP0811 - syphilis spirochete
C; Species: Treponema pallidum subsp. pallidum (87philis spirochete)
C; Species: Treponema pallidum subsp. pallidum (87philis spirochete)
C; Species: Treponema pallidum subsp. pallidum (87philis spirochete)
C; Accession: A71278
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUID:98332770; PMID:965876
A; Accession: A71278
A; Molecule type: DNA
A; Residues: 1-41 < COL>
A; Residues: 1-41 < COL>
A; Residues: 1-41 < COL>
A; Reperimental source: strain Nichols
C; Genetics:
A; Genetics:
A; Genetics:
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T18887
hypothetical protein C03D6.2 - Caenorhabditis elegans
C;Species: 21939
R;Burton, J.
R;Burton,
hypothetical protein (B2 element) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: S12207
R;Oberbaeumer, I.
submitted to MIPS, January 1991
A;Reference number: S12205
A;Accession: S12207
A;Molecule type: mRNA
A;Residues: 1-40 <OBE>
A;Cross-references: UNIPROT:Q8K081; UNIPROT:Q8K0H2; UNIPROT:Q8R1U0; UNIPROT:Q99JK9; EMBI
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100.0%; Pred. No. 2.9e+02;
ive 0; Mismatches 0; Indels
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100.0%; Pred. No. 2.8e+02;
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100.0%; Pred. No. 2.8e+02;
ive 0; Mismatches 0;
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Matches 3; Conservative
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Best Local Similarity
Matches 3; Conser
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PHG 24
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hypothetical protein yqcG [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86823
C;Accession: B86823
C;Accession: B86823
C;Accession: B86823
C;Accession: B86823
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis segnence number: A86625; MUID:21235186; PMID:11337471
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: B86823
A;Accession: B86823
A;Accession: B86823
A;Cross-references: UNIPROT:Q9CF95; GB:AE005176; PID:g12724591; PIDN:AAK05684.1; GSPDB:GNA;Experimental source: strain IL1403
C;Genetics:
A;Gene: yqcG
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 16-Aug-2004
C;Accession: S66330; SS8271
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Reference number: S66314
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S57791
probable beta-glucosidase - black mustard (fragment)
C,Species: Brassica nigra (black mustard)
C,Date: 27-Oct-1995 #sequence_revision 10-May-1996 #text_change 09-Jul-2004
C,Accession: S57791
R;Malboobi, M.A.; Lefebvre, D.D.
Plant Mol. Biol. 28, 859-870, 1995
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100.0%; Pred. No. 3.9e+02;
iive 0; Mismatches 0;
                             Pred. No. 3.6e+02;
Mismatches 0;
100.0%; Pr
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H81124
hypothetical protein NMB1079 [imported] - Neisseria meningitidis (strain MC58 serogroup C; Species: Neisseria meningitidis
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: H81124
R; Tettelin, H.; Salzberg, S.L.; White, O.; Fries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Frieschmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A; Reterence number: A81000; MUID:20175755; PMID:10710307
A; Recession: H81124
A; Residues: 1-52 < TET>
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T50885
hypothetical soluble protein [imported] - Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Species: Rubrivivax gelatinosus
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50885
R;Nagashima, K.V.; Igarashi, N.; Harada, J.; Nagashima, S.; Matsuura, K.; Shimada, K.
submitted to the EMBL Data Library, November 1999
A;Description: Determination of Nucleotide Sequences of Rubrivivax gelatinosus Photosynt
A;Reference number: Z25270
A;Reference number: Z25270
A;Residues: DNA
A;Residues: 1-48 kNAG>
A;Residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROT:Q9JZF4; GB:AE002458; GB:AE002098; NID:g7226311; PIDN:AAF4147
serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                             PROT:Q8CYU7; GB:AE007317; PIDN:AAK99713.1; PID:g15458516; GSPDB:d
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                y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.
A; Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A; Reference number: A97872; MUID:21429245; PMID:11544234
A; Accession: E97985
A; Accession: E97985
A; Molecule type: DNA
A; Residues: 1-46 < KUR>
A; Residues: 1-46 < KUR>
A; Cross-references: UNIPROT:Q8CYU7; GB:AE007317; PIDN:AAK99713.1; PIC; Genetics:
A; Genetics:
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100.0%; Pred. No. 3.3e+02;
vative 0; Mismatches 0;
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Best Local Similarity
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T49863
hypothetical protein B24P11.190 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Species: Neurospora crassa
C;Date: O2-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49863
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Recession: T49863
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-57 <SCH;
A;Residues: 1-50 <A;Residues: 1-50 <A;Re
          expression levels in phosphate-s
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A33811
tracheobronchial mucin - human (fragments)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C; Accession: A33811
R; Rose, M.C.; Kaufman, B.; Martin, B.M.
J. Biol. Chem. 264, 8193-8199, 1989
A; Title: Proteolytic fragmentation and peptide mapping of human carboxyamidomethylated A; Reference number: A33811; MUID:89255255; PMID:2656675
A; Accession: A33811
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-57 < ROS>
A; Cross-references: UNIPROT:Q7M4S5
                                                                                                           sequence not shown; not compared with conceptual translation
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4e+02;
0; Indels
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A; Title: Isolation of cDNA clones of genes with altered A; Reference number: S57791; MUID:95367647; PMID:7640358 A; Accession: S57791
A; Status: nucleic acid sequence not shown; not compared A; Molecule type: mRNA
A; Residues: 1-57 < MAL>
A; Residues: 1-57 < MAL>
Cross-references: UNIPROT:024434
C; Superfamily: Agrobacterium beta-glucosidase
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Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 3; Conservative 0; Mismatches 0;
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0; Mismatches
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Best Local Similarity 100.
Matches 3; Conservative
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RESULT 21

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(p) ppGpp 3-pyrophosphohydrolase homolog RC1099 [imported] - Rickettsia conorii (strain Mc; Species: Rickettsia conorii
C; Species: Rickettsia conorii
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: C97837
R; Ogata, H; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rou Science 293, 2003-2098, 2001
A; Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A; Reference number: A97700; MUID:21442074; PMID:11557893
A; Accession: C97837
A; Accession: C97837
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-57 < KUR>
A; Cross-references: UNIPROT:Q92GM4; GB:AE006914; PIDN:AAL03637.1; PID:g15620223; GSPDB:GP
C; Genetics:
A; Genetics:
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A45765
cre protein - Streptomyces hygroscopicus
C; Species: Streptomyces hygroscopicus
C; Species: Streptomyces hygroscopicus
C; Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C; Accession: A45765
R; Ogura, M.; Tanaka, T.; Seto, H.; Otake, N.
J. Antibiot. 43, 873-882, 1990
A; Title: Molecular cloning and characterization of the gene conferring curromycin resists
A; Reference number: A45765; MUID:90354306; PMID:2117601
A; Accession: A45765
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-58 < OGU>A; Cross-references: UNIPROT:P16961; GB:M28599; NID:g153217; PIDN:AAA26721.1; PID:g153218
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c; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Species: Oryza sativa (rice)
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C; Accession: T03588
R; Umeda, M.; Hara, C.; Matsubayashi, Y.; Li, H.; Lui, Q.; Tadokoro, F.; Aotsuka, S.; Uchi Plant Mol. Biol. 25, 469-478, 1994
A; Title: Expressed sequence tags from cultured cells of rice (Oryza sativa L.) under stre A; Reference number: Z14962; MUD:94325471; PMID:8049371
A; Accession: T03588
A; Accession: T03588
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-59 <UME>
A; Residues: 1-59 <UME>
A; Catus: mRNA
A; Residues: 1-59 <UME>
A; Catus: manala source: callus
C; Genetics:
A; Note: AK99
C; Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructokir
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Best Local Similarity
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Best Local Similarity 100.
Matches 3; Conservative
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C, Genetics: <GEN3>
A, Gene: VCA0297
A, Map position: 2
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A;Gene: VCA0353
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A86485
protein F2809.16 [imported] - Arabidopsis thaliana
c;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86485
C;Accession: A86485
R;Theologis, A.; Ecker, J.R.; Pallm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizon, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizon, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromsome i of the plant Arabidopsis.
A;Accession: A86485
A;Accession: A86485
A;Accession: A86485
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A;Cossion: A86485
A;Coss
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D82459
hypochetical protein VCA0435 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82459
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E
I, R.R.; Mekalence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-59 <HEI>
A;Residues: 1-59 <HEI>
A;Cross-references: UNIPROT:Q9XMC7; GB:AE004377; GB:AE003853; NID:g9657831; PIDN:AAF9634
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 2
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serogroup O1; strain N16961; biotype El Tor
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ilarity 100.0%; Pred. No. 4.1e+02;
Conservative 0; Mismatches 0;
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Pred. No. 4.1e+02;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 3; Conservative (
3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Appointment of protein Vng0548c [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84213
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Froc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Lit
A;Title: Genome sequence of Halobacterium species NRC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Userical protein VCA0336 VCA0353 VCA0297 [imported] - Vibrio cholerae (strain N16961 C.Species: Vibrio cholerae
C.Species: Colorio chole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: A84213
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-60 <STO>
A;Cross-references: UNIPROT:Q9HRT9; GB:AE004437; NID:g10580147; PIDN:AAG19069.1; GSPDB:GN
C;Genetics:
A;Gene: VNG0548C
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100.0%; Pred. No. 4.2e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 3; Conservative
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RESULT 31
S1021

hypothetical protein, 7.3K - human adenovirus 41
C;Species: Mastadenovirus h41 (human adenovirus 41)
C;Species: Mastadenovirus h41 (human adenovirus 41)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: S10211
R;Slemenda, S.B.; Pieniazek, N.J.; Velarde Jr., J.; Pieniazek, D.; Luftig, R.B.
Nucleic Acids Res. 18, 3069, 1990
A;Title: Nucleotide sequence of the region coding for 100K and 33K proteins of human ente A;Reference number: S10206; MUID: 90272433; PMID: 2349115
A;Reference number: S10206; MUID: 90272433; PMID: 2349115
A;Reference number: S10206
A;Reference number: S10206
A;Reference number: S10206; MUID: 90272433; PMID: 2349115
A;Reference number: S10201
A;Reference number: S10206; MUID: 90272433; PMID: 2349115
A;Cross-references: UNIPROT: P23691; EMBL: X52532; NID: 958438; PIDN: CAA36764.1; PID: 958444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 32
G75258
Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75258
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; P.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Maj. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUD:20036896; PMID:10567266
A;Accession: G7528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-65 <WHI>
A;Residues: 1-65 <WHI>
A;Residues: 1-65 <WHIS
A;Residues: 1-65 <WHIS
A;Residues: Brain R1
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
A;Residues: 1-64 «KIL»
A;Cross-references: UNIPROT:P30816; GB:S75996; NID:g243000; PIDN:AAB21001.1; PID:g243001
C;Comment: Simian herpes B virus is an alpha herpesvirus which causes a mild, recurring
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100.0%; Pred. No. 4.5e+02;
ive 0; Mismatches 0;
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100.0%; Pred. No. 4.5e+02;
tive 0; Mismatches 0;
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; Pred. No. 4.5e+02;
0; Mismatches 0;
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S39675
ywbE protein - Bacillus subtilis
N;Alternate names: hypothetical protein ipa-20r
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ilarity 100.0%;
Conservative 0
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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E86800
prophage pi3 protein 32 [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86800
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Accession: E86800
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-64 &STO>
A;Residues: 1-64 &STO>
A;Experimental source: strain IL1403
C;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                 A; Note: host Home sapiens (man)
C; Date: 13-Mar-1990 #text_change 09-Jul-2004
C; Accession: B31162
B; Flomenberg, P.R.; Chen, M.; Horwitz, M.S.
J. Virol. 62, 4431-4437, 1988
A; Title: Sequence and genetic organization of adenovirus type 35 early region 3.
A; Reference number: A93039; MUD:89012230; PMID:3172347
A; Accession: B31162
A; Molecule type: DNA
A; Residues: 1-61 <FLO>
A; Residues: 1-61 <FLO>
A; Residues: 1-61 <FLO>
C; Superfamily: adenovirus early E3 6.4K protein
C; Superfamily: adenovirus early B3 6.4K protein
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PQ0277
hypothetical protein 1 - cercopithecine herpesvirus 1 (fragment)
C; Species: cercopithecine herpesvirus 1
C; Species: oercopithecine herpesvirus 1
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C; Accession: PQ0277
C; Accession: PQ0277
R; Killeen, A.M.; Harrington, L.; Wall, L.V.M.; Kelly, D.C.
J. Gen. Virol. 73, 195-199, 1992
A; Title: Nucleotide sequence analysis of a homologue of herpes simplex virus type 1 gene A; Reference number: JQ1406; MUID:92113572; PMID:1309859
A; Accession: PQ0277
A; Molecule type: DNA
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91.3%; Score 21; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                      early E3 6.4K protein - human adenovirus 35
C;Species: Mastadenovirus h35 (human adenovirus 35)
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Best Local Similarity 100.
Matches 3; Conservative
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probable phage tail protein STY4622 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C; Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C; Accession: AC1037
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serove A; Reference number: AB0502; MUID:21534947; PMID:11677608
A; Stevens preliminary
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AG0927
probable phage tail protein [imported] - Salmonella enterica subsp. enterica serovar Typl
c;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0927
C;Accession: AG0927
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T25844
R;Fulton, L.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid M03F4.
A;Reference number: Z20097
A;Reference number: Z20097
A;Reference number: Z20097
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-67 <FUL>
A;Residues
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A;Residues: 1-67 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06744.1; PID:g16505395; GSPDB:GN00176
C;Genetics:
A;Gene: STY4622
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100.0%; Pred. No. 4.7e+02;
tive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 4.7e+02;
Conservative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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T25844
hypothetical p
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C;Species: Bacillus subtilis
C;Accession: 538675, G70051
A;A;Appport, G;Danchin, A93
A;Title: Bacillus sublishing support.
A; Rappport.
G;Danchin, A93
A;Title: Bacillus sublishing squame project: cloning and sequencing of the 97 kb region ft.
A;Reference number: 538655, MUD: 5302537; PMID: 7934828
A;Reference number: 538655, MUD: 5302037; PMID: 7934828
A;Retus: preliminary; nucleic acid sequence not shown; translation not shown
A;Retus: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-65 cGLA-
A;Residues: 1-65 cGLA-
A;Residues: 1-65 cGLA-
A;Residues: 1-65 cGLA-
A;Retus: preliminary; Nogare, I: A; Alberini, A.M.; Alloni, G.; Azovedo, V.; Berter
C; Bron, S; Broullier, S.; Brunlier, C.V.; Caldwell, B.; Captano, V.; Carter, N.M.; CARCE: T.; Carter, N.M.; CARCE: T.; Carter, N.M.; CARCE: T.; Remainer, S. P.; Brunlich, S. Brunlich, S. Brunlich, S. D.; Emmerson, P.; Extington, J.; Pabret, C.; Ferrari, E.
A; Bhrlich, S. D.; Emmerson, P.; Rinder, M.; Ringer, M.; Ringler, M.; Milloni, G.; Rrogh, S.; Kumano, M.; Kurin, R.; Patro, Y.; Poll, T.M.; Portor, V.; Poll, T.M.; Portor, V.; Poll, T.M.; Portor, V.; Poll, T.M.; Portor, V.; Poll, M.; Ringer, M.; Rivolte, C.; Roche, B.; Rose, M.; Sadada, Y.; Sadoo, T.; Schroenter, R.; Schr
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B31048
phosphotransferase system enzyme II (EC 2.7.1.69), mannitol-specific, factor III - Staph
NiAlternate names: phosphotransferase system enzyme III, mannitol-specific
C; Species: Staphylococcus carnosus
C; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004
C; Accession: B31048
R; Reiche, B.; Frank, R.; Deutscher, J.; Meyer, N.; Hengstenberg, W.
Biochemistry 27, 6512-6516, 1988
A; Title: Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system: purific
Carnosus and homology with the enzyme II(mtl) of Escherichia coli.
A; Reference number: A31048
A; Reference number: A31048
A; Accession: B31048
A; Accession: B31048
A; Readus: preliminary
A; Molecule type: protein
A; Readus: 1-67 aREI>
A; Cross-references: UNIPROT:P17876
C; Keywords: phosphotransferase system mannitol-specific enzyme II factor III; phosphot C; Keywords: phosphotransferase system mannitol-specific enzyme II factor III homolog
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Best Local Similarity 100.
Matches 3; Conservative
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PHG 35
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C;Species: phage P2
C;Species: phage P2
C;Date: 15-Oct-1996 #text_change 09-Jul-2004
C;Accession: B55855
C;Accession: B55855
R;Ziermann, R.; Bartlett, B.; Calendar, R.; Christie, G.E.
J. Bacteriol. 176, 4974-4984, 1994
A;Title: Functions involved in bacteriophage P2-induced host cell lysis and identificati
A;Reference number: A55855; MUID:94327465; PMID:8051010
A;Accession: B55855
A;Accession: B55855
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <ZIE>
A;Cross-references: UNIPROT:P51772; GB:L29304; NID:g508561; PID:g508562
C;Genetics:
A;Genet
                                                                         B, K.;
         Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
                                                                       Skelton, J.; Stevens,
Salmonella enterica s
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C;Species: Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Bccession: T17586
R;Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17586
A;Accession: T17586
A;Accession: T17586
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-67 <GRA>
A;Cross-references: UNIPROT: Q84417; EMBL: U42580; NID: g4028896; PIDN: AAC96464.1
A;Experimental source: specific host Chlorella strain NC64A
C;Genetics:
A;Gene: a96R
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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, I, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelle; Complete genome sequence of a multiple drug resistant Salne; Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0927
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-67 <PAR>
A;Residues: 1-67 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09441.1; PID:g16504558; GSC;Genetics:
A;Gene: STY3680
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4.7e+02;
hes 0; Indels
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100.0%; Pred. No. 4.7e+02;
ive 0; Mismatches 0; Indels
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Matches 3; Conservative
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hypothetical protein SMa1017 (imported) - Sinorhizobium meliloti (strain 1021) magaplasmy cystato sinorhizobium meliloti cybesion: Shorhizobium meliloti cybecies: Sinorhizobium meliloti cybecies: Sinorhizobium meliloti cybecies: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 cybecession: G95330 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowsi risk man, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C., Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloty A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95330
A;Status: preliminary
A;Molecule type: DNA
A;Residues: Je68 «KUR>
A;Cross-references: UNIPROT:Q922D7; GB:AE006469; PIDN:AAK65209.1; PID:g14523656; GSPDB:G3
A;Accession: G95330
A;Status: preliminary
A;Residues: 1-68 «KUR>
A;Cross-references: UNIPROT:Q922D7; GB:AE006469; PIDN:AAK65209.1; PID:g14523656; GSPDB:G3
A;Accession: G95330
A;Status: Preliminary
A;Residues: 1-68 «KUR>
A;Cross-references: UNIPROT:Q922D7; GB:AE006469; PIDN:AAK65209.1; PID:g14523656; GSPDB:G3
A;Authors: Kahn, P:; Cowie, A.; Davis, R.W.; Dreano, S.; Federapiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss E.; Komp, C.; Lelaure, A;Title: The composite genome of the lecume symbiont Sinorhizobium meliloti.
A;Genetics:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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OM protein - protein search, using sw model

June 15, 2005, 13:53:11 ; Search time 83.5 Seconds (without alignments) 30.663 Million cell updates/sec Run on:

US-10-074-225A-7 23 1 XXPHG 5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

segs, 512079187 residues 1612378 Searched:

1612378 Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Q6X700 Q8VJV6 Q81TC9 Q9RUH4 Q6EES4 Q9NC67 Q6X702 Q6X702 Q48911 Q48911 Q48911 Q48911	C C C C C C C C C C C C C C C C C C C	PRT; , Created) , Last seque , Last annot bacteriopha RNA stage; RNA stage; tion system phiSfi21.";
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MEDLINE=21663216; PubMed=11804559; DOI=10.1089/088922202753394745;
MEDLINE=21663216; PubMed=11804559; DOI=10.1089/088922202753394745;
Taniguchi Y., Takehsia J., Bikandou B., Mboudjeka I.,
N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
Ido E., Hayami M., Ichimura H., Parra H.Joseph.;
IGenetic subtypes of HIV type 1 based on the vpu/env sequences in the
                                                                                                                                                            Gaps
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1808 MW; E01CB44EF83834E2 CRC64;
                                                                               1856 MW; 8FA82D3270B9A959 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Thrombopoietin receptor (Fragment).
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01-DEC-2001 (TrEMBLrel. 19, Created)
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AIDS Res. Hum. Retroviruses 18:79-83(2002).
EMBL; AF127551; AAK84917.1; -.
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Virology 237:148-158(1997).
EMBL; AF013584; AAC48909.1; -.
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Mammalia; Eutheria;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
1-aminocyclopropene-1-carboxylate synthase 1b (Fragment)
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El Sharkawy I., Lelievre J.M., Latche A., Pech J.C.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
EMBL; AX514041; AAS66777.1; -.
                                               2A83630189068236 CRC64;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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100.0%; Pred. No. 5.9e+02;
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Q6X6Z8
ID Q6X6Z
AC Q6X6Z
DT 05-JU
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                                                                                                                                                                                                                                                                                                                   TISSUE=Hemolymph;

X MEDLINE=87242376; PubMed=3109474;

X Shipman B.A., Ryan R.O., Schmidt J.O., Law J.H.;

Shipman B.A., Ryan R.O., Schmidt J.O., Law J.H.;

The hemolymph of the honeybee Apis mellifera.";

Biochemistry 26:1885-1889(1987).

-!- FUNCTION: Unknown (it might play a role in lipid transport and/or storage protein metabolism during metamorphosis).

-!- SUBUNIT: Homodimer.

-!- SUBCELLULAR LOCATION: Extracellular.

-!- SUBCELLULAR LOCATION: Extracellular.

-!- TISSUE SPECIFICITY: Hemolymph.

-!- DEVELOPMENTAL STAGE: Present in high amounts in hemolymph only at the end of larval life.

PIR; A27108; A27108.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95164756; PubMed=7532194;
Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
"Characterization of trout galanin and its distribution in trout brain
                    Gарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and pituitary.";
J. Comp. Neurol. 350:63-74(1994).
-!- FUNCTION: Contracts smooth muscle of the gastrointestinal and genitourinary tract, regulates growth hormone release, modulates
                                                                                                                                          PRT; 27 AA.

PO9355;

01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-MAR-1989 (Rel. 14, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Larval-specific very high density lipoprotein (VHDL) (Fragment).
Apis mellifera (Honeybee).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
NCBI_TaxID=7460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
NCBI_TaxID=8022;
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                   Indels
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2885 MW; A9DDF7A75A65D10D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct protein sequencing; Hemolymph; Lipoprotein.
NON TER 27 27
SEQUENCE 27 AA; 2885 MW; A9DDF7A75A65D10D CRC6
Pred. No. 8.2e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.3%; Score 21; DB 1; Le
llarity 100.0%; Pred. No. 8.5e+02;
Conservative 0; Mismatches 0;
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33, Last sequence update)
44, Last annotation update)
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   100.0%;
                   3; Conservative
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Best Local Similarity
Matches 3; Consera
  Best Local Similarity
Matches 3; Conserv
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01-FEB-1996 (Rel.
05-JUL-2004 (Rel.
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MEDLINE=95164756;
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P47213;
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SEQUENCE
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GALA_ONCMY
                                                                                                                  RESULT 7
LSP_APIME
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Poluda L., Alonso C., Fernandez-Caldas E.;

"Purification, characterization, and partial sequencing of two new allergens of Olea europaea.";

J. Allergy Clin. Immunol. 101:210-216(1998).

-I. FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems (By similarity).

-!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).

-!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 34, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e v) (Fragment).
01 (Pragment).
01 (Superoxide dismutase (Common olive).
02 (Superoxide dismutase) (Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Lamiales; Oleaceae; Olea.
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insulin release, and may be involved in the control of adrenal
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-!- SIMILARITY: Belongs to the Cu-Zn superoxide dismutase family. InterPro; IPR001424; SOD_CU_ZN.
Pfam; PF00080; Sod_Cu; 1.
PROSITE; PS00087; SOD_CU_ZN 1; PARTIAL.
PROSITE; PS00332; SOD_CU_ZN 2; PARTIAL.
Allergen; Antioxidant; Copper; Direct protein sequencing; Metal-binding; Oxidoreductase; Zinc.
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                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the galanin family.
InterPro; IPR008174; Galanin.
Pfam; PF01296; Galanin; 1.
PRINTS; PR00273; GALANIN.
ProDom; PD005962; Galanin; 1.
PROSITE; PS00861; GALANIN; 1.
Amidation; Direct protein sequencing; Hormone; Neuropeptide.
MOD RES 29 Alanine amide.
SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;
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100.0%; Pred. No. 9.2e+02;
tive 0; Mismatches 0;
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05-JUL-2004 (TrEMBLrel. 27, Created)
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MEDLINE=98160390; PubMed=9500754;
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Q8R398;
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                                                                                                                                                                                                                                                                       Petersen A., Jensen L.B.;

"Analysis of gyrA and parC mutations in enterococci from environmental
samples with reduced susceptibility to ciprofloxacin.";

EMBL; AY252100; AAP84069.1; -.

EMBL; AY252100; AAP84069.1; -.

R GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0003677; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.

GO; GO:0006265; P:DNA topoisomerase activity; IEA.

R GO; GO:0006265; P:DNA topoisoiv.

R GO; GO:0006265; P:DNA topoisoiv.

R InterPro; IPR002205; DNA topoisoiv.

ProDom; PD000742; DNA topoisoiv; 1.
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                                                                                    Enterococcus gallinarum.
Bacteria, Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCB_TaxID=1353;
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Bacteria, Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCB_TaxID=37735;
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Pred. No. 9.2e+02;
0; Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Topoisomerase (Fragment).
                                                                                                                                                                                                                                                    PubMed=14769469; DOI=10.1016/S0378-1097(03)00929-7;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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29 AA;
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STRAIN=ATCC 35
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                                                                            Name=parC;
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Q6X701;
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Q6X701
 SO DE REPRESENTATION OF SO DE STATEMENT DE S
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EXPAINS TROUGH IN TISSUE=Mammary tumor;

KRY STRAINS TROUGH IN TISSUE=Mammary tumor;

KRY STRAINS TROUGH IN TISSUE Mammary tumor;

KRY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KRA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

KRA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.R., Bhat N.K.,

KRA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

KRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

KRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

KRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

KRA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

KRA Brownstein M.J., Usdin T.B., Toshiyki S., Carninci P., Prange C.,

KRA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

KRA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

KRA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

KRA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

KRA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

KRA Mhiting M., Madan A., Young A.C., Shewchenko Y., Bouffard G.G.,

KRA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

KRZywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

KR Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025886; AAH25886.1; -.
EMBL; BC025886; AAH25886.1; -.
RGD; MGI:108563; Ptpns1.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005887; C:integral to plasma membrane; IDA.
GO; GO:0005515; F:protein binding; IPI.
R GO; GO:0007015; P:actin filament organization; IMP.
GO; GO:0007016; P:cell motility; IMP.
R GO; GO:0007010; P:cytoskeleton organization and biogenesis; IMP.
R GO; GO:0006928; P:cell-matrix adhesion; IMP.
R GO; GO:0007010; P:phagocytosis, engulfment; IDA.
R GO; GO:0006911; P:phagocytosis, recognition; IDA.
R GO; GO:0005016; P:positive regulation of phagocytosis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
  DB 2; Le
9.2e+02;
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Score 21; DB
Pred. No. 9.2
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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0
  91.3%;
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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Name=Ptpns1;
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Best Local Similarity 100.
Matches 3; Conservative
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Euteleostomi; Canis.

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Q989K8

RESULT Q989K8

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Pubmed=15077118; DOI=10.1038/nbt959;
Rheidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T., Rolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Nationay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M., Nalson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Nalson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J., Natherenson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Reldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; "The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio vulgaris Hildenborough."; Nat. Biotechnol. 22:554-559(2004).
REMBL, AE017311; AAS95278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21015404; PubMed=11130975;
Brouillette J.A., Andrew J.R., Venta P.J.;
"Estimate of nucleotide diversity in dogs with a pool-and-sequence
method.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 31;
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31 31
31 AA; 3787 MW; 4E3B9EC795537E72 CRC64;
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Mammalia; Butheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0372F1F0B349FDE5 CRC64;
                                                                                                                                                                             Q9GKL4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Cardiac ryanodine receptor (Fragment).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=DVU0798;
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100.0%; Pred. No. 9.8e+02;
iive 0; Mismatches 0;
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EMBL; AF203021; AAG35635.1; -.

EMBL; AF203022; AAG35635.1; JOINED.

GO; GO:0004872; F:receptor activity; IEA.
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3; Conservative
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Q72DY1
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RX MEDLINE=21082930; PubMed=11214968;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Rawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., RA Takeuchi C., Yamada M., Tabata S.;
RY Toomplete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
RY Mesorhizobium loti.";
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Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Ms16380 protein.
OrderedLocusNames=ms16380;
Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 9.5e+02;
0; Mismatches 0; Indels
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EMBL; AF240632; AAF86958.1; -.
NON TER 30
SEQUENCE 30 AA; 3355 MW; 94F779DCE226E2AD CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Sialomucin complex (Fragment).
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sialomucin complex cells.";
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Hypothetical protein
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0736U2;
05-JUL-2004
05-JUL-2004
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Rhodococcus fascians.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI TaxID=1828;
                                                                                                                                                                                                                                                     91.3%; Score 21; DB 2; Length 32;
100.0%; Pred. No. 1e+03;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1e+03;
vative 0; Mismatches 0; Indels
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=NRRL-B-15096;
Dorado G., Roldan J.M., Lesher J.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY534865; AAS45278.1; -.
Hypothetical protein.
                                                                                 Q7M553;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Ribosomal protein S4.eR (Fragment).
Halobacterium salinarium (Halobacterium halobium).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
NCBI_TaxID=2242;
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32
3507 MW; DC612E3DC957273A CRC64;
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3463 MW; BCA73D0B5B1D338A CRC64;
 red. No. 9.8e+02;
Mismatches 0;
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 Pred. No.
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Best Local Similarity 100.
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Pecheux C., Gall A.L., Kaplan J.C., Dode C.;
"Sequence analysis of the CAG triplet repeats region in the Huntington disease gene (IT15) in several mammalian species.";
Ann. Genet. 39:81-86(1996).
EMBL; S83377; AAB50771.1; -.
NON_TER 33
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
PubMed=14960714; DOI=10.1093/nar/gkh258;
PubMed=14960714; DOI=10.1093/nar/gkh258;
Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pXO1.";
Nucleic Acids Res. 32:977-988(2004).
EMBL; AE017273; AAS41720.1; -.
TIGR; BCE2808; -.
Complete proteome; Hypothetical protein.
SEQUENCE 32 AA; 3635 MW; 6866784DFC0EADA3 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last annotation update)
Huntingtin protein (Fragment).
Name=IT15;
Gorilla gorilla (gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                                                                                                                                                                        Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes; Bacillales; Bacillus
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                                                    (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Created)
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Matches 3; Conservative
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O66384
ID O6638
AC O6638
DT 01-AU
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
GO; GO:0006265; P:DNA topological change; IEA.
InterPro; IPR002205; DNA topoisolV.
Pfam; PF00521; DNA topoisolV; 1.
ProDom; PD000742; DNA topoisolV; 1.
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GO; GO:0005524; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
GO; GO:0006265; P:DNA topoisolv.
InterPro; IPR002205; DNA topoisolv.
Ffam; PF00521; DNA topoisolv; 1.
Probom; PD000742; DNA topoisolv; 1.
                                                                                                                                                               Methylophilus methylotrophus (Bacterium W3A1).
Bacteria, Proteobacteria, Betaproteobacteria, Methylophilales;
Methylophilaceae; Methylophilus.
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Methylobacterium extorquens.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Methylobacteriaceae; Methylobacterium.
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0; Indels
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Kim H.J., Kim J.H., Kim K.S., Kim Y.M.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF287969; AAG17770.1; -.

HSSP; P09097; 1AB4.
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF287968; AAG17769.1; -.
HSSP; P09097; 1AB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 AA; 3791 MW; 32CC2C756A0FF45C CRC64;
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33 AA; 3791 MW; 32CC2C756A0FF45C CRC64;
                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gyrase subunit A (Fragment).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gyrase subunit A (Fragment).
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100.0%; Pred. No. 1e+03;
tive 0; Mismatches (
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Matches 3; Conservative
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Q9F711;
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C STRAIN=SK1;

Kim H.J., Kim J.H., Kim K.S., Kim Y.M.;

A Kim H.J., Kim J.H., Kim K.S., Kim Y.M.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

B SUBMITTER (JUL-2000) to the EMBL/GenBank/DDBJ databases.

R SUBMI
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STRAIN=ATCC27807T;
MEDLINE=99045881; PubMed=9828441;
Hiraishi A., Nagashima K.V.P., Matsuura K., Shimada K., Takaichi S., Wakao N., Katayama Y.;
"Phylogeny and photosynthetic features of Thiobacillus acidophilus and related acidophilic bacteria: its transfer to the genus Acidiphilium as Acidiphilium acidophilum comb. nov.";
Int. J. Syst. Bacteriol. 48:1389-1398(1998).
EMBL; AB013379; BAA26096.1; -.
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                                                                      Name=pufB;
Thiobacillus acidophilus.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
Acetobacteraceae; Acidiphilium.
NCBI_TaxID=76588;
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Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales;
Methylophilaceae; Methylobacillus.
NCB TaxID=134932;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Beta subunit of light-harvesting 1 complex (Fragment)
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100.0%; Pred. No. __
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01-MAR-2001 (TrEMBLrel. 16, C
01-MAR-2001 (TrEMBLrel. 16, L
01-OCT-2003 (TrEMBLrel. 25, L
Gyrase subunit A (Fragment).
Name=gyrA;
Methylobacillus sp. SKI.
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Best Local Similarity
Matches 3; Conserv
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Q6LBRO;
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EMBL;
TIGR;
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STRAIN=ATCC 35405 / DSM 14222;

PubMed=15064399; DOI=10.1073/pnas.0307639101;

PubMed=15064399; DOI=10.1073/pnas.0307639101;

A Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F., A Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H., A Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F., A Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A., Gebregeorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B., A Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A., A Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E., A Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.;

"Comparison of the genome of the oral pathogen Treponema denticola with other spirochete genomes.";
                                                                                                                                                                                                                                                     and incomplet.";
Blochem. Blophys. Res. Commun. 155:622-625(1988).
-!- FUNCTION: Binds heme and transports it to the liver for breakdown and iron recovery, after which the free hemopexin returns to the circulation.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
                                                                                                                                         Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                        PubMed=3421961;
K.C., Mueller-Eberhard U.;
acid sequences of the hemopexins from chicken, rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=TDE0141;
Treponema denticola.
Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI TaxID=158;
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InterPro; IPR000585; Hemopexin.
PROSITE; PS00024; HEMOPEXIN; PARTIAL.
Direct protein sequencing; Glycoprotein; Heme; Plasma; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 21; DB 1; Length 34; 100.0%; Pred. No. 1.1e+03; tive 0; Mismatches 0; Indels
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3598 MW; 07A2EEAC27386C57 CRC64;
                                                                                      17, Created)
17, Last sequence update)
44, Last annotation update)
                                                                   34 AA
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                                                                   STANDARD;
                                                                                      01-FEB-1991 (Rel. 17,
01-FEB-1991 (Rel. 17,
05-JUL-2004 (Rel. 44,
Hemopexin (Fragment).
Name=HPX;
                                                                                                                                                                                                   SEQUENCE.
MEDLINE=88339942; Pu
Wellner D., Cheng K
"N-terminal amino a
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PHG
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Q73RE8;
                                                                                                                                                                                Gallus.
                                                                  HEMO CF
P20057;
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HEMO_CHICK
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Q73RE8
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MEDLINE=90063453; PubMed=2584927;
Brorson K.A., Hunt S.W., Hunkapiller T., Sun H.Y., Cheroutre H.,
Nickerson D.A., Hood L.;
"Comparison of exon 5 sequences from 35 class I genes of the BALB/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
T10 class I MHC gene (exon 5) (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae, Yersinia.
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                                                                                                                                                                                                      0; Indels
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Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
EMBL; X16216; CAE82028.1; -.
NON_TER 1 1 1
NON_TER 35 35
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                                                                                                       3643 MW; EC84B7F1133531C4 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Natl. Acad. Sci. U.S.A. 101:5646-5651(2004)
AE017246; AAS10639.1; -.
TDE0141; -.
                                                                                                                                                     Query Match 91.3%; Score 21; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 3; Conservative 0; Mismatches 0;
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STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16.4601-4611.2002;
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J. Exp. Med. 170:1837-1858(1989).
[2]
SEQUENCE FROM N.A.
STRAIN-Domesticus;
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Matches 3; Conservative
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OrderedLocusNames=y0064;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
ATP-binding.
             SIMILARITY: Belongs to the ABC transporter family
                                                                                                                        36 AA; 3753 MW; CDB46C744DC8610D CRC64;
                                                                                                                                   Query Match
Best Local Similarity 100.
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   Leukemia 7:13-13(1993)
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Best Local Similarity
3, Conserve
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Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry R.D.; "Genome sequence of Yersinia pestis KIM."; J. Bacteriol. 184:4601-4611(2002).

EMBL; AE013607; AAM83659.1; -. Hypothetical protein.

SEQUENCE 35 AA; 3936 MW; 10744A0FDF6AC04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                          Miller J.H.; "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
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MEDLINE=93368189; PubMed=8361216;
Allikmets R., Gerrard B., Stewart C., White M., Dean M.;
"Identification of P-glycoprotein/multidrug resistance genes from model organisms.";
                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11792869; DOI=10.1073/pnas.241636498; Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
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                                                                                                                         Length 35
                                                                                                                                                                                                                                                                                                                         Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
Thermoproteaceae; Pyrobaculum.
NCBI_TaxID=13773;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Multidrug resistance P-glycoprotein (Fragment).
Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                     Score 21; DB 2; Le; Pred. No. 1.1e+03; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009833; AAL63646.1; -.
Complete proteome.
SEQUENCE 36 AA; 4060 MW; 43CC1A624F2822C5 C
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                                                                                                                       91.3%;
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                                                                                                                                                                                                                                                                                                               OrderedLocusNames=PAE1672;
                                                                                                                                               Conservative
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Matches 3; Conser
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Saccharomycetales;
NCBI_TaxID=4932;
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Q8ZWQ4;
01-MAR-2002 (
01-MAR-2003 (
01-JUN-2003 (
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STRAIN=IM2;
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Q9URE9
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain;

A transberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A promistein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Robar S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Youchman J.W., Schen E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Schen E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                         Indels
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056177; AAH56177.1; -.
Hypothetical protein.
SEQUENCE 37 AA; 3977 MW; 5D7166A450809A2B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
91.3%; Score 21; DB 2; Lo
100.0%; Pred. No. 1.1e+03;
ive 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.2e+03;
Conservative 0; Mismatches 0;
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STRAIN=C57BL/6; TISSUE=Brain;
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Query Match
Best Local Similarity 100.
Matches 3; Conservative
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Q9RUH4;
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Q81TC9
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STRAIN=ATCC 25788;
STRAIN=ATCC 25788;
BubMed=14769469; DOI=10.1016/S0378-1097(03)00929-7;
Petersen A., Jensen L.B.;
Petersen A., Jensen L.B.;
Ramples with reduced susceptibility to ciprofloxacin.";
FEMS Microbiol. Lett. 231:73-76(2004).
EMBL; AY252098; AAP84067.1; -.
RGO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003577; F:DNA binding; IEA.
GO; GO:0003655; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
GO; GO:0006265; P:DNA topoisolv:
RGO; GO:0006265; P:DNA topoisolv:
RGO; GO:0006265; P:DNA topoisolv:
RFAM: PF00521; DNA topoisolv:
RFAM: PF00621; DNA topoisolv:
RFAM: PF00621; DNA topoisolv:
RFAM: PF00621; DNA topoisolv:
RFAM: PF00671; D
                                                                                                                                                                                                                                                                                                                                                environmental
                                                                                                                                                                                        Name=parC;
Enterococcus casseliflavus.
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=37734;
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STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M. Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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Bacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 2; Length 38;
Pred. No. 1.2e+03;
0; Mismatches 0; Indels
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4357 MW; CEB751F1C22440E8 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Topoisomerase (Fragment).
                                                                                      38 AA
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                                                                                     PRT;
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Q8VJV6;
Q1-MAR-2002 (TrEMBLrel. 20, C)
01-MAR-2002 (TrEMBLrel. 20, L;
01-MAR-2002 (TrEMBLrel. 20, L;
Hypothetical protein.
OrderedLocusNames=MT1909;
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3; Conservative
                                                                                     PRELIMINARY;
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Gill J., Mikula A.,
Fraser C.M.;
"Whole-genome compar
laboratory strains."
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38
38 AA;
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Q6X700;
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Q8VJV6
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STRAIN=Ames / isolate Porton;

MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,

Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,

Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

Asalzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;

"The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria.";

Nature 423:81-86(2003).
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Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Fed
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
Fraser C.M.;
                                                                                                                                                                                                 Length 38
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"Bacillus anthracis comparative genomics.";
"Bubilted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017028; AAP25301.1; -.
EMBL; AE017334; AAT30451.1; -.
TIGR; BA1355; -.
TIGR; GBAA1355; -.
Complete proteome; Hypothetical protein.
SEQUENCE 38 AA; 4456 MW; 965D6E445A9BE25C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                     461CADD7180DB359 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q81TC9 PRELIMINARY; PRT; 38 AA.
Q81TC9; Q6KVF5;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BA1355, GBAA1355;
Bacillus anthracis.
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100.0%; Pred. No. 1.2e+03;
tive 0; Mismatches 0;
                                                                                                                                                                                            91.3%; Score 21; DB 2; L. 100.0%; Pred. No. 1.2e+03; tive 0; Mismatches 0;
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J. Bacteriol, 184:5479-5490(2002).
EMBL; AE000516; AAK46180.1; -.
TIGR; MT1909; -.
Hypothetical protein.
SEQUENCE 38 AA; 4273 MW; 461CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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Enterococcus flavescens.
Bacteria, Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=37735;
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GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
GO; GO:0005265; P:DNA topoisolosical change; IEA.
InterPro; IPR002205; DNA_topoisolV.
Pfam; PF00521; DNA_topoisolV; 1.
ProDom; PD000742; DNA_topoisolV; 1.
NON_TER 1 1
NON_TER 39 39
                                                                                                                                                                                                                                                                                                                                              Alexander S.;
the anticancer drug cisplatin in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 39;
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STRAIN=CECT 4481;
Pubmed=14769469; DOI=10.1016/S0378-1097(03)00929-7;
Petersen A., Jensen L.B.;
"Analysis of gyrA and parC mutations in enterococci from samples with reduced susceptibility to ciprofloxacin.";
FEMS Microbiol. Lett. 231:73-76(2004).
EMBL; AY252096; AAP84065.1; -.
HSSP; P09097; 1AB4.
                                                                                                                                                                                                                                                                                                              MEDLINE=20431894; Pubmed=10974109; Li G., Alexander H., Schneider N., Alexander S.; Li G., Alexander H., Schneider N., Alexander S.; Molecular basis for resistance to the anticancer dr Dictyostelium."; Microbiology 146:2219-2227(2000).

EMBL; AF233610; AAF97870.1; -. DictyBase; DDB0214888; sglA.

GO; GO:0016829; F:lyase activity; IEA.

InterPro; IPR010916; TONB_BOX_N.

PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1
39
4140 MW; BBB528F43199727A CRC64;
                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sphingosine-1-phosphate lyase (Fragment).
Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                  39 AA
                                PRT;
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                                PRELIMINARY;
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Best Local Similarity
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39
39 AA;
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Q6X702;
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Q6X702
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266; DOI=10.1126/Science.286.5444.1571;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
Praser C.M.;
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TISSUE=Lung;
PubMed=15233991; DOI=10.1016/j.ygeno.2004.04.004;
Roginski R.S., Mohan Raj B.K., Birditt B., Rowen L.;
"The human GRINL1A gene defines a complex transcription unit, unusual form of gene organization in eukaryotes.";
Genomics 84:265-276(2004).
EMBL; AY350748; AAQ82541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1."; Science 286:1571-1577(1999).
EMBL; AE001986; AAF10978.1; -.
PIR; G75398; G75398.
                                                                                                                             Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus; Deinococcaceae;
Deinococcaceae; Deinococcus.
NCBI_TaxID=1299;
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3891 MW; OEEBEFAGAFA325A4 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein DR1412.
OrderedLocusNames=DR1412;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
GRINLIA combined protein Gcom12 (Fragment).
Name=GRINLIA;
Homo sapiens (Human).
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Indels

Gaps . 0 91.3%; Score 21; DB 2; Length 39; 100.0%; Pred. No. 1.2e+03; Live 0; Mismatches 0; Indels 39 AA; 4312 MW; CDB3CDD0246265F3 CRC64; Conservative Best Local Similarity Matches 3; Conser

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RESULT

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from environmental

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SEQUENCE FROM N.A.

MEDLINE=96254595; PubMed=8849234;

Yonezawa M., Takahata M., Banzawa-Futakuchi N., Matsubara N.,

A watanabe Y., Narita H., Matsunaga T., Igarashi H., Kawahara M.,

Onodera S.;

"DNA gyrase gyrA mutations in quinolone-resistant clinical isolates of staphylococcus haemolyticus.";

Antimicrob. Agents Chemother. 40:1065-1066(1996).

EMBL; D78568; BAA11412.1; -.

Antimicrob. Agents Chemother. 40:1065-1066(1996).

REMBL; D78568; BAA11412.1; -.

REMBL; D78568; BAA11412.1; -.

REMBL; D78568; P:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.

GO; GO:00035677; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.

GO; GO:0003657; P:DNA topoisomerase (ATP-hydrolyzing)

RO; GO:0003657; P:DNA topoisolv.

RO; GO:000425; P:DNA topoisolv.

RO; GO:000425; DNA topoisolv.

RO; GO:00042; DNA topoisolv; 1.

R Prodom; PD000742; DNA topoisolv; 1.

R Prodom; PD000742; DNA topoisolv; 1.

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SEQUENCE 40 AA; 4533 MW; A4C6842027AA7812 CRC64;
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Miller J.H.;
"Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009915; AAL64721.1; -.
Complete proteome.
SEQUENCE 40 AA; 4604 MW; B6C670022B6F64E7 CRC64;
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                                                                                                              Q8ZTN8 PRELIMINARY; PRT; 40 AA.
Q8ZTN8;
O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2003 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
PAREP2a.
OrderedLocusNames=PAE3166;
Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum.
NCBL_TaxID=13773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 91.3%; Score 21; DB 2; Length 40; Best Local Similarity 100.0%; Pred. No. 1.3e+03; Matches 3; Conservative 0; Mismatches 0; Indels
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P95768
ID P95768
PRELIMINARY;
AC P95768
AC P95768
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DF GryA (Fragment).
GN Name=gyrA;
OS Staphylococcus haemolyticus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1283;
OX NCBI_TaxID=1283;
OX NCBI_TaxID=1283;
OX NCBI_TaxID=1283;
OX NCBI_TaxID=1283;
OX NCBI_TaxID=1283;
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PHG 5
Db 13 PHG 15
Search completed: June 15, 2005, 14:21:22
Job time: 85.5 secs
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us-10-074-225a-8.rag

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version 5.1.6
- 2005 Compugen Ltd.
GenCore
Copyright (c) 1993
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- protein search, using sw model OM protein June 15, 2005, 13:52:01; Search time 90 Seconds (without alignments) 21.487 Million cell updates/sec Run on:

US-10-074-225A-8 37 1 HHPHG 5

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

segs, 386760381 residues 2105692 Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_16Dec04:\* 1: genesecm1980...

1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

uo.	Histidine	Rabbit HP	Cathepsin	Human bra	Human pol	Human col	Rabbit HP	PRM-P5-F1	Rabbit hi	Human his	Human HPR	Peptide #	Peptide #	Peptide #	Protein #	Human bon	Human bra	Human liv	Human pep	Drosophil	Propionib	Propionib	Protein e	M. catarr	Human gap
Description	Abb79809	Adh10415	Aau10991	Aae10907	Aao07477	Aag73663	Adh10412	Adm16706	Abb79807	Abb79806	Adh10411	Aam21476	Abb43818	Aam37725	Abb26753	Aam77540	Aam64782	Abg59189	Abg46564	Abb71093	Aau55932	Abm52451	Abu35012	Ad105482	Aay32079
ΠD	ABB79809	ADH10415	AAU10991	AAE10907	AA007477	AAG73663	ADH10412	ADM16706	ABB79807	ABB79806	ADH10411	AAM21476	ABB43818	AAM37725	ABB26753	AAM77540	AAM64782	ABG59189	ABG46564	ABB71093	AAU55932	ABM52451	ABU35012	ADL05482	AAY32079
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
Result No.	1	7	m	4	ß	9	7	60	თ	10	11	12	13	14	15	16	17		19		21		23	24	25

Adil7057 Human NOV Adil7060 Human NOV	Abuse449 Lung canc Abuse673 Lung canc	Adn39026 Cancer/an Adn39932 Cancer/an	Adn46756 Thermococ Abb66932 Drosophil	Ads30838 Bacterial Abb71820 Drosophil		Human Human	Adh10409 Human HPR Ad112335 Human ste	Abb79805 Rabbit hi Adh10410 Rabbit HP
ADI17057 ADI17060	ABU56449 ABU56673	ADN39026 ADN39932 ABR60468	ADN46756 ABB66932	ADS30838 ABB71820	ABB59479 ABO77799	ABB79804 ADE76897	ADH10409 ADL12335	ABB79805 ADH10410
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273	273 273 273	273 273	326	350 402	419 466	525 525	525 525	526 526
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37	37	37	37	37	37	37 37	37	37
27	9 6 0 9 7 8	322	ე ტ ტ ე <b>4</b> წ	36 37	9 B	40 41	42 43	4 4 5

## ALIGNMENTS

Histidine proline rich glycoprotein; HPRG; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian. Histidine proline rich glycoprotein pentapeptide Mazar AP; Plunkett ML, ABB79809 standard; peptide; 5 AA 14-FEB-2002; 2002WO-US004336. 14-FEB-2001; 2001US-0268370P (first entry) (ATTE-) ATTENUON LLC. Donate F, Harris S, WO200264621-A2. 22-AUG-2002. 25-NOV-2002 Synthetic ABB79809; ABB79809 RESULT 1 

WPI; 2002-666989/71. P-PSDB; ABN84910.

New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.

Claim 2; Page 67; 82pp; English

The present sequence is a specific example of claimed anti-angiogenic pentapeptides of the invention. Claimed anti-angiogenic polypeptides or peptides comprise: the histidine-proline-rich (H/P) domain of human histidine proline rich glycoprotein (HPRG, see ABB79806); an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808, such as the present peptide, or its variant having an additional 1 to 4 amino acids comprising His, Pro or Gly at its No or C-terminus. Also claimed are: chemically synthesised or

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the composition of periods and supposition and againosticatly of the diagnostically labeled anti-angioganic polypeptide, peptide or peptide multimer; a diagnostically labeled anti-angioganic polypeptide, peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the HPRG and which binds to HPRG or to any comprising of the domains in a way which inhibits the anti-angiogenic activity of the domains in a way which inhibits the anti-angiogenic activity of of the domain, or an antigen-binding fragment of the antibody; a constrowing a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis; a method for treating a subject having a disease or condition associated with undesired cell contrading appropriate in a subject; a method of stimulating or inhibiting angiogenesis in a subject; a method of stimulating or inhibiting angiogenesis in a subject; a method of stimulating or inhibiting angiogenesis in a subject; a method of stimulating or inhibiting angiogenesis or cells, in a method of providing to a cell, tissue or organ an abiological sample; isolated nucleic acids encoding the polypeptide, or peptide multimer; an expression vector; transfected cells; a method of providing to a cell, tissue or organ an angiogenesis-inhibitory amount of HPRG, an H/P domain of HPRG or its pentapeptide, or the peptide multimer; an affinity ligand useful for the binding molecule, comprising the polypeptide, peptide or peptide compositions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, invasion, invasion, compositions and methods are useful in diagnosing or treating a disease or conditions and methods are useful in diagnosing or treating a disease or conditions and methods are useful and each or angele and methods are useful and each or an each or an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or angiogenesis, such as cancer, atherosclerosis, diabetic or angiogenesis, such as cancer, atherosclerosis, diabetic nflammation, endometriosis, arthritis, peptic ulcers, or is especially useful in inhibiting the growth of primary astases, and may also be used in treating neurodegenerative Alzheimer's or Parkinson's disease. The antibodies are angiogenesis and are useful for promoting tion in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rich glycoprotein; HPRG; cytostatic; antidiabetic; antiinflammatory; gynaecological; antiarthritic; matological; cardiant; vasotropic; vulnerary; therapy; rabbit.
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   multimers; a diagnostically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 37; DB 5; Length 5; larity 100.0%; Pred. No. 1.8e+06; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit HPRG protein H/P rich domain repeat fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiangiogenic receptor;
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fractures. HPRG is espe
tumours or metastases,
diseases like Alzheimer
   recombinantly produced therapeutically labeled
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5; Conserv
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neovascularization
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Matches S
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ADH10415
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The invention relates to an isolated tropomyosin (Tpm)-related
antiangiogenic receptor polypeptide or peptide, which is a is a fragment
CC antiangiogenic receptor polypeptide or peptide, which is a surface of
c andothelial cells, or a variant of the fragment. It has a molecular mass
CC dabout 17 kDa and corresponds in its sequence to, or is a variant of,
an internal fragment of a native Tpm isoform which is a binding site for
antiangiogenic polypeptide agents; The isolated antiangiogenic receptor
CC antiangiogenic polypeptide agents; The isolated antiangiogenic receptor
polypeptide, peptide or variant has substantially the same biochemical
activity of binding to the antiangiogenic polypeptide agent that
cc native Tpm internal fragment. The antiangiogenic polypeptide agent that
binds to the isolated polypeptide or peptide is human histidine-proline
crich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic
c homologue, variant, domain or fragment of human or rabbit HPRG, two chain
cc rich glycoprotein (HPRG), the DS domain of HK, or a Tpm-binding,
conditiangiogenic homologue, variant, domain or fragment of the HK or its DS
cc domain. The Tpm-related antiangiogenic receptor polypeptide or peptide,
antibodies and compositions are useful for inhibiting endothelial cell
migration, invasion, proliferation or angiogenesis, for inducing
centionethy, neovascular glaucoma, vueitis, endometriosis, arthritis,
centhopathy, neovascular glaucoma, vueitis, endometriosis, arthritis,
conditions in which
contreased angiogenesis is desired, e.g. coronary artery disease or
concern in the rabbit HPRG protein His-Pro (H/P) rich domain.
                                                                                                                                                                      New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contrast agent; cancer; cardiovascular disease; inflammation; stroke; central nervous system disorder; infection; cardiac failure; embolism; myocardial infarction; atherosclerosis; thrombosis; aneurysm; haemorrhage; Alzheimer's disease; multiple sclerosis; bone disease; osteoporosis; apoptosis; necrosis; cathepsin D.
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                 Mazar AP;
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                              Juarez J,
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                                 Donate F,
                                                                                                    WPI; 2004-090604/09.
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                        Example 5;
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                                 Mccrae K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU10991;
                                                                                                                                                                                                                                                                                     cancer
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셤
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The invention relates to a contrast agent substrate (I) susceptible of changing pharmacodynamic and/or pharmacokinetic properties upon the influence of enzymatic activity. The contrast agent substrate is useful for detection of tissue or cells with abnormal metabolic activity, for identification and/or diagnosis of cancer, cardiovascular diseases, diseases on the central nervous system, inflammations, or infections and diseases on the central nervous system, inflammatic activity, where the substrate is administered to human or animal body and a contrast agent signal is detected as a result of the contrast agent changing pharmacodynamic and/or pharmacokinetic properties. The substrate is useful for manufacturing a medicament for detecting an area of disease of abnormal enzymatic activity. The contrast agent is useful in diagnosis of cardiac failure, myocardial infarction, atherosclerosis, thrombosis, embolism, aneurysms, stroke, haemorrhage, central nervous system diseases, preferably Alzheimer's disease or multiple sclerosis, bone diseases such as osteoporosis, viral infections, and for identification of apoptosis and necrosis. The metabolically sensitive contrast agents as early sign of disease/condition, the contrast agents have a potential for diagnosing disease at an early stage, which in many clinical situations are important for the outcome of stage, which in many clinical situations are important for the outcome of stage, which in many clinical situations are important for the outcome of stage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tions are important for the outcome of sensitive to treatment and can be used sequence represents the cathepsin D
                                                                                                                                                                                                                                                                                                                         Contrast agents susceptible of changing pharmacodynamic and/or pharmacokinetic properties upon enzymatic activity, useful in diagnosis of cancer, cardiovascular diseases and inflammation in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lent. The present sequence rethe method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agents are very sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 37; DB 100.0%; Pred. No. 4.8; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               53; 77pp; English
 /note= "Cys(Et)"
                                                                                                                        2001WO-NO000215
                                                                                                                                                               23-MAY-2000; 2000NO-00002644
                                                                                                                                                                                                                                             Tolleshaug H;
                                                                                                                                                                                                     (NYCO-) NYCOMED IMAGING AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the treatment. The agent
to follow up treatment.
                                                                                                                                                                                                                                                                                    WPI; 2002-097616/13.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    substrate, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HHPHG
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                                         WO200189584-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHPHG
                                                                                                                                                                                                                                           Klaveness J,
                                                                                                                       23-MAY-2001;
                                                                               29-NOV-2001
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Query Match
Best Local Similarity 100.0%
Matches 5; Conservative .
                                                                                                                                                                                                                                                                                                                            Sequence 33 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          Human; brain sodium channel 4 protein; BNaC4; cerebroprotective; acid-sensing ion channel; ASIC4; neuromodulation; vasotropic; neurotransmission; ischaemia; neurodegeneration; Alzheimer's disease; Huntington's disease; amyotrophic lateral sclerosis; antiinflammatory;
Gaps
                                                                                                                                                                                                                                                                                                                                                  channel 4 protein (BNaC4) C-terminal peptide
                                                                                                                                                                                                          peptide; 33 AA
                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                Human brain sodium
                                                                                                                                                                                                        AAE10907 standard
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Gaps

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Indels

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Mismatches

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HHPHG

100.0%; Score 37; DB 4; Length 33; 100.0%; Pred. No. 13;

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The inventor relates to numban Drain south actioning by procesh is the invention relates to numban Drain south (ASIC4). Human BNaC4 is useful for identifying compounds that modulate its activity, by measuring the for identifying compounds that modulate its activity, by measuring the for identifying compounds that modulate its activity by measuring the state of the modulator on the protein. BNaC4-dependent cytotoxicity or BNAC4-dependent activation of ion flux. Compounds discovered by screening test compounds using human BNaC4 protein is useful for treatment for a condition mediated by human BNaC4. BNaC4 antibody is useful for blocking the activity of the polypoptide. BNaC4 antibody is useful for blocking the activity of the polypoptide. BNaC4 classase, Huntington's disease, amyotrophic lateral sclerosis, cerebellar diseases, Huntington's disease, amyotrophic lateral sclerosis, cerebellar cataxias and For use as analgesics for intractable pain, complex. Conditions and for use as analgesics for intractable pain, complex. regional pain syndrome, arthritis (ostecarthritis, rheumatorid), ulcers, neurodegenerative diseases, asthma, chronic obstructive pulmonary diseases, irritable bowel syndrome, psoriaais, central nervous system classase, irritable bowel syndrome, psoriaais, central nervous system diseases, control of viscera innervated by the dorsal root ganglia and to disease, control of viscera innervated by the dorsal root ganglia and to disease, control of viscera innervated by the dorsal root ganglia and to disease, control of viscera innervated by the dorsal root ganglia and to disease, control of viscera innervated by the dorsal root gandide. There consistent in one of the DNA molecules. BNAC4 DNA is used in gene contrary. The present sequence is human BNAC4 c-terminal peptide. There were 2 bases in the BNAC4 coding sequence that were consistently consistently consistently consistent in one of 10 independent cDNA library clones. These ketc and different in one of 10 independent consistence is and the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of acid-sensing ion measuring the effect
pain; Parkinsonism; inflammatory condition; cerebellar ataxia; complex regional pain syndrome; osteoarthritis; rheumatoid arthritis; ulcer; neurodegenerative disease; asthma; irritable bowel syndrome; chronic obstructive pulmonary disease; central nervous system disease; psoriasis; intestinal tract disease; gene therapy; neuroprotective; nootropic; analgesic; osteopathic; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to human brain sodium channel 4 protein (BNaC4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l 4 protein, a member
modulators comprises
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                                                                                                                                                                                                Location/Qualifiers
2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 60; 94pp; English
                                                                                                                                                                                                                                                              label= Lys, Arg
                                                                                                                                                                                                                                                                                                             /label= Ala, Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channel family, for identifying of the modulator on the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-FEB-2001; 2001WO-US004525.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Erlander MG,
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                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                        Misc-difference
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 97 AA;
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                                                                                                      WO200122920-A2
                                                                                                                                                  28-SEP-2000;
                                                                                 Homo sapiens
                                                                                                                                                                         29-SEP-1999;
03-NOV-1999;
  03-SEP-2001
                                                                                                                              05-APR-2001.
                                                                                                                                                                                                                               Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to 1052,
                          Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                           cids and polypeptides, useful for preventing diagnosing leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the encoded proteins (AAO000010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                          Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human polynucleotides (AAI79941-AAI93841) and
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                                                                      Z
                                                                                                                                      SEQ ID NO 21369
                                                                     42
                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                            28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                                                                                     Drmanac RT
                                                                    protein;
                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-514838/56.
N-PSDB; AAI87408.
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Best Local Similarity
Matches 5; Conserv
(HYSE-) HYSEQ INC.
                                                                                                                                       Human polypeptide
                                                                    AAO07477 standard
                                                                                                                                                                                                                                                                                                                                                                                                                                    and treating e.g.
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HHPHG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42 AA;
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                                                                                                                                                                                                                                          WO200164835-A2
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                              07-SEP-2001
                                                                                                                06-NOV-2001
                                                                                           AA007477;
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              18
                                                         AA00747.
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AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal action and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the present invention. N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                       Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
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colon cancer antigen protein SEQ ID NO:4427
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                                                                                     colorectal carcinoma; chromosome 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH10412 standard; protein; 101 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for preventing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-235357/24.
N-PSDB; AAH33094.
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protein; 97

AAG73663 standard;

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RESULT 6 AAG73663 AAG73663

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                     Phlebotomus
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                                                                                                                                                                                                                                                                                                The invention relates to an isolated tropomyosin (Tpm) related
antiangiogenic receptor polypeptide or peptide, which is a is a fragment
C antiangiogenic receptor polypeptide or peptide, which is a surface of
endothelial cells, or a variant of the fragment. It has a molecular mass
of about 17 kDa and corresponds in its sequence to, or is a variant of,
an internal fragment of a native Tpm isoform which is a binding site for
c antiangiogenic polypeptide agents; The isolated antiangiogenic receptor
polypeptide, peptide or variant has substantially the same blochemical
activity of binding to the antiangiogenic polypeptide agent that
continuty of binding to the antiangiogenic polypeptide agent that
continuty of binding to the antiangiogenic polypeptide agent that
continuty of binding to the antiangiogenic polypeptide agent that
continuty of binding to the antiangiogenic polypeptide agent that
conformed to the isolated polypeptide or peptide is human histidine-proline
conformed to the isolated polypeptide or peptide is human histidine-proline
conformed to the bold of the bold of the proposition of the propositions are useful for inhibiting endothelial cell
migration, invasion, proliferation or angiogenesis, for inducing
conforted antiangiogenic endometriosis, arthritis,
conforted antiangiogenic or peptide in a biological sample, for
contreased angiogenesis is desired, e.g. coronary artery disease or
concition which
concept artery disease. The present sequence represents a rabbit HPRG
conception HIB-Pro (H/P) rich domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                         New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
11; cardiant; vasotropic; vulnerary;
rabbit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Length 101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                             Mazar AP
                                                                                                                                                                                                                                                                                 24; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 137 AA
                                                                                                                                                                             F, Juarez J,
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0
       cmatological;
s therapy; rał
                                                                                                          17-MAR-2003; 2003WO-US008060
                                                                                                                               15-MAR-2002; 2002US-0364047P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                        Oryctolagus cuniculus
                                                                                                                                                       ATTENUON LLC.
                                                                                                                                                                                                  WPI; 2004-090604/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conser
                   angiogenesis, gene
                                                                                                                                                                                                                                                                                 2
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        der
                                                                                                                                                                             Donate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM16706 standard;
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                                                             WO2003077872-A2
                                                                                                                                                                                                                                                                               Claim 6; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 101 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HHPHG
       antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-2004
                                                                                    25-SEP-2003
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                                                                                                                                                       (ATTE-)
                                                                                                                                                                              Mccrae
                                                                                                                                                                                                                                                          cancer
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ADM16706
       원
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The present invention relates to a substantially purified salivary Phlebotomus ariasi or Phlebotomus perniciosus polypeptide. The composition comprising the polypeptide or the nucleic acid encoding the polypeptide is useful for manufacture of a medicament. The polypeptides and nucleic acids are useful for inducing an immune response to a P. ariasi or P. perniciosus polypeptide. It is also useful for inhibiting a symptom of a Leishmania infection or preventing a Leishmania infection in a subject. The present sequence represents a purified Phlebotomus ariasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Histidine proline rich glycoprotein; HPGP; rabbit; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New substantially purified salivary Phlebotomus ariasi or Phlebotomus perniciosus polypeptide, useful for inhibiting, treating or preventing Leishmania infection in a subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 37; DB 8; Length 137; .larity 100.0%; Pred. No. 54; Conservative 0; Mismatches 0; Indels
ariasi; Phlebotomus perniciosus; Vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Belkaid Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kamhawi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI-) MERIAL LTD.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribiero JMC,
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                                                                                                                                                                                                                                                                                                  18-SEP-2003; 2003WO-US029833
                                                                                                                                                                                                                                                                                                                                                                19-SEP-2002; 2002US-0412327P
12-NOV-2002; 2002US-0425852P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Valenzuela JG, Ribierc
Audonnet J, Milward F;
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                                    Leishmania infection.
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                                                                                               Phlebotomus arisasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                  WO2004027041-A2
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The present sequence is the protein sequence of the histidine-proline-rich (HPP) domain of rabbit anti-angloganic histidine proline rich glycoprotein (HPRG, see also, ABB79806). Claimed anti-angloganic proliferidine proline rich (BPP) domain of rabbit HPRG, a variant of these that is capable of inhibiting anglogenesis, and chelial cell proliferation or endothelial cubbit HPRG, an HPP domain of rabbit HPRG, a variant of these that is capable of inhibiting anglogenesis, and chelial cell proliferation or endothelial cubbiting by propertied paving the generic sequence given in ABB79808. Also claimed are: chemicially synthesised or recombinantly produced peptide wultimers; a diagnostically useful HPRG, polypeptide, poptide or peptide multimer; and antibody specific for an epitope of HPRG that is present in the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any of the domains in a way which inhibites the anti-anglogenes cell invasion, carrier; an antipody specific for an epitope of HPRG or the antibody; a method for inhibiting all mispatch, and which binds to HPRG or to any of the domain or analysen-binding fragment of the antibody; a method for inhibiting anglogenesis; a method for treating a subject having a disease or condition associated with undesired cell a biological sample; isolated nucleic acids encoding the polypeptide, peptide multimer; an expression vector; transferred cells, a method of providing to a subject; transferred cells, a method of providing to a cell; tissue or organ an anglogenesis in mibiting and method of providing to a cell; transferred cells, or the peptide multimer; an expression vector; transferred cells, or the peptide multimer; an expression vector; transferred cells, or the peptide multimer; an expression vector; transferred cells, or the peptide multimer; an expression vector; from a complex minker or peptide multimer; or solating molecule or solating molecule, or solating molec
                                                                                                                                                                                                                New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iogenesis and are useful for promoting in pertinent disease states, and in various
                                                                                                          Mazar AP;
                                                                                                         Plunkett ML,
                                                                                                                                                                                                                                                                                                     82pp; English
                    14-FEB-2001; 2001US-0268370P
                                                           (ATTE-) ATTENUON LLC.
                                                                                                                                                  WPI; 2002-666989/71
P-PSDB; ABN84910.
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neovascularization
                                                                                                                                                                                                                                                                                                     Claim 1; Page 13;
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                                                                                                         Donate
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Sequence 148 AA;

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Gaps
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100.0%; Score 37; DB 5; Length 148; 100.0%; Pred. No. 58; ive 0; Mismatches 0; Indels
             Similarity
5; Conserv
Query Match
Best Local S
Matches 5
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39 Ŋ HHPHG HHPHG Н 35 ò

protein; 148 AA. ABB79806 standard; RESULT 10 ABB79806 ID ABB79

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Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian.
                     Human histidine proline rich glycoprotein His/Pro-rich domain.
            25-NOV-2002
    ABB79806;
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VO200264621-A2 Homo sapiens.

22-AUG-2002.

Mazar AP; Plunkett ML, 14-FEB-2002; 2002WO-US004336. 14-FEB-2001; 2001US-0268370P (ATTE-) ATTENUON LLC Harris S, WPI; 2002-666989/71. P-PSDB; ABN84910 Donate F,

New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.

Claim 1; Page 13; 82pp; English.

The present sequence is the protein sequence of the histidine-prolineCC Tich (HPP) domain of human anti-anglogenic histidine proline rich
glycoprotein (HPRG, see also ABB79804). Claimed anti-anglogenic and properties or peptides comprise: the HPP domain of human HPRG; an H/P
glycoprotein (HPRG, see ABB179804). Claimed anti-anglogenic and proliferation or endothelial of inhibiting anglogenesis, endothelial cell proliferation or endothelial cof inhibiting anglogenesis, endothelial cell proliferation or endothelial companition in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808. Also claimed are: chemically synthesised or recompinantly produced peptide multimers, a diagnostically labeled anti-anglogenic polypeptide, peptide or peptide multimer and carrier; a diagnostically useful HRRC-related composition, comprising cut the diagnostically labeled polypeptide, peptide or peptide multimer and carrier; an antibody specific for an epitope of HRRG that is present in the HRRG or the domains in a way which inhibits the anti-anglogenic activity of HRRG or the domains in a way which inhibits the anti-anglogenic activity of the domain of human or rabble HRRG, and which binds to HRRG or to and of the domain in a way which inhibits the anti-anglogenic activity of the domain and a disease or condition associated with undesired cell migration, invasion, proliferation, or anglogenesis, a method of cardiact having a disease or condition associated with undesired cell cetenting the presence of HRRG or its cleavage product or its peptide, peptide multimer; an affinity ligand useful for carnifected cells; a method of providing to a cell, tissue or organ an anglogenesis-inhibitory amount of HRRG, an HFR domain of HRRG-binding molecule, composition, and enthod of secretic cells; a method of providing or a cell, tissue or organ an anglogenesis-inhibitory amount of HRRG an HFR domain of HRRG-binding site or receptor, from a complex mixture. The expressing HRRG-binding site or receptor, from a complex m proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic retinopathy, inflammation, endometriosis, arthritis, peptic ulcers, or fractures. HPRG is especially useful in inhibiting the growth of primary tumours or metastases, and may also be used in treating neurodegenerative 7

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The invention relates to an isolated tropomyosin (Tpm)-related
antiangiogenic receptor polypeptide or peptide, which is a is a fragment
of a full-length native Tpm protein expressed on the surface of
endothelial cells, or a variant of the fragment. It has a molecular mass
of about 17 kDa and corresponds in its sequence to, or is a variant of,
an internal fragment of a native Tpm isoform which is a binding site for
antiangiogenic polypeptide agents; The isolated antiangiogenic receptor
polypeptide, peptide or variant has substantially the same biochemical
activity of binding to the antiangiogenic polypeptide agent that
contive Tpm internal fragment. The antiangiogenic polypeptide agent that
activity of binding to the antiangiogenic polypeptide agent that
contive Tpm internal fragment. The antiangiogenic polypeptide agent that
contive Tpm internal fragment, the antiangiogenic polypeptide or peptide is human histidine-proline
contive Tpm internal fragment, abbit HPRG, a Tpm-binding, antiangiogenic
conditions are using to the antiangiogenic receptor polypeptide or peptide,
antiangiogenic homologue, variant, domain or fragment of the HK or its D5
antiangiogenic homologue, variant, domain or fragment of the HK or its D5
antiangiogenic nompositions are useful for inhibiting endothelial cell
migration, invasion, proliferation or angiogenesis, for inducing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
                                                                                                                                                                     Gaps
diseases like Alzheimer's or Parkinson's disease. The antibodies are stimulators of angiogenesis and are useful for promoting neovascularization in pertinent disease states, and in various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rich glycoprotein; HPRG; cytostatic; antidiabetic; antiinflammatory; gynaecological; antiarthritic; matological; cardiant; vasotropic; vulnerary;
                                                                                                                                                                      ó
                                                                                                                               5; Length 148;
                                                                                                                                                                     0; Indels
                                                                                                                                 BB
                                                                                                                               100.0%; Score 37; DB
100.0%; Pred. No. 58;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiangiogenic receptor;
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                                                                                                                                                                                                                                                                                                                                      protein; 148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    H/P rich domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2002; 2002US-0364047P
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                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
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angiogenesis; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tpm; tropomyosin;
histidine-proline
ophthalmological;
                                                                                                                                                                                                                                                                                                                                      ADH10411 standard
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                                                                                                                                                                                                      1 HHPHG 5
                                                                                         Sequence 148 AA;
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                                                                                                                                                                                                                                            HHPHG
                                                     immunoassays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
            retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease or peripheral artery disease. The present sequence represents a human HPRG protein His-Pro (H/P) rich domain.
 tumours or cancer, diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #7910 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; human; microarray; gene expression; cervical epithelial cell;
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or for treating
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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2000US-0207456P.
2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US000670
endothelial cell apoptosis,
                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                         Conservative
                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                              Sequence 148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer.
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                                                                                                                                                                                                                                                             35 HHPHG
                                                                                                                                                                                                                                         1 HHPHG
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                       AAM21476;
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AAM21476
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RESULT 13 ABB43818

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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                               Peptide #11762 encoded by probe for measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein #8752 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                          Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
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Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 27; SEQ ID NO 37994; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                         Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression in human placenta
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genome-derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488897/53
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Best Local Similarity
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                                                                                                                                                             WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157274-A2
                                                                                                                               Homo sapiens
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                 17-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                Gaps
                                                                                                                                                                                                                                                                                                          Human; foetal liver; gene expression; single exon nucleic acid probe
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  4; Length 151;
                                                                                                                                                                                                                                                                          Peptide #11324 encoded by human foetal liver single exon
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100.0%; Score 37; DB 100.0%; Pred. No. 59;
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Pred. No. 59;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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                                                                                                                                                                                                                                              entry)
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Best Local Similarity
5, Conserve
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Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                         128 HHPHG 132
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                                                                                                                                                                          ABB43818 standard;
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                                                               1 HHPHG 5
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                                                                                                                                                                                                                                                                                                                                                                        WO200157277-A2
                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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Gaps

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RESULT 14 AAM37725

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(MOLE-) MOLECULAR DYNAMICS INC
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                             Hanzel
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                                                                                                                                                                                     Sequence 151 AA;
                                                                                                                                                                                                                                             HHPHG
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                                                                                                                                                                                                                                                                                                                                                      05-NOV-2001
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                             Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single
                                                                              gene
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                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                              measuring human gene expression in gample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                       exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                       The present invention relates to single exon nucleic acid probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed exon; gene expression analysis; probe; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expressed probe encoded protein SEQ ID NO: 37846.
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0
                                                                                                                                                                                                                                                                                                                                                      4; Length 151;
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                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 37; DB 100.0%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                   Claim 15; SEQ ID NO 28523; 530pp; English
                                                                                                                  Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 151 AA
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0
                04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                              DYNAMICS INC
                                                                                                                 Chen W,
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2001WO-US000666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow e
microarray; cancer;
                                                                                                                                    WPI; 2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                             128 HHPHG 132
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                                                                                              (MOLE-) MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                            S
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
30-JAN-2001;
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                                                                                                                 Penn SG,
                                                                                                                                                       Single hearts.
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AAM77540
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                                                                                                                      n genome-derived single exon nucleic acid probes useful for analyzing expression in human bone marrow.
                                                                                                                                                                                                                                                                                        The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human brain expressed single exon probe encoded protein SEQ ID NO: 36887.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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                                                                                                                                                                                                                             Example 4; SEQ ID NO 37846; 658pp + Sequence Listing; English.
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100.0%; Pred. No. 59;
iive 0; Mismatches
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Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM64782 standard; protein; 151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanzel DK,
                                                             WPI; 2001-488900/53
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Best Local Similarity
Matches 5; Consern
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
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          diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon nucleic acid probes useful for analyzing
  nervous system
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                  Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
hypercholesterolaemia; coronary heart disease.
                                                                                                                                  .
0
                                                                                                      4; Length 151
 treatment of
                                                                                                                                  0; Indels
 and improved
                                                                                                    100.0%; Score 37; DB
100.0%; Pred. No. 59;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome-derived single exon nuclexpression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                    peptide, SEQ ID No 37837
                                                                                                                                                                                                                                                                  peptide; 151 AA
 diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0234687P.
2000US-0234283.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                 vative
which may enable the
                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                   HHPHG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression in
                                                                                                    Query Match
Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                  ABG59189 standard;
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                                                                                                                                                              1 HHPHG 5
                                                                         Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200157273-A2
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                    Human liver
                                                                                                                                                                                                                                                                                                                          25-FEB-2003
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                                                                                                                                                                                         128
                                                                                                                                                                                                                                                                                            ABG59189
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                                                                                                                                                                                                                                    RESULT 18
ABG59189
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung acid expression in a sample derived from human lung the label detectably bound to each probe of the mrany; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene,
                                    ö
                                                                                                                                                                                                                                                                                                             SEQ ID 36229.
                                                                                                                                                                                                                                                                                                                                         Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of single exon nucleic acid probes, used to
                                      Gaps
                                      ô
Length 151;
                                                                                                                                                                                                                                                                                                           Human peptide encoded by genome-derived single exon probe
                                      ö
  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  measure gene expression in human lung samples
Score 37; DB Pred. No. 59; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; SEQ ID NO 36229; 634pp; English.
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                                                                                                                                                                                                   ABG46564 standard; peptide; 151
                                   °,
 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                                                                                        (first entry)
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                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyaline membrane disease
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                  Best_Local Similarity
Matches 5; Conserv
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                                                                         1 HHPHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                        19-AUG-2002
                                                                                                                                                                                                                                      ABG46564;
 Query Match
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ABG46564
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comprising (a) identifying exons from genomic sequence by the method
above and (b) measuring the expression of each of the exons in several
tissues and/or cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
expression of the exons in the tissues and/or cell types indicates that
the exons should be assigned to a single gene; a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORF). The probes are used for gene expression
analysis, and for identifying exons in a gene, particularly using human
cancer, chronic obstructive pulmonary disease such as asthma, lung
cancer, chronic obstructive pulmonary fibrosis, neurofibromatosis,
tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
budlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
chistiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis,
histiocytosis, pulmonary hypertension and hyaline membrane disease. The
present sequence is a peptide/protein encoded by a single exon probe of
the invention. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                               5; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster polypeptide SEQ ID NO 40071
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 37; 100.0%; Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 198 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic a
genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75.
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| HHPHG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABL15196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HHPHG 5
                                                                                                                                                                                                                                                                                                                                                                Sequence 151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila;
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ABB71093
ID ABB71093 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                       ö
                                                                                                                                                                                   4; Length 198;
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                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes immunogenic protein #16828.
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                                                                                                                                                                                  Score 37; DB Pred. No. 78; Mismatches
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Jen S, Carter
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0
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                              Similarity 100
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccinating against and
treating acne vulgaris.
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153 HHPHG 157
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                                                                                                                                                                                                                                                       HHPHG 5
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                                                                                                                                                Sequence 198 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-FEB-2002
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                              RESULT 21
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and

NO 40071; 21pp + Sequence Listing; English

Disclosure; SEQ ID

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13:0

Thu Jun 16

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concoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to polypeptides encoded by the polynucleotides. The invention and to additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; antibodies against polypeptides of the invention; antibodies appentic for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
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                                                                                                                                                                                                                          Gaps
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Jones R, Carter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acnes predicted ORF-encoded polypeptide #17127.
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                                                                                                                                                                                                                        0; Indels
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Benson DR,
                                                                                                                                                                                    Score 37; DB Pred. No. 98; ; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 17127; 1481pp; English
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                           protein; 248 AA
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Zhang Y, Wang S, Jen S, Loc
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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                                                                                                                                                                                                                                                                                                142 HHPHG 146
                                                                                                                                                                                                       Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA COR
                                                                                                                                                                                                                                                                                                                                                                                         ABM52451 standard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium
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                                                                                                                                                 Sequence 248 AA;
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Best Local S
Matches 5
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ABM52451
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           vulgaris, or for stimulating an immune response specific for a P. acnes protein. The polynucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zyskind JW;
Xu HH;
polypeptides are useful for diagnosing, preventing or treating acne
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                        100.0%; Score 37; DB 6; Length 248; 100.0%; Pred. No. 98; 1;ve 0; Mismatches 0; Indels
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Forsyth |
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Yamamoto R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABU35012 standard; protein; 259 AA
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                               Conservative
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Trawick JD,
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N-PSDB; ACA38882.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                      Sequence 248 AA;
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Wall D,
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the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained for the car, and the printed specification, but was obtained for the car.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding a Moraxella catarrhalis polypeptide, useful for preparing a composition for diagnosing, preventing or treating infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tes to an isolated nucleic acid encoding an Moraxellaptide. The nucleic acid is useful for preparing a agnosing, preventing or treating infection caused by lis. The present sequence represents the amino acid atarrhalis protein.
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                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 264 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lis; infection
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a catarrhalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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5; Conservative
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N-PSDB; ADL03562.
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caused by Moraxella
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229 HHPHG 233
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5
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 259 AA
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ADL05482
ID ADL05482
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                             Gap junction protein beta-4; human; neurological disease; epidermal disease; deafness; cataract; AIDS; therapy; diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents human gap junction protein beta-4, a protein that has homology to connexins. The invention relates to gap junction protein beta-4 polypeptides and polynucleotides (see also AAZ20259), recombinant materials and methods for their production. It also relates to methods for using such polypeptides and polynucleotides for the treatment of neurological diseases, epidermal diseases, deafness, cataract, and AIDS, and for identifying agonists, antagonists and/or inhibitors useful in treating conditions associated with gap junction protein beta-4 imbalance. Also provided are diagnostic assays for detecting diseases associated with inappropriate gap junction protein beta-4 activity or levels, e.g. by analysing for the presence or amount of polypeptide expression in a sample. The polypeptides are also useful for raising antibodies immunospecific to gap junction protein beta-4
                                                           Gaps
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                          Score 37; DB 8; Length 264; Pred. No. 1e+02; Mismatches 0; Indels
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                         AAY32079 standard; protein; 273 AA
                                                                                                                                                                                                                                                                                  Human gap junction protein beta-4.
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                           100.0%;
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           Query Match
Best Local Similarity 100.00
Lag 5; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                               230 HHPHG 234
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Sequence 264 AA;
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RESULT

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RESULT 27
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                                                           human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes; inflammation; autoimmune disorder; allergy; blood disorder; acquired immunodeficiency syndrome; AIDS; obesity; asthma; immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis; Alzheimer's disease; infection; str.
                                               homologue SeqID 593
       protein; 273 AA
                                                                                                                                                       2001US-0265395P.
2001US-0265412P.
2001US-0265414P.
2001US-0265514P.
2001US-0266975P.
2001US-0266975P.
2001US-0266975P.
2001US-0267459P.
2001US-0267459P.
2001US-0267459P.
2001US-0271839P.
2001US-0276449P.
2001US-02789775P.
2001US-0278978P.
2001US-0278978P.
2001US-0278979P.
2001US-0278979P.
2001US-02893974P.
2001US-0289324P.
2001US-0289324P.
2001US-0299324P.
2001US-0312908P.
2001US-0313390P.
2001US-0313390P.
2001US-0313390P.
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2001US-0318115P.
2001US-0318118P.
2001US-0318740P.
                                 (first entry)
                                              Human NOVX protein
       standard;
                                                                                                                 WO200268649-A2
                                                                                                                                           31-JAN-2002;
                                                                                                     sapiens
                                                                                                                                                              31-JAN-2001;
31-JAN-2001;
31-JAN-2001;
02-FEB-2001;
07-FEB-2001;
08-FEB-2001;
08-FEB-2001;
08-FEB-2001;
08-MAR-2001;
14-MAR-2001;
02-MAR-2001;
15-MAR-2001;
16-MAR-2001;
11-APR-2001;
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11-AUG-2001;
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                                 5-APR-2004
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      AD117057
                   AD117057
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ADI17057
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This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical corp physiological responses in a cell, tissue, organ or organism.

Corp physiological responses in a cell, tissue, organ or organism.

Corp diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diagnostic and independent of modulate their corp. The NOVX polypeptides, polymucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, anner and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune disorders, allergies, blood disorders, acquired immunodeficiency syndrome disorders, allergies, blood disorders, acquired immunodeficiency syndrome condisorders, and epilepsy. Accordingly, these molecules have many activities including cytostatic, cardiant, antiinflammatory, immunosuppressive, antiallergic, and epilepsy. Accordingly, these molecules have many activities including cytostatic, anti-HIV, antidiabetic, antiarteriosclerotic, antiallergic, naminathmatic, nephrotropic, antiarthritic, hepatotropic, antiathritic, hepatotropic, antiathritic, hepatotropic, antiathritic, nephrotropic, antiathritic, hepatotropic, antiathritic, nephrotropic, antiathritic, hepatotropic, an
                                                                                                                                                                                                                                                                                                                            CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing
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                                                                                                                                                                                                                                                                                  Patturajan M, Shimkets RA;
3on DW, Rastelli L, Miller
Lman SD, Wolenc AR, Pena CE
spley DM, Rieger DK, Burgee
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100.0%; Pred. No. 1.1e+02;
ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                         Zerhusen BD,
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                                                                                                                                                                                                                                                                                  Tchernev VT, Spytek KA, Zerhusen BD
Li L, Gangolli EA, Padigaru M, And
Gerlach VL, Taupier RJ, Gusev VY,
Furtak K, Grosse WM, Alsobrook JP,
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                         2001US-0330245P.
2001US-0330308P.
2001US-0332701P.
19-SEP-2001; 2001US-0323379P
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5, Conserve
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                                      18-OCT-2001;
18-OCT-2001;
                                                                                                                    14-NOV-2001;
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This invention relates to a novel nucleic acids, and encoded polypeptides thereof, which have properties related to the stimulation of biochemical or physiological responses in a cell, tissue, organ or organism.

Corpectifically, it refers to the use of biologically active fragments for diagnostic and prognostic assays and furthermore in the treatment of diagnostic and prognostic assays and furthermore in the treatment of diverse pathological conditions. The present invention describes novel numan and murine NOVX proteins, as well as methods to modulate their carpression using antisense oligos, ribozymes and peptide nucleic acids.

CC The NOVX polypeptides, polynucleotides and antibodies are useful in treating or preventing NOVX-associated disorders, e.g. cardiomyopathy, atherosclerosis, cancer and diabetes. Furthermore, they may be used in treating or preventing diseases such as inflammation, autoimmune CC treating or preventing diseases such as inflammation, autoimmune cc disorders, allergies, blood disorders, acquired immunodeficiency syndrome (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis, arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy and epilepsy. Accordingly, these molecules have many activities including cytostatic, antidiabetic, antidiatherities, antidiabetic, antidiathematory, immunosuppressive, antiallergic, antidiathematic, nephrotropic, antidatherities, distant and anticonvulsant. In addition, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, contropic, antiarthritic, the molecules that modulate or inhibit, for example, or elections, wound healing and angiogenesis. The nucleic acids are also the phasimancements. This polypeptide is a homologue of a human NOVX protein
                    New NOVX polypeptides and nucleic acids, useful for preventing or treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or
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100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
                                                                                                                Disclosure; SEQ ID NO 596; 1498pp; English.
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03-AUG-2001; 2001US-0310099P.
08-NOV-2001; 2001US-0343705P.
13-NOV-2001; 2001US-035066FP.
12-APR-2002; 2002US-0372246P.
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Best Local Similarity
Matches 5; Conserv
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                                                                             pharmacogenomics
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igaru M, Anderson DW, Rastelli L, Miller CE;
Gusev VY, Colman SD, Wolenc AR, Pena CEA;
lsobrook JP, Lepley DM, Rieger DK, Burgess CE;
 e; infection; str.
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Li L, Gangolli EA, Padigaru M, And
Gerlach VL, Taupier RJ, Gusev VY,
Furtak K, Grosse WM, Alsobrook JP,
                                                                                                                                                                                 2001US-0265395P.
2001US-0265412P.
2001US-0265514P.
2001US-0266406P.
2001US-0266406P.
2001US-0266405P.
2001US-0266405P.
2001US-0266423P.
2001US-0267823P.
2001US-0267823P.
2001US-0271855P.
2001US-0271855P.
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2001US-0271855P.
2001US-0271855P.
2001US-0271839P.
2001US-0275989P.
2001US-0275989P.
2001US-0275989P.
2001US-0275989P.
2001US-0275989P.
2001US-027649P.
2001US-027649P.
2001US-027649P.
2001US-027649P.
2001US-027649P.
2001US-027649P.
2001US-027649P.
2001US-027649P.
2001US-028932P.
2001US-029324P.
2001US-0299324P.
2001US-0299324P.
2001US-0299324P.
2001US-0299324P.
2001US-0299324P.
2001US-039324P.
2001US-0313390P.
2001US-0313390P.
2001US-0313390P.
2001US-0313379P.
2001US-03131974P.
2001US-0313197P.
2001US-0313379P.
2001US-0333779P.
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31-JAN-2001;
31-JAN-2001;
02-FEB-2001;
07-FEB-2001;
07-FEB-2001;
08-FEB-2001;
08-FEB-2001;
09-FEB-2001;
15-FEB-2001;
15-FEB-2001;
16-MAR-2001;
16-MAR-2001;
16-MAR-2001;
16-MAR-2001;
16-MAR-2001;
16-MAR-2001;
16-MAR-2001;
16-MAR-2001;
17-MAR-2001;
18-AMR-2001;
19-MAR-2001;
11-APR-2001;
11-APR-2001;
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11-APR-2001;
11-ANG-2001;
11-SEP-2001;
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11-SEP-2001;
11-SEP-2001;
11-SEP-2001;
11-NOV-2001;
                                     Homo sapiens
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Alzheimer's
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RESULT 30
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                                                                                                                                The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a cancer-associated proteins given in ABR48146 to ABR48242). Bladder cancer-associated proteins given in ABR48146 to have cytostatic activities, and can be used in antisense gene therapy and in vaccine production. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, such as hormones or antibodies. The nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications
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                                                             patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lung cancer-associated polypeptide; cytostatic; emphysema; atelectasis; antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis; small cell lung cancer; benign lesion; precancerous lesion; bronchitis; chronic obstructive pulmonary disease; hypersensitivity pneumonitis; interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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100.0%; Pred. No. 1.1e+02;
:ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung cancer-associated polypeptide #42
                                                                                                                English
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
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                                                                                                                                                                                                                                                                                                                                                                         Conservative
                              WPI; 2003-201532/19
N-PSDB; ACC51048.
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5; Conserv
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                                                                                                               Claim 10; Page 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABU56449 standard
         Aziz N;
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09-NOV-2001;
13-NOV-2001;
29-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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         Mack DH,
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Best Local S
Matches 5
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The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polyneptide are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated polypeptide, for cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, emphysema, bronchitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer-associated polypeptides of the
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                                                                                                         Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 37; DB 6; I ilarity 100.0%; Pred. No. 1.1e+02; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                      Claim 27; Page 222; 453pp; English.
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10-MAY-2001; 2001US-0290492P.
09-NOV-2001; 2001US-0339245P.
13-NOV-2001; 2001US-0350666P.
29-NOV-2001; 2001US-0334370P.
12-APR-2002; 2002US-0372246P.
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Best Local Similarity
WPI; 2003-093161/08.
N-PSDB; ABX76170.
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Mack DH,
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                                                                                                                                                                                The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful of the cancer in cancer, such as small cell lung cancer, non-small cell ung cancer, other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer-associated polypeptides of the inverse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differential expression; cancer; angiogenic disorder; lc disorder; psoriasis; ischaemia; heart disease; atherosclerosis; natory disease; autoimmune disease;
                                                                                         Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s/fibrosis-related polypeptide, SEQ ID NO:344
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                                                                                                                                                           Claim 27; Page 393; 453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 273 AA
EOS BIOTECHNOLOGY INC.
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                                                  WPI; 2003-093161/08.
N-PSDB; ABX76402.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conser
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                           Murray R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229 HHPHG 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADN39026 standard,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 273 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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(EOSB-)
                         Aziz N,
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ADN39026
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
ther diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and mucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosing or treating cancer, comprises detecting a nucleic acid in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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3, Zlotnik A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gish KC, Gl
Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; SEQ ID NO 344; 1385pp; English.
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Murray R, Watson SR,
03-DEC-2001; 2001US-0335394P.
14-DEC-2001; 2001US-0340376P.
08-JAN-2002; 2002US-0347211P.
10-JAN-2002; 2002US-0347349P.
08-FEB-2002; 2002US-0355250P.
13-FEB-2002; 2002US-0355714P.
20-FEB-2002; 2002US-0359077P.
29-MAR-2002; 2002US-0368809P.
04-APR-2002; 2002US-0372246P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EOSB-) EOS BIOTECHNOLOGY INC
                                                                                                                                                                                                                                                                                                                                                                          05-JUN-2002; 2002US-0386614P.
16-JUL-2002; 2002US-0396839P.
22-JUL-2002; 2002US-0397775P.
22-JUL-2002; 2002US-0397845P.
09-SEP-2002; 2002US-0409450P.
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N-PSDB; ADN39025.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HHPHG S
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The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
whose expression is upregulated or downregulated in specific cancers or
other diseases such as angiogenic or fibrotic disorders, and to methods
of determining the presence or absence of a pathological cell in a
patient by detecting a nucleic acid at least 80% identical to those of
the invention or by detecting a polypeptide of the invention. The
invention also relates to expression vectors and host cells comprising a
nucleic acid of the invention; use of such antibodies for drug targeting;
onlypeptide of the invention; use of such antibodies for drug targeting;
and methods of screening for modulators of activity or expression of the
polypeptides and mucleic acids. The nucleic acids, polypeptides,
antibodies and methods are useful for diagnosing, prognosing and treating
cancer and other conditions such as psoriasis, ischaemia, heart disease,
atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
neovascularistaion syndromes, scarring and uterine fibroids. They may
also be useful in wound healing and in contraception. The present
sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   esence or absence of a pathological cell in a patient, ing, prognosing or treating cancer, comprises detecting
retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glynne R, Hevezi
i, Zlotnik A;
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Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C302; 1385pp; English
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a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ginsburg WM,
                                                                                                                                                                                                         2001US-0350666P.
2001US-0332464P.
2001US-0334393P.
2001US-0340376P.
2002US-0347349P.
2002US-0347349P.
2002US-0355250P.
2002US-0355250P.
2002US-0356714P.
2002US-0356714P.
2002US-0356899P.
2002US-0372246P.
2002US-037246P.
2002US-0396839P.
2002US-0396839P.
2002US-0396839P.
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                                                                                                                                                                                2002WO-US036810
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Murray R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-468649/44
N-PSDB; ADN39715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 273 AA
                                                                                                                WO2003042661-A2
                                                                                                                                                                                                                                                                                                       10-JAN-2002;

08-FEB-2002;

13-FEB-2002;

20-FEB-2002;

29-MAR-2002;

04-APR-2002;

12-APR-2002;

15-AUL-2002;

16-JUL-2002;

22-JUL-2002;

22-JUL-2002;

22-JUL-2002;
                                                                                                                                                                                                                           21-NOV-2001;
29-NOV-2001;
03-DEC-2001;
14-DEC-2001;
08-JAN-2002;
                                                                                                                                                                             13-NOV-2002;
                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 12;
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Best Local S
Matches 5
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Mack
  SXCCCCCCCCCCCCCXXXTTTXXBAXXBABABABABABABABABABABABAAAA
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene disruption; gene targeting; marker gene; transformation;
homologous recombination; hyperthermostable archaebacterium; KOD1;
                                                                                                                                     Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 35196; 21pp + Sequence Listing;
                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 35196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 37; DB 4; 1
100.0%; Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                   Myers EW;
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               ABB69468 standard; protein; 323 AA
                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
                                                                                                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid
genes from Drosophila and
interactions.
                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                   Venter JC, Adams M,
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Best Local Similarity
5; Conserve
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                                                                                                                                                                                                                                                                                                                                                     (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABL13571
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                                                                                                                                                    pharmaceutical
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ADN46756
ID ADN46
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AC ADN46
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DT 01-JU
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DE Therm
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KW Gene
KW homol
ABB69468
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Similarity 5; Conser

229 HHPHG 233

HHPHG 5

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HINKLE (
                                                                                                                                                                                        interactions.
 27-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS30838;
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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(HINK/)
(SLAT/)
                                                                                                                                                                            genes
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ID ADS3
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                                                                                                                                                                                                                                                                                       This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least arbitrary region in the sequence, providing a vector that contains a sequence homologous with the selected region and a marker gene, transformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly thermococcus kodakaraensis KOD1. The method is for targeting the disruption of a gene in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug inspection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein encoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                     Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
ne function; enzyme activity; medicine; food; drug inspection; molecular biology; immunology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 37; DB 8; Length 326; 100.0%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 27588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                      634; 598pp; Japanese.
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                                                                                                      29-AUG-2003; 2003WO-IB003597
                                                                                                                            30-AUG-2002; 2002JP-00319011
                                  Thermococcus kodakaraensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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gene structure; gene
forensic science; foo
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                                                                                                                                                                                                 WPI; 2004-257583/24.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                     Claim 9; SEQ ID NO
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|HPHG 142
                                                                                                                                                  (NISC-) JAPAN SCI
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                                                         WO2004022736-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila;
                                                                                18-MAR-2004
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ABB66932
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL6175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 27588; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 37; DB 4; Length 327; 100.0%; Pred. No. 1.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                    Myers EW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADS30838 standard; protein; 350 AA.
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23-MAR-2001; 2001WO-US009231
                                                                    23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2003; 2003US-00369493
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5; Conservative
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                                                                                                                                                                                                                                                                 Venter JC, Adams M,
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N-PSDB; ABL11035.
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(PEKE ) PE CORP NY
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                           Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with the improved plant properties, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of nor plant disease, better growth rate by modification of the coll cycle pathway with plant growth regulators, increased rate of content, improved plant growth and development under at least one stress content, improved lignin production of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved lignin production or improved galactomannan conduction. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic correct form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                           promoter positioned to provide
                                                                                      New recombinant DNA construct comprising a promoter positioned to provi
for expression of a polynucleotide encoding a polypeptide from a
microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental biology; cell signalling; insecticide;
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                                       Goldman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB 8;
Pred. No. 1.4e+02;
; Mismatches 0;
                                                                                                                                               19871; 122pp; English
                                      Chen X,
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                                      Slater SC,
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11-JUL-2000; 2000US-00614150
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                                                               WPI; 2004-061375/06
                                                                                                                                              Claim 1; SEQ ID NO
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Best Local Similarity
Matches 5; Conser
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174 HHPHG 178
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(CHEN/) CHEN X.
(GOLD/) GOLDMAN B
                                      Hinkle GJ,
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                                      Cao Y,
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ABB71820
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                                                                                                                        solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                               Disclosure; SEQ ID NO 42252; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 5229; 21pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 5229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 37; DB 4; 100.0%; Pred. No. 1.6e+02; ive 0; Mismatches 0;
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 Myers EW;
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PWD,
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11-JUL-2000; 2000US-00614150.
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genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
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N-PSDB; ABL03582.
                                                   WPI; 2001-656860/75
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   Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 HHPHG 164
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                                                                         N-PSDB; ABL15923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 402 AA;
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                                                                                                                                                                             interactions.
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    The invention is
capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                      infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                    ;
0
                                                                                                                                Length 419;
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                                                                                                                            100.0%; Score 37; DB 4; I
100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                 aeruginosa polypeptide #9974
                                                                                                                                                                                                                                                  protein; 466 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENO-) GENOME THERAPEUTICS CORP.
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98US-0094190P
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                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                           aeruginosa.
                                                                                                                                      Similarity 5; Conserv
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253 HHPHG 257
                                                                                                                                                                                                                                                ABO77799 standard;
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                                                                                                          Sequence 419 AA;
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27-JUL-1998
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The present sequence is the protein sequence of human histidine proline rich glycoprotein (HPRG), a proteinaceous metal chelator that can be used to rich glycoprotein (HPRG), a proteinaceous metal chelator that can be used to phypeptides or peptides comprise: the histidine-proline-rich (H/P) domain (see ABB79806) of human HPRG; an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808.

Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or therapeutically labeled antiangiogenic polypeptide, peptide or peptide multimer; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled polypeptide, peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the H/P domain of human or rabbit HPRG, and which binds to HPRG or to any of the domains in a way which inhibits the anti-angiogenic activity of HPRG or the domain, New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis. Claim 1; Page 11; 82pp; English P-PSDB; ABN84910

The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The ABO84396 represent P. aeruginosa polypeptides of the invention.

this patent did not form part of the printed was obtained in electronic format from USPTO at

sequence.html

sequence data for specification but seqdata.uspto.gov/

Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.

NO 26545; 455pp; English.

Disclosure; SEQ ID

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Deloughery

Rubenfield MJ, Nolling J,

WPI; 2003-615309/58. N-PSDB; ABD11370.

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                                                                                                                                                                              Histidine proline rich glycoprotein; HPRG; human; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian; chelator.
                                  Gaps
                                                                                                                                                                                                                                                         /note= "Proline-rich domain"
350. .497
/note= "Histidine-proline-rich domain, region also specifically claimed in Claim 1"
                                  .
0
                Length 466;
                                 Indels
               Score 37; DB 7; Pred. No. 1.9e+02; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          Mazar AP;
                                                                                                                                                              Human histidine proline rich glycoprotein.
                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Plunkett ML,
                                                                                                            ABB79804 standard; protein; 525 AA
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               100.08;
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                                                                                                                                             (first entry)
                      Similarity 100.5; Conservative
                                                                                                                                                                                                                                                                                                                                                                         (ATTE-) ATTENUON LLC
                                                                                                                                                                                                                                                                                                                                                                                         Harris S,
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-666989/71.
                                                                 135 HHPHG 139
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Sequence 466 AA;
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                                                                                                                                                                                                                         Homo sapiens
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              Query Match
Best Local S
Matches 5
                                                                                                                             ABB79804;
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels

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Gaps

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Qy 1 HHPHG 5 (1) | | | | | Db 384 HHPHG 388

Search completed: June 15, 2005, 14:15:48 Job time : 93 secs us-10-074-225a-8.rai

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 15 Run on:

, 2005, 14:06:20 ; Search time 23.5 Seconds (without alignments) 15.883 Million cell updates/sec

US-10-074-225A-8 37 1 HHPHG 5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

513545 segs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

1: /cgn2 6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Patents\_AA:\* Issued Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	37	100.0			US-09-095-407-3	Sequence 3, Appli
7	37	100.0	11	m	US-09-095-407-1	7
m	37	100.0	-	4	US-09-742-494-1	H
4	37	100.0	-	4	US-09-809-657-1	٦,
Ŋ	37	100.0	26	m	US-08-785-636-1	٦,
9	37	100.0	7	ო	US-09-095-407-2	7
7	37	100.0	-	4	US-09-742-494-2	7
æ	37	100.0		4	US-09-809-657-2	Sequence 2, Appli
סי	37	100.0	ø	4	US-09-248-796A-24357	24
10	37	100.0	16	4,	US-09-902-540-13395	13
11	37	100.0	22	4	US-09-270-767-61056	6105
12	37	100.0	56	4,		
13	37	100.0	273	4	US-09-949-016-6606	,9099
14	37	100.0	28	4	09-949-016-910	9101,
15	37	100.0	46	4	US-09-252-991A-26545	26545,
16	37	100.0	52	4	US-09-976-594-64	64,
17	37	100.0	52	4	US-09-919-039-62	62
18	37	100.0	53	4	US-09-518-959-8	ω̈
19	37	100.0	53	4	US-09-518-959-9	δ
20	37	100.0	61	4	US-09-252-991A-23373	23.
21	37	100.0	81	4	US-09-248-796A-20281	Sequence 20281, A
22	37	100.0	92	₹'	US-09-270-767-45546	4554
23	31	83.8		4		29,
24	31	83.8		ന	US-08-776-265-12	12,
25	31	83.8		4	-09-398-1	Sequence 12, Appl
26	31	83.8	<b>ნ</b>	ന	-08-159-	10
27	31	83.8	15	m	US-09-082-092-14	14,

	Sequence 158, App Sequence 73, Appl Sequence 10688, A		Sequence 51249, A Sequence 23534, A	Sequence 653, App Sequence 58449, A		Sequence 160, App Sequence 24231, A	Sequence 2, Appli Sequence 1135, Ap	CA
US-09-885-722A-14 US-09-227-357-575	US-09-910-009A-158 US-09-716-129-73 US-09-489-039A-10688	US-09-270-767-57094 US-09-270-767-36032	US-09-270-767-51249 US-09-248-796A-23534	US-09-640-211A-653 US-09-270-767-58449	US-09-461-325-160 US-10-012-542-160	US-10-115-123-160 US-09-248-796A-24231	US-09-430-221-2 US-09-205-258-1135	US-08-470-179-26
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## ALIGNMENTS

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APPLICANT: Hutchens, T. William
Yip, Tai-Tung
TITLE OF INVENTION: Surface-Enhanced Neat Desorption for the
Detection of Analytes
                                                                                                                                                                                      Detection of Analytes
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,407
FILING DATE: 10-Jun-1998
CLASSIFICATION ATA:
APPLICATION NUMBER: WO PCT/US94/06064
FILING DATE: 28-MAY-1993
APPLICATION NUMBER: WO PCT/US94/06064
FILING DATE: 27-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Pa::1 Thomas D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Paul, Thomas D.
REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5639-PCT-US-D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-5325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-095-407-3
US-09-095-407-3
; Sequence 3, Application US/09095407
; Patent No. 6124137
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (713) 651-537
TELEFAX: (713) 651-5246
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
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Page

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Query Match
Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 5; Conser
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US-09-095-407-1
; Sequence 1, Application US/09095407
; Patent No. 6124137
; GENERAL INFORMATION:
; APPLICANT: Hutchens, T. William
; TITLE OF INVENTION: Surface-Enhanced Neat Desorption for the Detection of Analytes
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 100.0%; Score 37; DB 3; Length 6; 100.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 32,714
REFERENCE/DOCKET NUMBER: D-5639-PCT-US-D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 651-5325
TELEFAX: (713) 651-5246
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: HOUSEON
STATE: Texas
COUNTRY: USA
ZIP: 77010-3095
ZIP: 77010-3095
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,407
FILING DATE: 10-Jun-1998
CLASSIFICATION NUMBER: US 08/068,896
FILING DATE: 28-MAY-1993
APPLICATION NUMBER: WO PCT/US94/06064
FILING DATE: 27-MAY-1994
APPLICATION NUMBER: US 08/556,951
FILING DATE: 27-MAY-1995
ATTORNEY, AGENT INFORMATION:
NUMBER: US 08/556,951
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P
STREET: 1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 3
Pred. No. 0.83;
                                Mismatches
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IPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on US/09742494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no acid
                Similarity 100
5; Conservative
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MOLECULE TYPE: p.;
SEQUENCE DESCRIPTUS-09-095-407-1
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US-09-742-494-1
; Sequence 1, Application
; Patent No. 6528320
; GENERAL INFORMATION:
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APPLICANT: YIP, TAI-TUNG
TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES
FILE REFERENCE: P00798USE/09306611
CURRENT APPLICATION NUMBER: US/09/742,494
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-742-494-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09809657
; Sequence 1, Application US/09809657
; Patent No. 6734022
; GENERAL INFORMATION:
; APPLICANT: HUTCHENS, WILLIAM
; APPLICANT: YIP, TAI-TUNG
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES
; FILE REFERENCE: P00798USF/09306611
; CURRENT APPLICATION NUMBER: US/09/809,657
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 08/068,896
; PRIOR APPLICATION NUMBER: 08/068,896
; RIGHT FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 11
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US-08-785-636-1
; Sequence 1, Application US/08785636
; Patent No. 6027942
; GENERAL INFORMATION:
; APPLICANT: Yip, Tai-Tung
; APPLICANT: Hutchens, T. William
; ITLE OF INVENTION: Method and Apparatus for Desorption and Ionization of
; TILE OF INVENTION: Analytes
; TILE OF INVENTION: Analytes
; FILE REFERENCE: Hutchens
; CURRENT APPLICATION NUMBER: US/08/785,636
; CURRENT FILING DATE: 1997-01-17
; EARLIER FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SQ ID NO 1
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Unknown
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Pred. No. 0.83;
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US-09-809-657-2
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                                                                                                                                                                                                                                                                                                                                                NESULT 6
US-09-095-407-2
; Sequence 2, Application US/09095407
; Patent No. 6124137
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: Surface-Enhanced Neat Desorption for the Detection of Analytes
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                                                                                                                 3; Length 26;
                                                                                                                                                                          0; Indels
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                                Description of Unknown Organism:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1, Thomas D.
TON NUMBER: 32,714
//DOCKET NUMBER: D-5639-PCT-US-D1
ION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,407
FILING DATE: 10-Jun-1998
CLASSIFICATION SAPA:
APPLICATION NUMBER: US 08/068,896
FILING DATE: 28-MAY-1993
APPLICATION NUMBER: WO PCT/US94/06064
FILING DATE: 27-MAY-1994
APPLICATION NUMBER: US 08/556,951 ·
FILING DATE: 27-NAY-1995
ATTORNEY AGENT INFORMATION:
NAME: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Fulbright & Jaworski L.L.P. 301 McKinney, Suite 5100 ston
                                                                                                             100.0%; Score 37; DB
100.0%; Pred. No. 2;
iive 0; Mismatches
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IPTION: SEQ ID NO: 2:
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STREET:
CITY: Houst.
STATE: Texas
COUNTRY: USA
TP: 77010-3095
READABLE FORM:
TYPE: Floppy disk
TYPE: Floppy disk
TYPE: Ploppy disk
TYPE: Ploppy disk
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;
TOPOLOGY: linear
;
MOLECULE TYPE: peptide
;
SEQUENCE DESCRIPTION: SEQ ID
US-09-095-407-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright
STREET: 1301 McKinne
                                                                                                                                                                          Conservative
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TELECOMMUNICATI(
TELEPHONE:
                                                                                                               Query Match
Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 5; Conser
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COMPUTER READA
; FEATURE:
; OTHER INFORMATION:
US-08-785-636-1
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RESULT 7

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RESULT 9
US-09-248-796A-24357
i Sequence 24357, Application US/09248796A
j Patent No. 6747137
j GENERAL INFORMATION:
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
i TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
j FILE REFERENCE: 107196.132
j CURRENT APPLICATION NUMBER: US 60/074,725
j PRIOR FILING DATE: 1998-02-13
j PRIOR FILING DATE: 1998-08-13
j PRIOR FILING DATE: 1998-08-13
j PRIOR FILING DATE: 1998-08-13
j NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09809657

Sequence 2, Application US/09809657

Patent No. 6734022

GENERAL INFORMATION:
APPLICANT: HUTCHENS, WILLIAM
APPLICANT: YIP, TAI-TUNG
APPLICATION NUMBER: US/09/809,657
CURRENT FILING DATE: 2001-03-15
PRIOR FILING DATE: 1993-05-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
Sequence 2, Application US/09742494

Sequence 2, Application US/09742494

Batent No. 6528320

GENERAL INFORMATION:

APPLICANT: HUTCHENS, WILLIAM

APPLICANT: YIP, TAI-TUNG

TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES

FILE REFERENCE: P00798USE/09306611

CURRENT APPLICATION NUMBER: US/09/742,494

CURRENT FILING DATE: 2000-12-20

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 26

LENGTH: 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 37; DE
100.0%; Pred. No. 2;
:ive 0; Mismatches
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100.0%; Pred. No. 2
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-494-2
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US-09-809-657-2
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Best Local Similarity
Matches 5; Conserv
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US-09-902-540-13395
; Sequence 13395, Application US/09902540
; Patent No. 683347
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Slater, Steven C.
; APPLICANT: Miegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13395
; LENGTH: 163
; TYPE: PRT
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                                                                                                               100.0%; Score 37; DB 4; Length 69; 100.0%; Pred. No. 5.5;
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US-09-270-767-61056
; Sequence 61056, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and protei; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61056
; LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-61056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s xanthus
; SEQ ID NO 24357
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24357
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5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                               Query Match
Best Local Similarity
Matches 5; Conser
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US-09-902-540-13395
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Best Local S
Matches 5
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RESULT 12
US-09-540-236-3168
is Sequence 3168, Application US/09540236
j Sequence 3168, Application US/09540236
j Retent No. 6673910
j GENERAL INFORMATION:
it TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARF
it TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
it TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
j FILE REFERENCE: 2709.2005-001
j CURRENT APPLICATION NUMBER: US/09/540,236
j CURRENT FILING DATE: 2000-04-04
j NUMBER OF SEQ ID NOS: 3840
j SEQ ID NO 3168
j LENGTH: 264
j LENGTH: 264
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Sequence 666, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARKE: FastSEQ for Windows Version 4.0

SEQ ID NO 6606

LENGTH: 273
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-09-949-016-9101
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Sequence 62, Application US/09919039

Sequence 62, Application US/09919039

Patent No. 6727066

GENERAL INFORMATION:

APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION:

FILE REFERENCE: PA-0035 US

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 62

LENGTH: 525
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US-09-518-959-8
; Sequence 8, Application US/09518959
; Patent No. 6548270
; GENERAL INFORMATION:
; APPLICANT: Dubin, Adrienne E
; APPLICANT: Erlander, Mark G
; APPLICANT: Huvar, Rene
; APPLICANT: Pyati, Jayashree
; TITLE OF INVENTION: Channel BNaC4 (ASIC4)
; TITLE OF INVENTION: channel BNaC4 (ASIC4)
; TITLE OF INVENTION: channel BNaC4 (ASIC4)
; FILE REFERENCE: ORT-1197
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-518-959-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
    ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 085596CD1
US-09-976-594-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:

NAME/KEY: misc feature

CTHER INFORMATION: Incyte ID No. 6727066 085596CD1

US-09-919-039-62
                                                                              100.0%; Score 37; DB 100.0%; Pred. No. 44;
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Best Local Similarity 100.v-
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 5; Conserv
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384 HHPHG 388
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US-09-919-039-62
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Faquence 64, Application US/09976594

Facuence 64, Application US/09976594

GENERAL INFORMATION:

APPLICANT: Furness, Michael

APPLICANT: Buchbinder, Jenny

TITE OF GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL Program

SOFTWARE: PERL Program

LENGTH: 525

TYPE: PRT

CORGANISM: Homo sapiens

FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-09-252-991A-26545
; Sequence 26545, Application US/09252991A
; Sequence 26545, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICATION:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26545
; TYPE: PRT
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: Fast SEQ for Windows Version 4.0
LENGTH: 280
                                                                                                                                                                                                                                                        Score 37;
Pred. No.
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US-09-252-991A-26545
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Best Local Similarity
Matches 5; Conser
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236 HHPHG 240
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Best Local Similarity
Matches 5; Conser
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|135 HHPHG 139
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US-09-949-016-9101
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US-09-976-594-64
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Sequence 29, Application US/09546013
Sequence 29, Application US/09546013
Patent No. 6610504
GENERAL INFORMATION:
APPLICANT: Yuan, Chong-Shen
TITLE OF INVENTION: METHODS FOR ASSAYING S-ADENOSYLMETHIONINE-DEPENDENT Methyltransfer
TITLE OF INVENTION: WINDER: US/09/546,013
CURRENT APPLICATION NUMBER: US/09/546,013
CURRENT FILING DATE: 2000-04-10
EARLIER FILING DATE: 1999-07-06
EARLIER FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 5
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Sequence 45546, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 45546
LENGTH: 923
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             CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20281
LENGTH: 810
                                                                                                                                                                                                                                                                                                                                            Mismatches
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                      Candida albicans
                                                                                                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                       1 HHPHG 5
                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Candid
US-09-248-796A-20281
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US-09-270-767-45546
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US-09-248-796A-20281
; Sequence 20281, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECTION STATES APPLICATION US/09252991A

PATENT NO. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23373

LENGTH: 618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 37; DB 4; Length 539; 100.0%; Pred. No. 45; 0; Indels iive 0; Indels
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                                                                                                                                                                                                                                                          DNA encoding human acid-sensing ion channel BNaC4 (ASIC4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 37; DB 100.0%; Pred. No. 52;
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                                                                                           Sequence 9, Application US/09518959;
Patent No. 6548270;
GENERAL INFORMATION:
APPLICANT: Dubin, Adrienne E
APPLICANT: Brlander, Mark G
APPLICANT: Huvar, Rene
APPLICANT: Pyati, Jayashree
TITLE OF INVENTION: DNA encoding human acid-
TITLE OF INVENTION: channel BNaC4 (ASIC4)
FILE REFERENCE: ORT-1197;
CURRENT APPLICATION NUMBER: US/09/518,959;
CURRENT FILING DATE: 2000-03-03;
NUMBER OF SEQ ID NOS: 9;
COSTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
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; LENGTH: 539
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-518-959-9
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Best Local Similarity
Matches 5; Conser
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476 HHPHG 480
524 HHPHG 528
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US-09-252-991A-23373
                                                          RESULT 19
US-09-518-959-9
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1 YHPHG 5
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US-08-159-339A-1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BLANCHE, Francis
APPLICANT: CAMERON, Beatrice
APPLICANT: CAMERON, Beatrice
APPLICANT: CAMERON, Alain
APPLICANT: FARRERO, Lucia
TITLE OF INVENTION: No. 6001631e1 Topoisomerase IV, Corresponding
TITLE OF INVENTION: Nucleotide Sequences and Uses Thereof
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner, L.L.P.
STREET: 1300 I. Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIF: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Bar PC compatible

    Description of Artificial Sequence: synthetic peptide representing metal-binding protein surface domains from human histadine rich glycoprotien (HRG).
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Pred. No. 4.1e+05;
0; Mismatches 0; Indels
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80.0%; Pred. No. 4.18+05;
ive 1; Mismatches 0; Indels
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; OTHER INFORMATION: Descri

; OTHER INFORMATION: peptid

; OTHER INFORMATION: domain

; PUBLICATION INFORMATION:

; JOURNAL: J. Chromatogr.

; VOLUME: 604

; ISSUE: 1

; PAGES: 125-132

; DATE: 1992

US-09-546-013-29
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application Patent No. 6001631 GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conser
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US-08-776-265-12
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Best Local S
Matches 4
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Length 15;
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                  COMPUTER EDGE 11

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,092
FILING DATE: 20-MAY-1998
CLASSIFICATION:
APPLICATION NUMBER: 60/047,221
FILING DATE: 20-MAY-1997
APPLICATION NUMBER: 60/060,465
FILING DATE: 30-SEP-1997
APPLICATION NUMBER: 60/075,940
FILING DATE: 06-MAR-1998
ATPLICATION NUMBER: 60/077,033
FILING DATE: 06-MAR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461/7032
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 3;
Pred. No. 13;
0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nakao, Atauhito
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: ten Dijke, Peter
TITLE OF INVENTION: SMAD7 AND USES THEREOF
FILE REFERENCE: L00461.70117.US
CURRENT FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: US 09/082,092
PRIOR FILING DATE: 1998-05-20
PRIOR FILING DATE: 1998-03-06
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1997-09-30
PRIOR FILING DATE: 1997-09-30
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14

LUNGTH: 15
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; Sequence 14, Application US/09885722A
; Patent No. 6605443
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-09-082-092-14
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Pred. No. 4.1e+05;
0; Mismatches 0; Indels
 NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
Tree Townsend and Townsend a sireET: Two Embarcadero Center, Eig CITY: San Francisco STATE: CA COUNTRY: USA ZUP: 9411-3834

COUNTRY: USA ZUBALE FORM:
MEDIUM TYPE: Diskette COMPUTER: EABABLE FORM:
MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OBERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version CURRENT APPLICATION NUMBER: US/08/159,339A FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 06/027,746
FILING DATE: 05-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 106-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELEPHONE: (415) 576-030^
TELEPHONE: (415) 576-030^
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US-09-082-092-14

Sequence 14, Application US/09082092

Patent No. 6251628

GENERAL INFORMATION:

APPLICANT: Nakao, Atsuhito
APPLICANT: Heuchel, Rainer
APPLICANT: Heuchel, Rainer
APPLICANT: Afrakhte, Mozghan
APPLICANT: Afrakhte, Mozghan
APPLICANT: Landstrom, Marene
APPLICANT: Landstrom, Marene
APPLICANT: Heldin, Grager
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Carl-Henrik
APPLICANT: Heldin, Garl-Henrik
APPLICANT: Heldin, SMAD7 AND USES THEREOF
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1005:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
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; STRANDEDNESS: sir
; TOPOLOGY: linear
; MOLECULE TYPE: pept
US-08-159-339A-1005
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TYPE: am
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Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 52,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Only or all research. Foundary of APPLICANT: Only or all allowers and APPLICANT: Only or all allowers and APPLICANT: Only or all allowers by APPLICANT: Matkins, Maren APPLICANT: Watkins, Maren APPLICANT: Shon, Ki-Joon APPLICANT: Shon, Ki-Joon APPLICANT: Shon, Ki-Joon APPLICANT: Shon, Ki-Joon APPLICANT: Jacobsen, Richard APPLICANT: Jacobsen, Richard APPLICANT: Shen, Greg S. APPLICANT: Shen, Greg S. APPLICANT: Shen, Greg S. APPLICANT: Wagstaff, John D. TITLE OF INVENTION: Mu-Conopeptides FILE REFERENCE: 2314-242
CURRENT FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2001-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.8%; Score 31; DB 100.0%; Pred. No. 48 Live 0; Mismatches
                                           EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-08-18
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PATENTIN Ver: 2.0
SOFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 575
LENGTH: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 158, Application US/09910009A Patent No. 6727226 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-227-357-575
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Best Local Similarity
Matches 4; Conserv
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US-09-910-009A-158
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SEQ ID NO 158
LENGTH: 69
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                                                                                                                       Gaps
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                                                                       Length 15;
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                                                                          DB 4;
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123 Human Secreted Proteins
                                                                                                                      Mismatches
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NUMBER: PCT/US98/13684
1998-07-07
                                                                         Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER: US/09/227,357
                                                                                                                                                                                                                                                                             RESULT 29

US-09-227-357-575

Sequence 575, Application US/09227357

Sequence 575, Application US/09227357

Sequence 575, Application US/09227357

GENERAL INFORMATION:

APPLICATION NUMBER: US/09/227, 3

CURRENT PELING DATE: 1999-01-08

EARLIER APPLICATION NUMBER: 60/051,926

BARLIER PILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,925

EARLIER PILING DATE: 1997-07-08

EARLIER PILING DATE: 1997-08-18

EARLIER PILING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER: 60/051,926
1997-07-08
NUMBER: 60/052,793
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1997-07-08
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1997-07-08
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1997-07-08
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NUMBER: 60/052,795
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1997-08-18
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1997-08-18
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                                                                       83.8%;
                                                                   Query Match
Best Local Similarity 100.
Matches 4; Conservative
; ORGANISM: Mus musculus US-09-885-722A-14
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TYPE: PRT
CORGANISM: Drosophila melanogaster
US-09-270-767-57094
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; ORGANISM: Drosophila melanogaster
US-09-270-767-36032
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ORGANISM: Drosophila melanogaster
72 HHPH 75
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                                                   RESULT 33
US-09-270-767-57094
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US-09-489-039A-10688

i Sequence 10688, Application US/09489039A

j Patent No. 6610836

i GENERAL INFORMATION:

i APPLICANT: Gary Breton et. al

i TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

i FILE REFERENCE: 2709.2004001

i CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

i NUMBER OF SEQ ID NOS: 14342

i SEQ ID NO 10688

LENGTH: 76
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                                                                                                                                 Sequence 73, Application US/09716129; Sequence 73, Application US/09716129; Patent No. 6632920; Patent No. 6632920; GENERAL INFORMATION:
TITLE OF INVENTION: 36 Human Secreted Proteins; FILE REFERENCE: PZ025P1; CURRENT FILING DATE: 2000-11-17; PRIOR FILING DATE: 1998-02-26; NUMBER OF SEQ ID NOS: 186; SEO TH NOS: 186
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100.0%; Pred. No. 71;
ive 0; Mismatches (
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100.0%; Pred. No.
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10688
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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COTHER INFORMATION:
US-09-716-129-73
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ННРН 26
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HHPH 47
                HHPH 4
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LENGTH: 75
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Sequence 57094, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 57094

LENGTH: 84
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US-09-270-767-36032
; Sequence 36032, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster;
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36032
; LENGTH: 91
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US-09-270-767-51249
; Sequence 51249, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; TILE SPERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 51249
; LENGTH: 91
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                                              Sequence 58449, Application US/09270767
Sequence 58449.
Sequence 58449.
Sequence 58449.

APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 58449
LENGTH: 102
TYPE: PRT
ORGANISM: Drosophila melanogaster
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NAME/KEY: SITE
LOCATION: (100)
OTHER INFORMATION: Xaa equals any of the naturally occurring
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OTHER INFORMATION: Xaa equals any of the naturally occurring
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ITILE OF INVENTION: 94 Human Secreted Proteins
FILE REFERENCE: PZ029P1
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
EARLIER APPLICATION NUMBER: PCT/US99/13418
EARLIER FILING DATE: 1999-06-15
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
SOFTWARE: PATHON OF SEQ ID NOS: 532
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
NAME/KEY: SITE
NAME/KEY: SITE
NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-58449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 160, Application US/09461325A Patent No. 6475753 GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
Matches 4; Conserv
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                               US-09-270-767-58449
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US-09-248-796A-23534

is Sequence 23534, Application US/09248796A

is Sequence 23534, Application US/09248796A

is Sequence 23534, Application US/09248796A

is GENERAL No. 6747137

is GENERAL No. 6747137

is TILE OF INVENTION:

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Sequence 653, Application US/09640211A;
Patent No. 6833446;
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.;
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Modification of Gene Transcription;
TITLE OF INVENTION: Modification of Gene Transcription;
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 653
LENGTH: 99
TYPE: PRT
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Pred. No. 86;
                                                       Length 91
                                                                                                            0; Indels
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                                                    Score 31; DB '
Pred. No. 85;
0; Mismatches
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US-09-248-796A-23534
                                            Query Match
Best Local Similarity 100.
Matches 4; Conservative
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US-09-640-211A-653
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Best Local Similarity
Matches 4; Conser
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Matches 4; Conser
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US-09-270-767-51249
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US-09-640-211A-653
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US-10-012-542-160

is Sequence 160, Application US/10012542

patent No. 6627741

i GENERAL INFORMATION:

APPLICANT: Ruben et al.

TILLE OF INVENTION: 94 Human Secreted Proteins

FILE REFERENCE: E2029F1

CURRENT APPLICATION NUMBER: US/10/012,542

CURRENT APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507

PRIOR PILING DATE: BARLIER FILING DATE: 1998-06-16

PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-16

PRIOR PILING DATE: BARLIER FILING DATE: 1998-06-16

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFTWARE: PATENTING DATE: EARLIER FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SEQ ID NO 160

LENGTH: 115

TYPE: PATURE:

NAMELKEY: SITE

NAMELKEY: SIT
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; OTHER INFORMATION: X
; NAME/KEY: SITE
; LOCATION: (100)
; OTHER INFORMATION: X
US-10-012-542-160
                                                        104 HHPH 107
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1 HHPH 4
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15, 2005, 14:24:19

Search completed: June Job time : 24.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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- protein search, using sw model OM protein June 15, 2005, 14:21:52; Search time 79.75 Seconds (without alignments) 24.034 Million cell updates/sec Run on:

US-10-074-225A-8 37 1 HHPHG 5 score: Title: Perfect sc Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1710399

Searched:

1710399 of hits satisfying chosen parameters: Total number

segs, 383334425 residues

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

| cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/BCT\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
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| cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\* 

SUMMARIES

## Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 8, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli
ΩI	US-10-074-225A-8	US-10-153-312A-1	US-09-809-657-1	US-09-848-512A-1	US-09-742-494-1	US-10-153-312A-2	US-10-153-312A-3	US-09-809-657-2	US-09-848-512A-2	US-09-742-494-2	US-10-153-312A-4
DB	14	14	σ	σ	თ	14	14	σ	σ	0	14
% Query Match Length DB	2	9	11	11	11	11	16	26	26	26	26
& Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	37	37	37	37	37	37	37	37	37	37	37
Result No.		7	m	4	ß	9	7	8	თ	10	11

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277019, 4437, Ap 6, Appli 149790, 324288, 142824,	55, 1128, 128, 158, 158, 158, 158, 158, 158, 158, 15	65, Appl 344, App 1250, Ap 593, App 596, App 185, App	19871, A 205101, 8, Appli 62, Appl 1, Appli 42, Appli 2, Appli	8, Appli 290, Appli 3, Appli 1, Appli 25, Appli 12, Appli 24, Appl
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US-10-424-599-277019 US-10-106-698-4437 US-10-074-225A-6 US-10-437-963-149790 US-10-425-115-324288 US-10-437-963-142824	-10-074-225A-5 09-864-761-42051 -10-437-963-12847 -10-425-114-58759 -10-282-122A-6293	-09-981- -10-295- -10-295- -10-072- -10-188-	US-10-369-493-19871 US-10-424-599-205101 US-10-808-807-8 US-09-919-039-62 US-10-074-225A-1 US-10-868-577A-42 US-10-077-180A-2	09-772-1 09-772-1 09-772-1 00-084-8 10-419-8 10-373-2 10-683-7
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## ALIGNMENTS

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                                                                                                                                                                                                    100.0%; Score 37; DB 14;
100.0%; Pred. No. 1.5e+06;
iive 0; Mismatches 0;
                                                                                                                                                                            ; OTHER INFORMATION: Synthetic Peptide US-10-074-225A-8
                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 100.
Matches 5; Conservative
US-10-074-225A-8
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APPLICANT: HUTCHENS, WILLIAM
APPLICANT: HUTCHENS, WILLIAM
APPLICANT: YIP, TAI-TUNG
TITLE CANT: YIP, TAI-TUNG
TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES
FILE REFERENCE: P00798USF/09306611
CURRENT FILING DATE: 2001-03-15
PRIOR PILING DATE: 1993-05-28
PRIOR FILING DATE: 1993-05-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
LENGTH: 11
TYPE: PRT

ORGANISM: Homo sapiens
US-09-809-657-1
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RESULT 2
US-10-153-312A-1
; Sequence 1, Application US/10153312A
; Publication No. US20030040016A1
; GENERAL INFORMATION:
; APPLICANT: Singh, Sharat
; APPLICANT: Zivin, Robert Allan
; TITLE OF INVENTION: Analyzing Phosphorylated Proteins
; FILE REFERENCE: 50225-8086.US03
; CURRENT APPLICATION NUMBER: US/10/153,312A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/334,902
; PRIOR FILING DATE: 2001-10-24
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS FOR SEQUENCING BIOPOLYMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 37; DB 14;
100.0%; Pred. No. 1.5e+06;
iive 0; Mismatches 0;
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APPLICANT: HUTCHENS, WILLIAM; APPLICANT: YIP, TAI-TUNG; TILLE OF INVENTION: METHODS FOR SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09809657
Patent No. US20010014479A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
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5; Conservative
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Best Local Similarity
Matches 5; Conser
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US-10-153-312A-1
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US-09-848-512A-1
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APPLICANT: HUTCHENS, WILLIAM

APPLICANT: HUTCHENS, WILLIAM

APPLICANT: HUTCHENS, WILLIAM

APPLICANT: YIP, TAI-TUNG

TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES

FILE REFERENCE: P00798USE/09306611

CURRENT APPLICATION NUMBER: US/09/742,494

CURRENT FILING DATE: 2000-12-20

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.0

LENGTH: 11
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APPLICANT: Singh, Sharat
APPLICANT: Zivin, Robert Allan
TITLE OF INVENTION: Analyzing Phosphorylated Proteins
FILE REFERENCE: 50225-8086.US03
CURRENT APPLICATION NUMBER: US/10/153,312A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/334,902
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 16;
; Mismatches
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; Pred. No. 16;
0; Mismatches
FILE REFERENCE: P00798USG/09306611
CURRENT APPLICATION NUMBER: US/09/848,512A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 08/068,896
PRIOR FILING DATE: 1993-05-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 11
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: metal binding peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 2, Application US/10153312A; Publication No. US20030040016A1; GENERAL INFORMATION:
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100.0%;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                          TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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HHPHG 6
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US-10-153-312A-4
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US-09-742-494-2
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US-09-809-657-2
; Sequence 2, Application US/09809657
; Patent No. US20010014479A1
; GENERAL INFORMATION:
; APPLICANT: HUTCHENS, WILLIAM
; APPLICANT: YIP, TAI-TUNG
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES
; FILE REFERENCE: P00798USF/09306611
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US/09/809,657
; CURRENT FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; SEQ ID NO 2
; LENGTH: 26
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                                  Length 11
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                                                                                                                                       RESULT 7

US-10-153-312A-3

US-10-153-312A-3

Sequence 3, Application US/10153312A

Publication No. US20030040016A1

GENERAL INFORMATION:

APPLICANT: Singh, Sharat

APPLICANT: Zivin, Robert Allan

TITLE OF INVENTION: Analyzing Phosphorylated Proteins

FILE REFERENCE: 50225-8086.US03

CURRENT APPLICATION NUMBER: US/10/153,312A

CURRENT FILING DATE: 2002-05-21

PRIOR APPLICATION NUMBER: US 60/334,902

PRIOR FILING DATE: 2001-10-24

PRIOR FILING DATE: 2001-10-24

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 16
                                                                Indels
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0
                              100.0%; Score 37; DB 14;
100.0%; Pred. No. 16;
ive 0; Mismatches 0;
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                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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; ORGANISM: Homo sapiens
US-09-809-657-2
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Best Local Similarity
Matches 5; Conser
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US-10-153-312A-2
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Sequence 2, Application US/09742494

Fatent No. US20020155620A1

GENERAL INFORMATION:

APPLICANT: HUTCHENS, WILLIAM

APPLICANT: YIP, TAI-TUNG

TITLE OF INVENTION: METHODS AND APPARATUS FOR DESORPTION AND IONIZATION OF ANALYTES

FILE REFERENCE: P00798USE/09306611

CURRENT APPLICATION NUMBER: US/09/742,494

CURRENT FILING DATE: 2000-12-20

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin version 3.0

SEQ ID NO 2

LENGTH: 26
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Sequence 2, Application US/09848512A
; Sequence 2, Application US/09848512A
; GENERAL INFORMATION:
; APPLICANT: HUTCHENS, WILLIAM
; APPLICANT: YIP, TAI-TUNG
; TITLE OF INVENTION: METHODS FOR SEQUENCING BIOPOLYMERS
; FILE REFERENCE: P00798USG/09306611
; CURRENT APPLICATION NUMBER: US/09/848,512A
; CURRENT FILING DATE: 2000-05-03
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4. Application US/10153312A
; Publication No. US20030040016A1
; Publication No. US20030040016A1
; GENERAL INFORMATION:
; APPLICANT: Zivin, Robert Allan
; TITLE OF INVENTION: Analyzing Phosphorylated Proteins
; FILE REFERENCE: 50225-8086.US03
; CURRENT APPLICATION NUMBER: US/10/153,312A
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/334,902
; PRIOR FILING DATE: 2001-10-24
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 37; DB 100.0%; Pred. No. 34;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: HOMO SAPIENS
US-09-848-512A-2
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: PLUNKETT, Marian L

APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

APPLICANT: MAZAR, Andrew P

TITLE OF INVENTION: ANTI-TUMOR AGENT

FILE REFERENCE: 38342-178463

CURRENT FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/268,370

PRIOR FILING DATE: 2001-02-14

DRIOR FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.1
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
; SEQ ID NO 4437
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; OCTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC_FEATURE
; LOCATION: (29)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; LOCATION: (33)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-4437
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100.0%; Pred. No. 1.1e+02;
ative 0; Mismatches 0;
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; Sequence 149790, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Bachave, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 6
LENGTH: 101
TYPE: PRT
ORGANISM: Lepus americanus
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Best Local Similarity
Matches 5; Conserv
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US-10-424-599-277019
; Sequence 277019, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Cao Yongwei
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 18-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 277019
; LENGTH: 84
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US-10-106-698-4437
; Sequence 4437, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR FILING DATE: 1999-09-29
; PRIOR FILING DATE: 1999-11-03
; PRIOR FILING DATE: 1999-11-03
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                                                                                                                                                                                                                                                  Similarity 100.0%; Score 37; DB 14; Similarity 100.0%; Pred. No. 34; 5; Conservative 0; Mismatches 0;
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 PRIOR APPLICATION NUMBER: US 60/292,548
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 26
                                                                                                                                                                                         metal binding peptide
                                                                                                                          TYPE: PRT
CORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: metal bindi
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FEATURE:
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ORGANISM: Glycine m:
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(84)
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Best Local Similarity
Matches 5; Conser
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Sequence 5, Application US/10074225A
; Sequence 5, Application US/10074225A
; Publication No. US20030082740A1
; GANEAL INFORMATION:
; APPLICANT: DONATE, Fernando
; APPLICANT: DONATE, Fernando
; APPLICANT: DONATE, Scott
; APPLICANT: MAZAR, Andrew P
; TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC ;
; TITLE OF INVENTION: ANTI-TUMOR AGENT
; TITLE OF INVENTION: ANTI-TUMOR AGENT
; FILE REFERENCE: 38342-178463
; CURRENT APPLICATION NUMBER: US/10/074,225A
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 60/268,370
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 148
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| Sequence 42051, Application US/09864761
| Patent No. US20020048763A1
| GENERAL INFORMATION:
| APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Rank, David R. APPLICANT: Chen, Wensheng
| TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FILE REFERENCE: Acomica-X-1
| CURRENT APPLICATION NUMBER: US/09/864,761
| CURRENT APPLICATION NUMBER: US 60/180,312 |
| PRIOR FILING DATE: 2000-05-26 |
| PRIOR FILING DATE: 2000-05-26 |
| PRIOR FILING DATE: 2000-06-03 |
| PRIOR FILING DATE: 2000-08-03 |
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                                                                           TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
COTHER INFORMATION: Clone ID: PAT_MRT4530_43793C.1.pep
US-10-437-963-142824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 37; DB 16;
100.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 0;
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     NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 142824
LENGTH: 138
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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US-10-074-225A-5
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US-10-437-963-142824

i Sequence 142824, Application US/10437963

j Publication No. US20040123343A1

j GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Abou, Yihua
    APPLICANT: Cao, Yongwei
    APPLICANT: Wu, Wei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Brbazuk, Brad
    APPLICANT: Li, Ping
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REFERENCE: 38-21(53221)B
    CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 149790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 16
US-10-425-115-324288
; Sequence 324288, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 324288
; SEQ ID NO 324288
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      Clone ID: PAT_MRT4530_50089C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone ID: MRT4577_58824C.1.pep
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                    ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Zea mays
FEATURE:
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US-10-437-963-149790
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Sequence 58759, Application US/10425114

Sequence 58759, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Yihua

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 58759

LENGTH: 185
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CTHER INFORMATION: Clone ID: PAT_MRT4530_30821C.1.pep
US-10-437-963-128472
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100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.6e+02;
vative 0; Mismatches 0;
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US-10-425-114-58759
       CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 128472
LENGTH: 152
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                     TYPE: PRT
ORGANISM: Oryza sativa
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24 HHPHG 28
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                1 HHPHG 5
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US-10-437-963-128472
; Sequence 128472, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
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N: EXPRESSED IN BONE MARROW, SIGNAL = 2.4

N: EXPRESSED IN HEART, SIGNAL = 3.8

N: EXPRESSED IN LUNG, SIGNAL = 2.5

N: EXPRESSED IN PLACENTA, SIGNAL = 2.4

N: EXPRESSED IN ADULT LIVER, SIGNAL = 2.7

N: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2

N: EXPRESSED IN HELA, SIGNAL = 3.2

N: EXPRESSED IN HELA, SIGNAL = 3.4

N: EXPRESSED IN BRAIN, SIGNAL = 2.6

N: EXPRESSED IN BRAIN, SIGNAL = 2.6

N: EXPRESSED IN BRAIN, SIGNAL = 2.6

N: EXT HUMAN HIT: BE182360.1, EVALUE 3.00e-64

N: SWISSPROT HIT: 095377, EVALUE 2.00e-89
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
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ORGANISM: Homo sapi
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SEQ ID NO 42051
LENGTH: 151
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229 HHPHG 233
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US-09-981-151A-64
IS-09-981-151A-64
School Catterion No. US20030212256A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R
APPLICANT: Malyankar, Muriel M
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Smithson, Glennda
APPLICANT: Stimkes, John A
APPLICANT: Stimkes, John A
APPLICANT: Stimkes, John A
APPLICANT: Stimkes, Razen
APPLICANT: Shimkes, Razen
APPLICANT: Shimkes, Richard A
APPLICANT: Shimkes, Richard A
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tauglaru, Muralidhara
APPLICANT: Gangolli, Esha A
APPLICANT: Gangolli, Esha A
APPLICANT: Germandes, Elma R
APPLICANT: Germandes, Elma R
APPLICANT: Gramm, Linda
ITTLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-168
FURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR PRIOR APPLICATION NUMBER: 60/241,040
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100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0;
          NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,1
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-27
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data remove NUMBER: Patentin version 3.1
SEQ ID NO 62936
LENGTH: 259
TYPE: PRT
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5; Conservative
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A-62936
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Best Local S
Matches 5
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PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 344
LENGTH: 273
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                                                                                                                                                                                                                                                                                                            Length 273;
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100.0%; Pred. No. 2.7e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                             0
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 5; Conserv
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US-10-295-027-344

Sequence 344, Application US/10295027

Publication No. US2003023250A1

Sequence 344, Application US/10295027

Publication No. US2003023250A1

SEREAL INFORMATION:

APPLICANT: Aziz, Natasha

APPLICANT: Glynne, Richard

APPLICANT: Glynne, Richard

APPLICANT: Glynne, Richard

APPLICANT: Markson, Richard

APPLICANT: Markson, Susan R.

APPLICANT: Markson, Susan R.

APPLICANT: Warkson, Susan R.

APPLICANT: Sos Blotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer

TITLE OF INVENTION: Warkser: US/10/295,027

CURRENT FILING DATE: 2002-11-13

PRIOR PLICATION NUMBER: US 60/335,394

PRIOR FILING DATE: 2001-11-12

PRIOR PLICATION NUMBER: US 60/334,335

PRIOR FILING DATE: 2001-11-21

PRIOR PLICATION NUMBER: US 60/340,376

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR PLING DATE: 2002-01-10

PRIOR PLING DATE: 2002-01-10

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR APPLICATION NUMBER: US 60/347,211

PRIOR PLING DATE: 2002-01-10

PRIOR PRIING DATE: 2002-01-10

PRIOR PLING DATE: 2002-01-10

PRIOR PRIING DATE: 2002-01-10

PRIOR PRIING DATE: 2002-01-10

PRIOR PRIING DATE: 2002-01-10

PRIOR PRIOR PLING DATE: 2002-01-10
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/241,243
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,880
PRIOR FILING DATE: 2000-10-24
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LOCATION: (41)
OTHER INFORMATION: W
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|HPHG 233
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ORGANISM: Homo s
FEATURE:
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Best Local S
Matches 5
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NUMBER OF SEQ ID NOS: 1391
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Argger, Daniel A.

APPLICANT: Argger, Daniel A.

TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-258

CURRENT APPLICATION NUMBER: US/10/072,012

CURRENT PILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: 60/265,102

PRIOR APPLICATION NUMBER: 60/265,514

PRIOR PILING DATE: 2001-01-31

PRIOR APPLICATION NUMBER: 60/265,517

PRIOR PILING DATE: 2001-01-31

PRIOR PILING DATE: 2001-01-31

PRIOR PILING DATE: 2001-01-31

PRIOR PILING DATE: 2001-01-01-31

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-05

PRIOR PILING DATE: 2001-02-07

PRIOR PILING DATE: 2001-02-07

PRIOR FILING DATE: 2001-02-07

PRIOR PILING DATE: 2001-02-07
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100.0%; Pred. No. 2.7e+02;
tive 0; Mismatches 0;
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COTHER INFORMATION: Wherein Xaa is anya mino acid
US-10-072-012-596
                                                                       Sequence 596, Application US/10072012; Publication No. US20040033493A1; GENERAL INFORMATION:
APPLICANT: Tchernev, Velizar
APPLICANT: Spytek, Kimberly
APPLICANT: Zerhusen, Bryan
APPLICANT: Patturajan, Meera
APPLICANT: Shimkets, Richard
                                                                                                                                                                                                                                                                                                       Li, Li
Gangolli, Bsha
Padigaru, Muralidhara
Anderson, David W.
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller, Charles E. Gerlach, Valerie
Taupier Jr, Raymond J. Gusev, Vladimir Y. Colman, Steven D. Wolenc, Adam R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Furtak, Katarzyna
Grosse, William M.
Alsobrook II, John P.
Lepley, Denise M.
Rieger, Daniel K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carol E. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pena,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HHPHG
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LENGTH: 273
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100.0%; Pred. No. 2.7e+02;
iive 0; Mismatches 0;
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                                                                                                                                            Sequence 593, Application US/10072012
Sequence 593, Application US/10072012
Sequence 591, Application US/10072012
Sequence 593, Application US/10072012
Sequence 591
Publication No. US20040033493A1
APPLICANT: Spick, Kimberly
APPLICANT: Spick, Kimberly
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Shimkets, Richard
APPLICANT: Anderson, David W.
APPLICANT: Anderson, David W.
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Guner, Valerie
APPLICANT: Gerlach, Valerie
APPLICANT: Guner, Valerie
APPLICANT: Guner, Valerie
APPLICANT: Guner, Steven D.
APPLICANT: Guner, Steven D.
APPLICANT: Guner, Steven D.
APPLICANT: Guner, Adam R.
APPLICANT: Lepley, Denise W.
APPLICANT: Rigger, Daniel K.
APPLICANT: Burges, Catherine E.
TITLE OF INVENTION: Proceins and Nuclei.
FILE REFERENCE: 21402-258
CURRENT APPLICATION NUMBER: 60/265,514
PRIOR FILING DATE: 2001-01-31
PRIOR PILING DATE: 2001-02-07
PRIOR PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 100
5; Conservative
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CRGANISM: Homo
US-10-072-012-593
                                                                                                 RESULT 27
US-10-072-012-593
                 229
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; Sequence 8, Application US/10808807
; Publication No. US20040253663A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont deNemours and Co., Inc.
; APPLICANT: Cheng, Qiong
; APPLICANT: Tao, Luan
; APPLICANT: Tao, Luan
; TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
; TITLE OF INVENTION: GENES ENCODING CAROTENOID COMPOUNDS
; TITLE OF INVENTION GENES ENCODING CAROTENOID COMPOUNDS
; FILE REFERENCE: CL2365 US NA
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: US 60/477,874
; PRIOR FILING DATE: 2003-06-12
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PATENTIN Version 3.2
; TYPE: PRT
; ORGANISM: Pantoea agglomerans strain DC404
US-10-808-807-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

Corner ID: PAT_MRT3847_27235C.1.pep US-10-424-599-205101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 37; DB 15; Best Local Similarity 100.0%; Pred. No. 4.2e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 37; DB 16; Best Local Similarity 100.0%; Pred. No. 4.5e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(460)
OTHER INFORMATION: unsure at all Xaa locations
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19871
LENGTH: 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                      APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-002330US
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US, 60/302,814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 37; DB 15; Length 273; 100.0%; Pred. No. 2.7e+02; ative 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 3.3e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: No. US20030233675Altoc punctiforme
US-10-369-493-19871
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-07-03
PRIOR PLING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR FILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19871, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                    S-10-188-832-185
Sequence 185, Application US/10188832
Publication No. US20040076955A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 185
LENGTH: 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-10-188-832-185
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
229 HHPHG 233
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US-10-369-493-19871
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; Sequence 3, Application US/10074225A; Sequence 3, Application WS/10074225A; Publication No. US20030082740A1; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: DONATE, Fernando
; APPLICANT: HARRIS, Scott
; APPLICANT: MAZAR, Andrew P
; TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC ;
; TITLE OF INVENTION: HATI-TUMOR AGENT
; TITLE OF INVENTION: ANTI-TUMOR AGENT
; FILE REFERENCE: 38342-178463
; CURRENT APPLICATION NUMBER: US/10/074,225A
; CURRENT APPLICATION NUMBER: US 60/268,370
; PRIOR APPLICATION NUMBER: US 60/268,370
; PRIOR APPLICATION NUMBER: US 50/268,370
; PRIOR APPLICATION NUMBER: US 50/268,370
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 526
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; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS; FILE REFERENCE: 28967/39359A; CURRENT APPLICATION NUMBER: US/10/868,577A; CURRENT FILING DATE: 2004-06-14; PRIOR APPLICATION NUMBER: US 60/478,390; PRIOR FILING DATE: 2003-06-12; PRIOR FILING DATE: 2003-09-23; NUMBER OF SEQ ID NOS: 69; SOFTWARE: Patentin version 3.2; SEQ ID NO 42; LENGTH: 525; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 37; DB 17;
100.0%; Pred. No. 4.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 37; DB 14; 100.0%; Pred. No. 4.7e+02;
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APPLICANT: David C. Harrison
APPLICANT: Sharon Bingham; APPLICANT: Sharon Bingham; APPLICANT: Simon Topp; TITLE OF INVENTION: NOVEL COMPOUNDS; FILE REFERENCE: GH-30021-C1; CURRENT APPLICATION NUMBER: US/09/772,180A; CURRENT FILING DATE: 2001-01-29; PRIOR APPLICATION NUMBER: 09/063,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Lepus americanus
US-10-074-225A-3
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100
Matches 5; Conservative
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384 HHPHG 388
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US-10-074-225A-3
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                                                                                   Sequence 62, Application US/09919039

Publication No. US20030108871A1

GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 62
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Incyte ID No. US20030108871A1 085596CD1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10074225A; Publication No. US20030082740A1; GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: PLUNKETT, Marian L
APPLICANT: HARRIS, Scott
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GL
TITLE OF INVENTION: ANTI-TUMOR AGENT
TILE REFERENCE: 38342-178463
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2002-02-14
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 5; Conservative
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US-10-074-225A-1
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Best Local Similarity
Matches 5; Conserv
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US-10-868-577A-42
                                                RESULT 33
US-09-919-039-62
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US-10-074-225A-1
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LENGTH: 525
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100.0%; Pred. No. 4.8e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09772180A; Sequence 8, Application US/09772180A; Publication No. US20030027749A1; GENERAL INFORMATION:
APPLICANT: David C. Harrison
APPLICANT: Sharon Bingham
APPLICANT: Sharon Bingham
APPLICANT: Trudy R. Doe
APPLICANT: Simon Topp
TITLE OF INVENTION: NOVEL COMPOUNDS; FILE REFERENCE: GH-30021-C1
CURRENT APPLICATION NUMBER: US/09/772,180A; CURRENT FILING DATE: 1998-04-21; PRIOR APPLICATION NUMBER: 9708936.1
PRIOR FILING DATE: 1997-05-01
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 8
SOUTHARE: FASTESQ for Windows Version 3.0
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 9708936.1
PRIOR FILING DATE: 1997-05-01
PRIOR FILING DATE: 1997-05-01
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 539
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APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsherg, Wendy M.
APPLICANT: Ginsherg, Mendy M.
                                                                                                                                                                                                                                                                                                                             vative
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US-09-772-180A-2
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US-10-295-027-290
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US-09-772-180A-8
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US-09-772-180A-8
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539
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- 2005 Compugen Ltd
GenCore (c) 1993
           Copyright
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OM protein - protein search, using sw model

Run on:

June 15, 2005, 14:04:57 ; Search time 17.5 Seconds (without alignments) 27.491 Million cell updates/sec

US-10-074-225A-8 37 1 HHPHG 5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

seqs, 96216763 residues 283416 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMADIES

	* Query Match	Length	DB	SUMMARIES ID .	Description
}			}		
10	0.0	419	Н	870617	homeotic protein g
10	100.0	445	N	A60488	histidine-rich gly
7	0.0	491	N	H83979	lysine decarboxyla
7	0.0	525	Н	KGHUGH	histidine-rich gly
10	0.0	602	7	D75618	hypothetical prote
ĭ	100.0	721	~	E70766	cal
ä	0.0	753	~	D72660	ble alde
ä	0.00	1441	~	T13717	CRAG protein - fru
w	س	16	7	F97793	hypothetical prote
œ	m m	84	~	AH3162	u
œ	3.8	94	~	A49832	DNA gyrase A - Sta
80	щ	95	~	S49447	DNA topoisomerase
Φ	Э.	95	~	S54254	DNA topoisomerase
w	щ	105	7	S62940	probable membrane
ω	ъ М	110	~	F69760	hypothetical prote
œ	т М	113	7	E82687	e O
œ	щ	130	7	S14983	
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Φ,	m.	136	0	E72759	hypothetical prote
œ	ъ.	146	7	I40541	
Ф.	m.	147	7	I39542	DNA gyrase - Aerom
w	ن	147	7	AC1898	urease accessory p
w	е	148	7	F89956	conserved hypothet
_	ო	155	7	S25846	
	m	156	~	T31664	DAP-kinase homolog
_	е Н	164	7	158201	MHC class I antige
ω	33.8	171	7	T13554	cal
ш	щ	178	7	T36013	probable integral
Φ	3.8	188	7	B49773	ecdysone-dependent

Asolate solution of the disulphide bridge arrangement of bovine (fragments)
NyAlternate names: autorosette inhibition factor
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1993 #sequence\_revision 23-Mar-1995 #text\_change 07-Jul-1995
C;Accession: S35687; JC2196; A60488
R;Sorensen, C.B.; Krogh-Pedersen, H.; Petersen, T.E.
FEBS Lett. 328, 285-290, 1993
A;Title: Determination of the disulphide bridge arrangement of bovine histidine-rich glyc
A;Reference number: S35687; MUID:93351678; PMID:8348977
A;Accession: S35687
A;Accession: S35687
A;Molecule type: protein
A;Residues: 1-25;26-52;57-75;82-88;95-119;146-173;175-206;210-309;313-445 <SOR>
A;Note: 355-Gln and 368-Tyr were also found
R;Halkier, T.; Andersen, H.; Vestergaard, A.; Magnusson, S.

thioredoxin BH1717	hypothetical prote	guanylate kinase [	pyroglutamyl-pepti	Myb26 protein - ga	glutamate decarbox	DNA gyrase chain A	hypothetical prote	pyruvate decarboxy	conserved hypothet	probable phage min	hypothetical prote	probable dapB prot	conserved hypothet	nitrous-oxide redu	hypothetical prote
E83864	S50686	G87457	JX0244	T06455	159173	835735	T40889	S65426	H82360	AB0259	A84729	D70882	AB0957	AE3631	F84845
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## ALIGNMENTS

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A; Restauces: 1-525 extor.

A; Restaus: 1-525 extor.

A; Recess-references: UNIPROT:P04196; GB:AB005803; NID:g2280513; PIDN:BAA21613.1; PID:g2280
R; Riemnis: B.; Havelaar, A.; Kluft, C.
Submitted to the EMBL Data Library, October 1991
A; Description: PCR detection of a dinucleotide repeat in the human histidine-rich glycopy A; Recession: 829669
A; Recession: 829669
A; Accession: 829669
A; Status: preliminary
A; Residues: Data Library, October 1991
A; Residues: Data Library, October 1991
A; Residues: Data Library, D
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hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: D75618

C;Accession: D75618

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F., M.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

S; Smith, H.O.; Venter, J.C.; Fraser, C.M.

A; Reference number: A75250; MUID:20036896; PMID:10567266

A; Residues: 1-602 <WHI>

A; Residues: 1-602 <WHI>

A; Residues: 1-602 <WHI>

A; Residues: Brain R1

C; Genetics:

A; Genet
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C;Superfamily: Deinococcus radiodurans hypothetical
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100.0%; Pred. No. 45;
ive 0; Mismatches
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384 HHPHG 388
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Biochem. Biophys. Res. Commun. 200, 78-82, 1994

A; Title: Bovine histidine-rich glycoprotein is a substrate for bovine plasma factor XIII

A; Accession: JC2196; MUID: 94220160; PMID: 7909439

A; Accession: JC2196

A; Molecule type: protein

A; Residues: 1-23;35-54, "WK',57-101,"R'; TVGEYTEG',116,"N',118,"R',120-136;137-145;150-20

A; Residues: 1-23;35-54, "WK',57-101,"R'; TVGEYTEG',116,"N',118,"R',120-136;137-145;150-20

A; Residues: 1-23;35-54,"WK',57-101,"R'; TVGEYTEG',116,"N',118,"R',120-136;137-145;150-20

A; Title: Histidine-rich glycoprotein inhibits contact activation of blood coagulation.

A; Reference number: A60488; MUID: 91196010; PMID: 2084959

A; Reference number: A60488; MUID: 91196010; PMID: 2084959

A; Reference number: A60488

A; Reference number: A60488; MUID: 91196010; PMID: 2084959

A; Reference number: A60488; MUID: 91196010; PMID: 2084959

C; Comment: This protein is a single-chained plasma protein which participates in transglenge in the protein is a single-chained plasma protein which participates in transglenge in the protein is a single-chained plasma protein which participates in transglenge in the protein is a single-chained plasma protein which participates in transglenge in the protein in plasma

C; Superfamily: histidine-rich glycoprotein; cystatin homology (fragments)

F; 2-113/Domain: cystatin homology (fragments)

F; 2-207/Domain: cystatin homology (fragments)

F; 7-424,60-71,87-109,165-346,180-203,258-288/Disulfide bonds: #status experimental

F; 74,107,164,266/Binding site: carbohydrate (Asn) (covalent)
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C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: H83979
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Reference number: DNA
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Reference number: A;References: UNIPROT:09K9K5; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB063
A;Experimental source: strain C-125
C;Genetics:
A;Gene: cad
C;Superfamily: lysine decarboxylase
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NiAlternate names: HRG
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A01287; S29669
C;Accession: A01287; S29669
R;Koide, T.; Foster, D.; Yoshitake, S.; Davie, B.W.
Biochemistry 25, 2220-2225, 1986
A;Title: Amino acid sequence of human histidine-rich glycoprotein derived from the 1A;Reference number: A01287; MUID:86216149; PMID:3011081
A;Accession: A01287
A;Molecule type: mRNA
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H83979
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A;Reference number: Z17709; MUID:99030403; PMID:9813038
A;Accession: T13717
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1441 <XUX>
A;Cross-references: UNIPROT:096957; EMBL:Y17918; NID:g3893100; PIDN:CAA76938.1; PID:g3895:C;Genetics:
A;Gene: CRAG
A;Cross-references: FlyBase:FBgn0025864
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F97793
hypothetical protein RC0750 [imported] - Rickettsia conorii (strain Malish 7)
C; Species: Rickettsia conorii
C; Species: Rickettsia conorii
C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C; Accession: F97001
R; Accession: F97001
A; Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A; Reference number: A97700; MUID:21442074; PMID:11557893
A; Accession: F97793
A; Accession: F97793
A; Reference number: A97700; MUID:21442074; PMID:11557893
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A; Attle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
A; Reference number: AB2577; MUID:21608550; PMID:11743193
A; Residues: 1-84 <KUR>
A; Residues: 1-84 <KUR>
A; Residues: 1-84 <KUR>
A; Residues: 1-84 <KUR>
A; Genetics: A; Gene
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AH3162
IS21 family transposase (truncated) tnp [imported] - Agrobacterium tumefaciens (strain C
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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Pred. No. 65;
1; Mismatches
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Best Local Similarity 80.0
Matches 4; Conservative
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1119 HHPHG 1123
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HHPYG 11
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D72660
probable aldehyde oxidoreductase APE0708 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Accession: D72660
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Accession: D72660
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Residues: 1-753 <KAW>
A;Residues: 1-753 <KAW>
A;Residues: 1-753 <KAW>
A;Residues: BNA
A;Re
                                                                                                                                                                                                                                                        E70766
hypothetical protein Rv2082 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-011-1998 #sequence_revision 17-011-1998 #text_change 09-011-2004
C;Accession: E70766
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atile: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Recession: E70766
A;Accession: E70766
A;Accession: E70766
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-721 <-COL>
A;Cross-references: UNIPROT:Q10690; GB:Z73966; GB:AL123456; NID:g3261577; PIDN:CAA98194.
C;Genetics:
A;Genetics:
A;Genetics:
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C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C; Accession: T13717
C; Accession: T13717
R; Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C. R; Xu, X.Z.; Wes, P.D.; Chen, H.; Li, H.S.; Yu, M.; Morgan, S.; Liu, Y.; Montell, C. J. Biol. Chem. 273, 31297, 1998
A; Title: Retinal targets for calmodulin include proteins implicated in synaptic transmis
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411 HHPHG 415
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591 HHPHG 595
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A;Reference number: S54254
A;Accession: S54254
A;Accession: S54254
A;Accession: S54254
A;Accession: S54254
A;Residues: 1-95 <RUI>
A;Cross-references: UNIPROT: P37411; EMBL: X86695; NID: G799016; PIDN: CAA60388.1; PID: G79901
C;Comment: The A chain is the target of quinolone antibiotics such as nalidixic acid and C;Genetics:
A;Gene: gyrA
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase (F;Superfamily: DNA topoisomerase (ATP-hydrolyzing) medium chain homology (fragme F;1-95/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology (fragme F;51/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable membrane protein YNL028w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N2758
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S62940; S62940
R;Andre, B.; Iraqui Houssalni, I.; Urrestarazu, L.A.; Vissers, S.
R;Andre, B.; Iraqui Houssalni, I.; Urrestarazu, L.A.; Vissers, S.
R;Ancession: S62940
A;Reference number: S62940
A;Reference number: S62940
A;Residues: 1-105 <AND>
A;Residues: 1-105 <AND>
A;Residues: 1-105 <AND>
A;Residues: 1-105 <AND>
A;Residues: 1-105 <AND
A;Residues: S62944
A;Reserence number: S62944
A;Reference number: S62944
A;Reference number: S62950
A;Molecule type: DNA
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F69760
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 95
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Pred. No. 82;
1; Mismatches
   Library, April 1995
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Best Local Similarity 80.0%;
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
submitted to the EMBL Data A; Reference number: S54254
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YHPHG 10
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S49447

DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain A - Acinetobacter baumannii (fra
N;Alternate names: DNA gyrase chain A
C;Species: Acinetobacter baumannii
C;Date: 20-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S49447
R;Vila, J.; Ruiz, J.; Goni, P.; Marcos, M.; Jimenez de Anta, M.T.
R;Vila, J.; Ruiz, J.; Goni, P.; Marcos, M.; Jimenez de Anta, M.T.
R;Vila, J.; Ruiz, J.; Goni, P.; Marcos, M.; Jimenez de Anta, M.T.
A;Accession: S49447
A;Accession: S49447
A;Accession: S49447
A;Residues: 1-95 <VIL>
A;Molecule type: DNA
A;Residues: 1-95 <VIL>
A;Conestration: CASTOSS CASTO
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S54254
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain A - Salmonella typhimurium (frag
DNA topoisomerase chain A, type II DNA topoisomerase chain A
C;Species: Salmonella typhimurium
C;Species: Salmonella typhimurium
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S54254
R;Ruiz, J.; Castro, D.; Goni, P.; Borrego, J.J.; Vila, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A49832; MUID:92102204; PMID:1662027
A; Accession: A49832
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-94 <SRE>
A; Cross-references: UNIPROT:P54112; GB:S72603; NID:9240996; PIDN:AAB20672.1; PID:9240997
A; Note: sequence extracted from NCBI backbone (NCBIN:72603, NCBIP:72604)
C; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase (C; Keywords: ATP
C; Heywords: ATP
F; 1-94/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology (fragm
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A49832
DNA gyrase A - Staphylococcus epidermidis (fragment)
C; Species: Staphylococcus epidermidis
C; Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change C; Accession: A49832
C; Accession: A49832
R; Sreedharan, S.; Peterson, L.R.; Fisher, L.M.
Antimicrob. Agents Chemother. 35, 2151-2154, 1991
A; Title: Ciprofloxacin resistance in coagulase-positive and -negresults.
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YHPHG 12
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78 YHPHG 82
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HHPH 50
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RESULT 17
S14983
extensin class I (clone w10-1 L) - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Accession: S14983
R;Showalter, A.M.; Zhou, J.; Rumeau, D.; Worst, S.G.; Varner, J.E.
Plant Mol. Biol. 16, 547-565, 1991
A;Title: Tomato extensin and extensin-like cDNAs: structure and expression in response to A;Reference number: S14970; MUID:91329690; PMID:1714316
A;Accession: S14983
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <SHO>
A;Cross-references: EMBL:X55694
A;Cross-references: EMBL:X55694
C;Keywords: cell wall; glycoprotein; hydroxyproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein APE1531 - Aeropyrum pernix (strain K1)
C; Species: Aeropyrum pernix
C; Species: Aeropyrum pernix
C; Species: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C; Dacession: D72634
R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kn DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Residues: DNA
A; Residues: 1-134 < KAW>
A; Extras: Preferences: UNIPROT:Q9YBR8; DDBJ:AP000061; NID:g5104821; PIDN:BAA80530.1; PID:g51
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetical protein APE1531
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B72759
hypothetical protein APE0066 - Aeropyrum pernix (strain K1)
C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C; Accession: B72759
R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. Jille. Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Accession: E72759
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-136 < KAW>
A; Residues: 1-136 < KAW>
A; Residues: 1-136 < KAW>
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100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 4; Conservative
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A;Reference number: A69580; MUID:98044033; PMID:934377
A;Residues: 1-110 <KUN>
A;Residues: 1-110 <KUN>
A;Residues: 1-110 <KUN>
A;Residues: 1-110 <KUN>
A;Coss-references: UNIPROT:P42402; GB:299105; GB:AL009126; NID:g2632457; PIDN:CAB12134.
A;Experimental source: strain 168
C;Genetics:
A;Genetics:
A;Genetics
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100.0%; Pred. No. 95;
ive 0; Mismatches
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Pred. No. 97;
0; Mismatches
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100.0%; Pre
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4; Conservative
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Best Local Similarity
Matches 4; Conser
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Best Local S
Matches 4
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A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 12-Jul-2004 C;Accession: AC1898 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Reference number: AC1898 A;Reference number: AC1898 A;Residues: 1-147 <KUR> A;Residues: 1-147 <KUR> A;Residues: 1-147 <KUR> A;Cross-references: UNIPROT:Q8YYW0; GB:BA000019; PIDN:BAB72690.1; PID:g17130078; GSPDB:G7 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr0733 C;Superfamily: urease accessory protein (nickel metallochaperone) UreE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 23
F89956
conserved hypothetical protein SA1543 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F89956
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 125-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Residues: DNA
A;Residues: 1-148 cKUR>
A;Residues: 1-148 cKUR>
A;Residues: 1-148 cKUR>
A;Cross-references: UNIPROT:Q99TE2; GB:BA000018; PID:g13701517; PIDN:BAB42811.1; GSPDB:GN
A;Genetics:
A;Genetics:
A;Gene: SA1543
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S25846
homeotic protein Hox A4, testicular - mouse (fragment)
N;Alternate names: homeotic protein Hox 1.4
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 06-Feb-1998 #text_change 16-Aug-2004
C;Accession: S25847; S25846
R;Rubin, M.R.; Nguyen-Huu, M.C.
DNA Seq. 1, 329-334, 1991
A;Title: Murine embryonic spinal cord and adult testis Hox-1.4 cDNAs are identical 3'
A;Reference number: S25846; MUID:92190549; PMID:1686835
A;Accession: S25847
A;Molecule type: DNA
A;Residues: 1-28 <RUBI>A;Cross-references: EMBL:X17346; NID:951375; PID:951376
A;Accession: S25846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 83.8%; Score 31; DB 2; Length 147; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.8%; Score 31; DB 2; Length 148; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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140541
hypothetical protein X - Pseudomonas solanacearum
C; Species: Pseudomonas solanacearum
C; Species: Pseudomonas solanacearum
C; Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C; Accession: 140541
R; Huang, J.; Carney, B.F.; Denny, T.P.; Weissinger, A.K.; Schell, M.A.
J. Bacteriol. 177, 1259-1267, 1995
A; Title: A complex network regulates expression of eps and other virulence genes of Pseu A; Reference number: 140539; MUID:95173103; PMID:7868600
A; Reference number: 140541
A; Reference number: 140541
A; Returns: preliminary; translated from GB/EMBL/DDBJ
A; Accession: I40541
A; Residues: 1-146 < RES>
A; Cross-references: UNIPROT:Q45417; EMBL:U18135; NID:g603068; PIDN:AAA66241.1; PID:g6030
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                                                                                               pernix hypothetical protein APE0066
                                                                                                                                              Query Match 83.8%; Score 31; DB 2; L Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 4; Conservative 0; Mismatches 0;
             strain K1
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Best Local Similarity
    A;Experimental source: st
C;Genetics:
A;Gene: APE0066
C;Superfamily: Aeropyrum
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Best Local Similarity
Matches 4; Conser
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C;Species: Nostoc sp. P
                                                                                                                                                                                                                                                                                                                            132 HHPH 135
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45 YHPHG 49
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AC1898
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probable integral membrane protein - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36013
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A;Reference number: Z21574
A;Reference number: Z21574
A;Reference number: Z21574
A;Reference number: Z21574
A;Residues: 1-178 <SEE>
A;Molecule type: A;Residues: 1-178 <SEE>
A;Residues: 1-178 <SEE>
A;Cross-references: UNIPROT:Q8CK12; EMBL:AL096839; PIDN:CAB50766.1; GSPDB:GN00070; SCOEDF
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCC22.23c
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C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: B49773
R;Apple, R.T.; Fristrom, J.W.
Bev. Biol. 146, 569-582, 1991
A;Title: 20-Hydroxyecdysone is required for, and negatively regulates, transcription of I
A;Reference number: A49773; MUID:91323677; PMID:1713868
A;Accession: B49773
A;Residues: Preliminary
A;Accession: B49773
A;Accession: B49773
A;Accession: B49773
A;Accession: B49773
A;Coss-references: UNIPROT:P27780; GB:M71249; NID:g157324; PIDN:AAA28501.1; PID:g157325
C;Genetics:
A;Gene: FlyBase:Edg84A
A;Cross-references: FlyBase:FBgn0000552
           09-Jul-2004
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0
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-C;Accession: T13554
R;Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y. submitted to the EMBL Data Library, July 1998
A;Description: Complete nucleotide sequence of Bacillus subtilis pha;Reference number: Z17688
A;Accession: T13554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-171 <KOB>A;Residues: 1-171 <KOB>A;Cross-references: UNIPROT:Q9ZXC1; EMBL:AB016282; PIDN:BAA36671.1
C;Superfamily: Bacillus phage phi-105 hypothetical protein 14
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 171;
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                                                                                                                                                                                                                                                                                                                                                                                              83.8%; Score 31; DB 2; Le ilarity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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T36013
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histocompatibility antigen; immunoglobulin homology
lobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROT: Q94426; EMBL: Z80904; NID: e1007749; PID: e274125; PIDN: CAB0258
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T31664
DAP-kinase homolog COS1.3 - sea squirt (Ciona intestinalis) (fragment)
C;Species: Ciona intestinalis
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31664
R;Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Lennard, N.; Tweedie, S. submitted to the EMBL Data Library, October 1996
A;Reference number: Z21050
A;Reference number: Z21050
A;Accession: T31664
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-156 <BIR>
A;Cross-references: UNIPROT:Q94426; EMBL:Z80904; NID:e1007749; PID:e274125; PIDI C;Genetics:
A;Introns: 75/2; 131/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC class I antigen - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C;Accession: I58201

R;Lalanne, J.

Nucleic Acids Res. 10, 1039-1049, 1982

A;Title: Comparison of nucleotide sequences of mRNAs belonging to the mouse h-2 as Accession: I58201

A;Reference number: I58201

A;Reference number: I58201

A;Accession: I58201
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  A; Molecule type: mRNA
A; Residues: 27-155 <RUB2>
A; Cross-references: EMBL:X13538; NID:951373; PIDN:CAA31889.1; PID:951374
C; Superfamily: homeobox homology
C; Keywords: DNA binding; homeobox; nucleus; transcription regulation
F; 10-66/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                Query Match 83.8%; Score 31; DB 2; Length 155; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 4; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.8%; Score 31; DB 2; Length 156; 100.0%; Pred. No. 1.3e+02; ative 0; Mismatches 0; Indels
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phi-105
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Best Local Similarity
Matches 4; Conserv
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A;Cross-references: UNIE
C;Superfamily: class I F
F;13-78/Domain: immunocl
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T13554
hypothetical protein 14
C;Species: Bacillus phag
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Best Local Similarity
Matches 4; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                98 HHPH 101
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RESULT 33
JX0244
pyroglutamyl-peptidase I (EC 3.4.19.3) - Bacillus amyloliquefaciens
N;Alternate names: 5-oxoprolyl-peptidase; pyroglutamyl aminopeptidase
C;Becies: Bacillus amyloliquefaciens
C;Bate: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 09-Jul-2004
C;Accession: JX0244
R;Yoshimoto, T.; Shimoda, T.; Kitazono, A.; Kabashima, T.; Ito, K.; Tsuru, D.
J. Biochem. 113, 67-73, 1993
A;Title: Pyroglutamyl peptidase gene from Bacillus amyloliquefaciens: Cloning, sequencing
A;Reference number: JX0244; MUID:93203177; PMID:8095933
A;Reference number: JX0244
A;Molecule type: DNA
A;Residues: 1-215 <YOS>
A;Cross-references: UNIPROT:P46107; DDBJ:D11035; NID:g216315; PIDN:BAA01791.1; PID:g21633
C;Superfamily: pyrrolidone-carboxylate peptidase (N-terminal pyroglutamyl peptidase)
C;Keywords: hydrolase; omega peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myb26 protein - garden pea
C; Species: Pisum sativum (garden pea)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C; Accession: T06455
R; Uimari, A.; Strommer, J.
Plant J. 1273-1284, 1997
A; Title: Myb26: A MYB-like protein of pea flowers with affinity for promoters of phenylpy A; Reference number: Z15690; MUID:98112025; PMID:9450341
A; Reference number: Z15690; MUID:98112025; PMID:9450341
A; Reference number: Z15690; MUID:98112025; PMID:9450341
A; Residues: L-217 < UIM>
A; Residues: L-217 < UIM>
A; Residues: L-217 < UIM>
A; Cross-references: UNIPROT:P93474; EMBL:Y11105; NID:g1841474; PIDN:CAA71992.1; PID:g1841
C; Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology < WYB1>
F; 64-113/Domain: myb DNA-binding repeat homology < WYB1>
                                A;Molecule type: DNA
A;Residues: 1-213 <STO>
A;Cross-references: UNIPROT:Q9A7N9; GB:AE005673; NID:g13423091; PIDN:AAK23659.1;
C;Genetics:
A;Gene: CC1681
C;Superfamily: guanylate kinase; guanylate kinase homology
                                                                                                                                                                                                                                                                                                       Length 213;
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                                                                                                                                                                                                                                                                                                    83.8%; Score 31; DB 2; Ld 100.0%; Pred. No. 1.8e+02; iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Consera
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preliminary
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5 HHPH 8
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                                                                                                                                      RESULT 30
E83864
thioredoxin BH1717 [imported] - Bacillus halodurans (strain C-125)
C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Daccession: Ba3864
C; Accession: E83864
R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A; Recession: E83864
A; Recession: E83864
A; Recession: E83864
A; Recession: E83864
A; Recession: E93864
A; Recession: E93864
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-193 <STO>
A; Residues: 1-193 <STO>
A; Residues: 1-193 <STO>
A; Experimental source: strain C-125
C; Genetics:
A; Genetics:
A; Genetics:
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G87457
guanylate kinase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87457
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
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S50686
hypothetical protein YER183c - yeast (Saccharomyces cerevisiae)
C; Species: Saccharomyces cerevisiae
C; Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-J
C; Accession: $50686
R; Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A; Description: The sequence of S. cerevisiae cosmids 9163 and 9132.
A; Reference number: $50431
A; Reference number: $50431
A; Residues: 1-211 < DIE>
A; Cross-references: UNIPROT: P40099; EMBL: U18922; NID:g603405; PID:g6
C; Genetics:
A; Genetics:
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100.0%; Pred. No. 1.8e+02;
vative 0; Mismatches 0;
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Pred. No. 1.7e+02;
0; Mismatches 0;
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100.0%; Pr
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Best Local Similarity
Matches 4; Conser
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Best Local Similarity
Matches 4; Conser
                                   179 HHPH 182
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A.Cross-references: UNIPROT:Q9KVL5; GB:AE004103; GB:AE003852; NID:g9654523; PIDN:AAF93304
A.Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0127
A;Map position: 1
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H82360
conserved hypothetical protein VC0127 [imported] - Vibrio cholerae (strain N16961 serogrc C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C; Accession: H82360
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Aleidelberg, J.F.; Eisen, J.A.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
Nature 406, 477-483, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pycuvate decarboxylase (EC 4.1.1.1) - fava bean (fragment)

C;Species: Vicia faba (fava bean)
C;Species: Vicia faba (fava bean)
C;Species: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 12-Jul-2004
C;Accession: $65426
R;Muecke, U.; Wohlfarth, T.; Fiedler, U.; Baeumlein, H.; Ruecknagel, K.P.; Koenig, S. Eur. J. Biochem. 237, 373-382, 1996
A;Title: Pyruvate decarboxylase from Pisum sativum. Properties, nucleotide and amino & A;Reference number: $65423; MUID:96215432; PMID:8647075
A;Accession: $65426
A;Accession: $65426
A;Accession: $65426
A;Kerus: preliminary
A;Molecule type: mRNA
A;Residues: 1-228 <MUE>
A;Residues: 1-228 <MUE>
A;Cross-references: UNIPROT:Q7M228
C;Superfamily: thiamin pyrophosphate-binding domain homology
C;Keywords: carbon-carbon lyase; carboxy-lyase
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AB0259
probable phage minor tail protein YPO2123 [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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A, Map position: 3
C, Superfamily: Caenorhabditis elegans hypothetical protein K07Bl.4
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100.0%; Pred. No. 2e+02;
ative 0; Mismatches 0;
                                                                                                                                      Query Match 83.8%; Score 31; DB 2; Best Local Similarity 80.0%; Pred. No. 2e+02; Matches 4; Conservative 1; Mismatches
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Best Local Similarity 100.
Matches 4; Conservative
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118 YHPHG 122
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T40889
hypothetical protein SPCC1235.15 - fission yeast (Schizosaccharomyces pombe) (fragment)
C; Species: Schizosaccharomyces pombe
C; Species: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 03-Nov-2000
C; Accession: T40889
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
Submitted to the EMBL Data Library, September 1998
A; Reference number: 221954
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA gyrase chain A - Spiroplasma citri (fragment)
C;Species: Spiroplasma citri
C;Species: Spiroplasma citri
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S35735
R;Ye, Fr. Jaigret, F. Bove, J.
Submitted to the EMBL Data Library, December 1992
A;Description: Nucleotide sequence and genetic organization at the replication origin (c
A;Reference number: S35732
A;Accession: S35735
A;Accession: S35735
A;Accession: S35735
A;Residues: DNA
A;Residues: 1-227 <YEF>
A;Cross-references: UNIPROT: P34030; EMBL: Z19108; NID: g49345; PIDN: CAA79524.1; PID: g49345
C;Genetic code: SGC3
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain A; phage T4 DNA topoisomerase (C;Keywords: ATP; DNA binding
F;7-227/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology (frag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nding
4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology (frag
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                                                                                glutamate decarboxylase - rat
c;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I59173
R;Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.
R;Bond, R.W.; Wyborski, R.J.; Gottlieb, D.I.
Proc. Natl. Acad. Sci. U.S.A. 87, 8771-8775, 1990
A;Title: Developmentally regulated expression of an exon containing a stop codon in the
A;Reference number: I59173; MUID: 91062362; PMID: 2247446
A;Reference number: I59173
A;Accession: I59173
A;Accession: I59173
A;Molecule type: mRNA
A;Residues: 1-223 <RES>
A;Cross-references: UNIPROT: Q63211; GB:M38350; NID: g204231; PIDN: AAA41185.1; PID: g204232
C;Superfamily: human glutamate decarboxylase
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84 YHPHG 88
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0259
C;Accession: AB0259
R;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; WUD:21470413; PMID:11586360
A;Ratus: AB0259
A;Ratus: AB0259
A;Ratus: DNA
A;Residues: 1-236 <KUR>
A;Residues: 1-236 <KUR>
A;Residues: 1-236 <KUR>
C;Genetics: The Company
A;Gene: YP02123
C;Superfamily: phage lambda tail assembly protein K
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15, 2005, 14:22:47

Search completed: June 1 Job time : 21.5 secs

|||:| 205 HHPYG 209

g

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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OM protein - protein search, using sw model

June 15, Run on:

2005, 13:53:11; Search time 83.5 Seconds (without alignments) 30.663 Million cell updates/sec

Title: US-10-074-225A-8 Perfect score: 37 Sequence: 1 HHPHG 5

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

seqs, 512079187 residues 1612378

Searched:

1612378 Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

	Description	3 yersinia pe	porana co		drosophi			~		og brachydanio		_			synechoc	-	thermus	thermus	i4 thermus the	19 brachydanio	c5 brachydanio			18 brachydanio	30 brachydanio	33 brachydanio					drosop	2 rattus norv
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SUMMARIES	ΙD	Q8CLE3	Q6E2P7	Q6E2S2	Q9W4B3	Q8TDG7	Q87QR5	CXB5_HUMAN	Q9VAN2	Q9W7B8	Q65F52	Q7QID0	Q68DR3	Q67PX1	Q8DJ31	Q9X6C8	Q8GEA7	Q9X6D3	Q74614	073679		HRG_BOVIN	GSC_DROME	Q9PWC8	038860	Q98SS3	Q98SS2	Q98SS1		SPEA_BACHD	OMIA60	Q9ESB2
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Q99ps7 rattus norv Q80xk4 mus musculu P04196 homo sapien Q99ps5 mus musculu Q99ps6 mus musculu Q99ps8 rattus norv Q9esb3 mus musculu Q28640 oryctolagus Q6yk32 mus musculu Q6yk32 mus musculu Q9nqa4 homo sapien Q7tns7 mus musculu Q9jhs6 rattus norv	iconments  ied)  sequence update)  annotation update)  annotation update)  coteobacteria; Enterobacteriales;  ioo2;  III, Boutin A., Mayhew G.F., Liss P.,  nou S., Schwartz D.C.,  the M.L., Matson J.S., Blattner F.R.,  is KIM.";  i	:; 189 AA. :ed) sequence update) annotation update) annotation ydate) phyta; Embryophyta; Tracheophyta; licotyledons; core eudicots; asterids; licotyledons; Porana.
Q99PS7 Q80XK4 HRG HUMAN Q99PS5 Q99PS6 Q99PS8 Q9ESB3 HRG RABIT Q6YXA2 Q9VXA2 Q9UQA4 Q9JHS6	ALIGNMEN PRT; 7 reated) ast sequer ast annota ast annota lis; 2430; 11.2002; G. III, E Zhou S., Brubakex Nilles M. Nilles M. D2C5B430EE C2C5B430EE Score 37; Pred. No. Mismatc	7 2  06E2P7  06E2P7;  25-OCT-2004 (TrEMBLrel. 28, Created) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation updat Ribosomal protein L2 (Fragment).  Name=rpl2; Porana commixta. Chloroplast. Chloroplast. Chloroplast. Spermatophyta; Magnoliophyta; eudicotyledons; cox lamiids; Solanales; Convolvulaceae; Dichondreae; [1]
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Ribosomal protein L2 (Fragment).
Name=rpl2;
Ipomoea pes-tigridis.
Chloroplast.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Convolvulaceae; Ipomoeae.
NCBI TaxID=89657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
SEQUENCE FROM N.A.
Stefanovic S., Olmstead R.G.;
"Testing the Phylogenetic Position of a Parasitic Plant (Cuscuta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ogenetic Position of a Parasitic Plant (Cuscuta, steridae): Bayesian Inference and the Parametric Drawn from Three Genomes.";
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                                                                                    Doctatrap on Data Drawn from Three Genomes.";

Syst. Biol. 53:384-399(2004).

Syst. Biol. 53:384-399(2004).

Rembl, AV596770; AAT69100.1; -..

GO; GO:0009507; C:chloroplast; IEA.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003735; F:structural constituent of ribosome; IEA.

GO; GO:0003735; F:structural constituent of ribosome; IEA.

GO; GO:0006412; P:protein biosynthesis; IEA.

R InterPro; IPR008994; Nucleic acid OB.

R InterPro; IPR008994; Nucleic acid OB.

R InterPro; IPR008991; Tanasl L2.

R InterPro; IPR008991; Tanasl L2.

R Fam; PF00181; Ribosomal L2.:

R Fam; PF00181; Ribosomal L2.:

R TIGRFAMS; TIGR01171; rplB bact; 1.

R TIGRFAMS; TIGR01171; rplB bact; 1.

R NON TER

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I SEQUENCE 189 AA; 20451 MW; 2C81496B6779C7B5 CRC64;
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Stefanovic S., Olmstead R.G.;

Stefanovic S., Olmstead R.G.;

"Testing the Phylogenetic Position of a Parasitic Plant (Cuscre Convolvulaceae, Asteridae): Bayesian Inference and the Parame Tomoretrap on Data Drawn from Three Genomes.";

Bootstrap on Data Drawn from Three Genomes.";

R Bootstrap on Data Drawn from Three Genomes.";

Syst. Biol. 53:384-399(2004).

R EMBL; AYS96745; AAT69075.1; -.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005622; F:RNA binding; IEA.

GO; GO:0006412; F:RNA binding; IEA.

GO; GO:0006412; F:Structural constituent of ribosome; IEA.

R GO; GO:0006412; F:Structural constituent of ribosome; IEA.

R GO; GO:0006412; F:Structural constituent of ribosome; IEA.

R InterPro; IPR005880; Ribosomal L2; 1.

R TIGRFAMS; TIGR01171; rplB bact; 1.

R TIGRFAMS; TIGR01171; rplB bact; 1.

R TIGRFAMS; TIGR01171; rplB bact; 1.
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                                                                             teridae): Bayesian Inferenc
Drawn from Three Genomes.";
-399(2004).
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Pred. No. 76;
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REDGINGE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.

RA Abril J.F., Agbayani A., An H.J., Andrews-Prannkoch C., Baldwin D.,

Ballew R.M., Banna P.V., Bernan B.P., Bhandari D., Bladbakov S.,

Raberson K.Y., Benos P.V., Bernan B.P., Brokstein P., Bortleak B.M.,

Borkova D., Botchan M.R., Butler H., Cadleu E., Center A., Chandra I.,

RA Boris K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Buris K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Gengen K., Doup L.B., Downes M. Dugan-Rocha S., Plunkov S.,

RA Goon K., Doup L.B., Downes M. Dugan-Rocha S., Plunkov B.C., Dunn P.,

RA Harris M.L., Harvay D., Hahman T.J., Herrandez J.R., Houck J.,

RA Goon K., Doup L.B., Mannan T.J., Herrandez J.R., Houck J.,

RA Harris M.L., Harvay D., Hahman T.J., Herrandez J.R., Houck J.,

RA Harris M.L., Harvay D., Hahman T.J., Mei M.H., Ibegwam C.,

RA Harris M.L., Harvay D., Hahman T.J., Mei M.H., Degwam C.,

RA Jalli M., Kalush F., Karpen G.H., Kazi, Kulp D., Laiz Z.,

Liu X., Mattei B., McIntoen T.C., Morleod M.P., McPherson D.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

Reinert K., Remington K.A., Howley R., Strong J., Strong L.S., Shen H.,

Spier E., Spradling A.C., Stadn-Kames I., Strong M., Strong R., Sne H.,

RA Williams S.M., WoodagaT, Woolfey K., Zhong S., Yao Q., And S., Shen H.,

RA Williams S.M., WoodagaT, Wolley K., Zhang G., Zhao Q., Zhao Q., Zheng L.,

RA Harris M.L., Hower B.W., Rubin G.M., Venter J.C.,

Ra Harris M.L., WoodagaT, Wolley M., Wolley S., Shon H.,

Rance S., Siden-Klames I., Simpson M., Strong S., Yao B.,

Rance S., Shan M., WoodagaT, Wolley W., Zh
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Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                   Length 192;
                                                              69D683AEFS5FEE0D CRC64;
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George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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t P., Gribben J.G.;
1) to the EMBL/GenBank/DDBJ databases.
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Catarrhini; Hominidae; Homo
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaste
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seque:
01-MAR-2004 (TrEMBLrel. 26, Last annot.
CLL-associated antigen KW-6 (Fragment)
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Chordata;
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Krackhardt A.M., Witzens M.,
Chessia M., Barrett P., Gribb
Submitted (OCT-2001) to the E
EMBL; AF432219; AAL99925.1; -
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IntAct; Q9W4B3; -.
FlyBase; FBgn0029774; CG1578
SEQUENCE 198 AA; 21401 MW
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Submitted (SEP-2002)
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
NCBI TaxID=9606;
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Submitted (MAR-200
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SEQUENCE FROM N.A.
STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
MADLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
                                              Gaps
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein VP1084.
OrderedLocusNames=VP1084;
Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                 Indela
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Xia J.-H., Liu C.-Y., Zheng D., Pan Q., Xie W.;
"Molecular cloning of human connexin 31 and 31.1.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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Complete proteome.
SEQUENCE 246 AA; 27594 MW; 3F130DD284361E45 CRC64;
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100.08;
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229 HHPHG 233
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                                         TISSUE-Pancreas;

X MEDINE-238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Magner L., Shenmen C.M., Schuler G.D.,

X Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina V., Peters G.J., Abramson R.D., Mullah S.J.

B Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

R Bas S., Mocley K.C., McKernan K.J., Malek J.A., Gunarane P.H.,

R Richards S., Worley K.C., McKernan K.J., Malek J.A., Gunbs R.A.,

R Richards S., Worley K.C., Stetteman M., Madan A., Young A.C., Sharchenko Y., Bouffard G.G.,

R Richards S., Worley W. Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley W. Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley W. Schein J.S., Schmutz J., Myers R.M.,

R Rahseley R.W., Arzywinski M.I., Skalska U., Smallus D.E.,

R Butterfield Y.S. N. Krzywinski M.I., Skalska U., Smallus D.E.,

R Butterfield S. S. N. Krzywinski M.I., Skalska U., Smallus D.E.,

R Beneration and initial analysis of more than 15,000 full-length human mouse CDNA sequences "," Namera M.A.

R Rodersation and initial analysis of more than 15,000 full-length human mouse CDNA sequences "," Namera M.A.

R Rodersation and initial analysis of more than 15,000 full-length human mouse CDNA sequences "," Namera M.A.

R Rodersation and initial analysis of more call to a neighboring collustrials of low MW diffuse from one call to a neighboring collustrials and part of the connexons, through which materials of Low My diffuse from one call tower connexons, through which subfamily.

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Institute of Bioinformatics and the EMBL outstation -
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it institutions as long as its content is in no way
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a license agreement (See http://www.isb-sib.ch/announce/
o license@isb-sib.ch).
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EMBL; AF052693; AAD18005.1; -.
EMBL; AL121988; CAB90271.1; -.
EMBL; BC004379; AAH04379.1; -.
Genew; HGNC:4287; GJBS.
MIM; 604493; -.
GO:0008544; P:epidermal differentiation; TAS.
InterPro; IPR000500; Connexin.
InterPro; IPR0002270; Connexin311.
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CONNEXINS 2; 1.
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PRINTS; PR00206; CONNEXIN.
SMART; SM00037; CNX; 1.
PROSITE; PS00407; CONNEXINS_1;
PROSITE; PS00408; CONNEXINS_2;
Gap junction; Transmembrane.
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RAMBAR M.D. CELNIREA S.E., Holf R.A., Evans C.A., Gocapue J.D.

RA Amanatides P.G., Scherer S.E., Ii P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RAM Abril J.F., Agbayari A., An H.J. Andrews-Péanhocch C., Baldwin D.,

RA Abril J.F., Agbayari A., An H.J. Bhandari D., Bolahakov S.,

Ballew R.M., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,

RAM Abril J.F., Agbayari A., An H.J. Bucketein P., Brottler P.,

Burkova D., Botchen M.R., Bouck J., Broketein P., Brottler P.,

Burkis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RAM Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,

Burkis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RAM Cherry J.M., Cawley S., Dahlke C., Davenpoort L.B., Davies P.,

Burkis K.C., Gabrielian A.E., Gars C., Perraz C., Perraz C., Perraz C., Perraz C., Davies P.,

RAM Goldek A., Gong F., Gorrell J.H., Gu Z., Gulbart W.M., Glasser K.,

RAM Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAM Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RAM Harris N.L., Marvey D., McIntosh T.C., McIeod M.P., McBherson D.L.,

RAM Harris N.W., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RAM Harris N.W., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RAM Harris N.W., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RAM Harris N., Kalush F., Karpen G.H., K. Z., Liang Y., Lia Y., Masarman D.A., Wohlare E., Wang A.H., Wang Z.Y., Wassarman D.A., Weinstood M., Stupek M., Stupek M., Shue H.,

Spier E., Spradinian A.C., Perrac C., Pollard J., Worley K., Smith H.O.,

RAM Harris M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

Ram J. H., Harry R., Rubin G.M., Weinsenbech J.,

Ram J. H., Ram R., Zaveri J.S., Zhan M., Zhou X., Zh
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MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                 (TrEMBLrel. 22, Last sequence update) (TrEMBLrel. 23, Last annotation update)
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                                                                                            Created)
                                               PRT;
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                                                                                           (TrEMBLrel. 13,
                                               PRELIMINARY;
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                                                                                                                                                                                    ORFNames=CG14509;
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SEQUENCE 294 A
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                                           elements of the Drosophila melanogaster euchromatin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-NOV-1999 (TrEMBLrel. 12, Created)

01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

01-NOV-1999 (TrEMBLrel. 26, Last annotation update)

01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

Transcription factor Tcf3b (Fragment).

Name=tcf7l1b; Synonyms=tcf3b;

Brachydanio rerio (Zebrafish) (Danio rerio).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danio.
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                                                                                                SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110-10; tcf7llb.
DNA binding; IEA.
regulation of transcription, DNA-dependent; IEA.
    Svirskas
                                                                                                                                                                                                                                  Drosophila melanogaster euchromatic genome: a
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MEDLINE=99376682; PubMed=10446273; DOI=10.1016/S0925-4773(9A)

DOSEKY R.I., Snyder A., Cretekos C.J., Grunwald D.J., Geisla Haffter P., Moon R.T., Raible D.W.;

"Maternal and embryonic expression of zebrafish lefl.";

Mech. Dev. 86:147-150(1999).

EMBL; AF136456; AAD41491.1; -.

R SSP; P27782; 2LEF.

ZPIN; ZDB-GENE-991110-10; tcf711b.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-depender InterPro; IPR009071; HMG-box.

R InterPro; IPR00910; HMG_box.

R Pfam; PF00505; HMG_box; 1.
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 gman C.M., Kronmiller B., Carlson J., Wheeler D.A., Lewis S.E., Rubin G.M.
                                                                                                                                                                                                                                                                                                                                                                              4) to the EMBL/GenBank/DDBJ databases
F56872.2; -.
47; CG14509.
31482 MW; A94AA7075D40446C CRC64;

 to the EMBL/GenBank/DDBJ databases

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Pred. No. 1.2e+02;
; Mismatches 0;
Kaminker J.S., Bergman C.M., Kronmiller B., Car
Patel S., Frise E., Wheeler D.A., Lewis S.E., F
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila me
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
                                                                                                                                                                                                                Lewis S.E.;
"Annotation of the Drosophila melanogaster euc
systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
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3; PSS0118; HM
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                                                                                                                                                                                                                                                                                                         FlyBase;
Submitted (SEP-200)
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003768; AA FlyBase; FBgn00396 SEQUENCE 284 AA;
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                                                    Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=DSM 13;
PubMed=15383718;
Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
Ehrenreich A., Gottschalk G.;
"The Complete Genome Sequence of Bacillus licheniformis DSM13,
Organism with Great Industrial Potential.";
J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 14580;
Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky Tang M.W., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D., Berka R.M.;
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  Length 287;
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                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=yuxN; ORFNames=BL00748, BLi03485;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 AA; 34659 MW; 8C74565AlABA478C CRC64;
                                                                                                                                                                                                                                                                                                                                     25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
YuxN (Homeodomain-like).
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Score 37; DB 2; I
Pred. No. 1.2e+02;
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Name=agCG52960; ORFNames=ENSANGG0000017877;
                                                                                                                                                                                                                                                                                      294 AA
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100.0%;
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5; Conservative
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les 5; Conserv
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Symbiobacterium thermophilum
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nes 5; Conser
                                                                                                                     SEQUENCE FROM N.A.
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                                  Bacteria, Actinol
NCBI_TaxID=2734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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Q8DJ31
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Q9X6C8
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                                                                                                          Preliminary data.

REBL; AAAB01008807; EAA04166.1; -.

RISSP; Q99958; 1D5V.

RGO; GO:0005634; C:nucleus; IEA.

RGO; GO:0003700; F:transcription factor activity; IEA.

RGO; GO:000375; F:transcription of transcription, DNA-dependent; IEA.

RICETPRO; IPR00176; TF Fork head.

RICETPRO; IPR009058; Wing hlx DNA bnd.

RICETPRO; IPR009058; Wing hlx DNA bnd.

RRINTS; PR00150; Fork head; 1.

RROSITE; PS00657; FORK HEAD.

RROSITE; PS00657; FORK HEAD.

RROSITE; PS00659; FORK HEAD.

RROSITE; PS00659; FORK HEAD.

RROSITE; PS00659; FORK HEAD.

RROSITE; PS0099; FORK HEAD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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iemann S.;
4) to the EMBL/GenBank/DDBJ databases.
H18157.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 37; DB 2; Length 295; 100.0%; Pred. No. 1.2e+02; vative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp779H1622 (Fragment)
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Last annotation update)
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Koehrer K., Beyer A., Mewes H
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2004) to the E
EMBL; CR749302; CAH18157.1; -
Hypothetical protein.
NON TER
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SEQUENCE 312 AA; 35124 MW;
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25-OCT-2004 (TrEMBLrel. 28, C
25-OCT-2004 (TrEMBLrel. 28, L
25-OCT-2004 (TrEMBLrel. 28, L
Hypothetical protein.
ORFNames=STH1287;
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Name=DKFZp779H1622;
Homo sapiens (Human)
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Mammalia; Eutheria
NCBI_TaxID=9606;
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TISSUE=Liver;
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Best Local S
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Q68DR3
ID Q68DR
AC Q68DR
DT 25-OC
DT 2
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Q67PX1
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                                                                                                         STRAIN=IAM14863;
Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
Worimura K., Ikeda H., Hattori M., Beppu T.;
"Complete genome sequence of an uncultured bacterium Symbiobacterium
thermophilum.";
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AP006840; BAD40272.1; -.
Hypothetical protein.
SEQUENCE 331 AA; 36263 MW; 2EF2D7BD61A84880 CRC64;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

XTRAIN=BP-1;

Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Matanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,

Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,

Kiyokawa C., Kohara M., Takeuchi C., Yamada M., Tabata S.;

Kiyokawa C., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;

Complete genome structure of the thermophilic cyanobacterium

Thermosynechococcus elongatus BP-1.";

DNA Res. 9:123-130(2002).

In EMBL; AP005373; BAC08950.1; -.

R InterPro; IPR007087; Znf_C2H2.

R InterPro; IPR007087; Znf_C2H2.

Pfam; PF01903; Cbix; 2.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_1.

Complete proteome.

Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 331;
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100.0%; Pred. No. 1.4e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBL_TaxID=32046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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O9X6C8,
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Galactose-1-phosphate uridylyltransferase homolog.
Name=galT;
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 37; DB 2; Lilarity 100.0%; Pred. No. 1.4e+02; Conservative 0; Mismatches 0;
Actinobacteria; Symbiobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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OrderedLocusNames=tll1398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8DJ31;
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 5; Conservative
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us-10-074-225a-8.rup

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-I- PATHWAY: Galactose metabolism; second step.
-I- SIMILARITY: Belongs to the galactose-1-phosphate
uridylyltransferase family 1.

BMBL; AY130259; AAN05445.1; -.

RBSP; P09148; 1GUQ.

GO; GO:0008108; F:UDP-Glucose-hexose-1-phosphate uridylyltran. . .; IEA.

GO; GO:0008108; F:UTP-hexose-1-phosphate uridylyltransferase . . .; IEA.

GO; GO:0006012; P:galactose metabolism; IEA.

InterPro; IPR001937; Galp_Uptransf1.

InterPro; IPR01937; Galp_Utransf1.

InterPro; IPR01987; Galp_Utransf1.

InterPro; IPR01087; Galp_Utransf1.

PINSF; PINSF000808; Galf_1: 1.

PINSF; PINSF000808; Galf_1: 1.

PRODOM; PD005051; Galp_Utransf; 2.

TIGRFAMS; TIGR00209; galf_1: 1.

PROSITE; PS00117; GAL_P_UDP_TRANSF_I; 1.

Carbohydrate metabolism; Galactose metabolism; Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMs; TIGR00209; galt 1; 1.
Carbohydrate metabolism; Galactose metabolism; Nucleotidyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
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GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0008108; F:UDP-glucose-hexose-1-phosphate uridylyltrans.
GO; GO:0008102; F:UTP-hexose-1-phosphate uridylyltransferase.
GO; GO:0006012; P:galactose metabolism; IEA.
InterPro; IPR001937; Galp_Utransfl.
InterPro; IPR0015850; Galp_Utransf.
InterPro; IPR005850; Galp_Utransf.
InterPro; IPR005849; Galp_Utransf.
Pfam; PF01087; Galp_Utransf.
                                                                                                                                                                                                                                                                                                                                                                                                   349 AA; 39736 MW; DF8A239FA7C59607 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Galactose-1-phosphate uridylyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 37; DB 2; I
100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Utransf; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
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SEQUENCE
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                                                                                                   Fridjonsson O., Watzlawick H., Gehweiler A., Rohrhirsch T., Mattes R.; "Cloning of the gene encoding a novel thermostable alpha-galactosidase from Thermus brockianus ITI360."; Appl. Environ. Microbiol. 65:3955-3963(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   льскамв; TIGR00209; galt 1; 1.
PROSITE; PS00117; GAL P UDP TRANSF I; 1.
Carbohydrate metabolism; Galactose metabolism; Nucleotidyltransferase;
Transferase.
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                                                                                                                                                                                                                                                                                                                                Fridjonsson O., Watzlawick H., Mattes R.;
"The structure of the alpha-galactosidase gene loci in Thermus
brocklanus ITI360 and Thermus thermophilus TH125.";

Extremophiles 4:23-33(2000).

-I- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose 1-phosphate
alpha-D-glucose 1-phosphate + UDP-galactose.

-I- PATHWAY: Galactose metabolism; second step.

-I- SIMILARITY: Belongs to the galactose-1-phosphate
uridylyltransferase family 1.

EMBL; AF135398; AAD33669.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=IB-21;
Kang S.K., Cho K.K., Ahn J.K., Choi Y.J.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose 1-phosphate alpha-D-glucose 1-phosphate + UDP-galactose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0016740; F:UDP-glucose-hexose-l-phosphate uridylyltran. . .;
GO; GO:000108; F:UDP-glucose-hexose-l-phosphate uridylyltrans. . .;
GO; GO:0003982; F:UTP-hexose-l-phosphate uridylyltransferase . . .;
GO; GO:0006012; P:galactose metabolism; IEA.

R InterPro; IPR001937; Galp_UDPtransf1.

R InterPro; IPR001937; Galp_Utransf2.

R InterPro; IPR005850; Galp_Utransf2.

R InterPro; IPR005849; Galp_Utransf2.

R Pfam; PF01087; Galp_UDP_transf3.

R Pfam; PF02744; Galp_UDP_transf3.

R Pfam; PF02744; Galp_UDP_transf4.

R PTGRFAMS; TIGR00209; GalT_1; 1.

R PROSITE; PS00117; GAL_P_UDP_TRANSF_1; 1.
Thermus brockianus.
Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
Thermus.
NCBL_TaxID=56956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
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Q1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Galactose-1-phosphate uridylyltransferase-like protein.
Thermus sp. IB-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39855 MW; BF6CA7EEA85DC904 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    349 AA
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                                                                                                                                                                                                                                                                                                                       PubMed=10741834;
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5; Conservative
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|HPHG 187
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MEDLINE=20203878;
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Thermus

RESULT 16
Q8GEA7
1D Q8GEA
AC Q8GEA
DT 01-MA
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Q8GEA7

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Gaps

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Indels

349;

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us-10-074-225a-8.rup

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Pfam; PF03131; bZIP Maf;
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Q98UKS
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P. SEQUENCE FROM N.A.

PubMed=15064768;

A Henne A., Brueggemann H., Raasch C., Wiezer A., Hartsch T.,

A Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,

Jacobi C., Starkuviene V., Schlenczeck S., Dencker S., Huber R.,

Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;

The genome sequence of the extreme thermophile Thermus

T "The genome sequence of the extreme thermophile Thermus

I "The genome sequence of the extreme thermophile Thermus

C -I- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose I-phosphate

C -I- PATHWAY: Galactose metabolism; second step.

C -I- SIMILARITY: Belongs to the galactose-I-phosphate

-I- SIMILARITY: Belongs to the galactose-I-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2:547-553(2004).

VITY: UDP-glucose + alpha-D-galactose 1-phosphate te 1-phosphate + UDP-galactose.

Ctose metabolism; second step.

Clongs to the galactose-1-phosphate emily 1.
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REMBL; AE017222; AAS82401.1;

RGO; GO:0008108; F:UDP-glucose-hexose-1-phosphate uridylyltran.

RGO; GO:0008108; F:UTP-hexose-1-phosphate uridylyltransferase.

RGO; GO:0006012; P:galactose metabolism; IEA.

RILETPRO; IPR001937; Galp_UDPtransfl.

R InterPro; IPR011573; Galp_Utransf.

R InterPro; IPR05880; Galp_Utransf.

R InterPro; IPR058849; Galp_Utransf.

R InterPro; IPR05849; Galp_Utransf.

R Pfam; PF01087; Galp_UDP_transf.

R Pfam; PF01087; Galp_UDP_transf.

R Pfam; PF02744; Galp_UDP_tr_C; 1.

R Pfam; PF02744; Galp_Utransf; 2.
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Carbohydrate metabolism; Complete proteome; Galactose metabolism; Nucleotidyltransferase; Transferase.
SEQUENCE 349 AA; 39576 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10).
OrderedLocusNames=TTP0071;
Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039)
Plasmid pTT27.
                                         Length 349;
                                                                                     Indels
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0B2284608704339A CRC64;
                                     Score 37; DB 2; L
Pred. No. 1.4e+02;
; Mismatches 0;
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100.0%; Pred. No. 1.4e+02;
ative 0; Mismatches 0;
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 39451 MW;
                                       100.0%;
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073679;
01-AUG-1998 (TrEMBLrel. 07,
01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                             Similarity 5; Conserv
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Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                    183 HHPHG 187
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 349 AA;
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                                     Query Match
Best Local S
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SEQUENCE
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Q746I4;
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Q74614
ID Q74614
ID Q74611
DT Q77461
DT Q77461
OS-JU
DT Q77461
OS-JU
DT Q7761
OS-JU
DT Q760
OS GB
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PEQUENCE FROM N.A.

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Giorgianni M.W., M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Candella S.P., Giorgianni M.W., M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Candella S.P., Giorgianni M.W., M.W., Barsh G.S., Kimmel C.B.;

Moens C.B., Cordes S.P., Candella S.P., Giorgianni M.W., M.W.
Ol-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transcription factor Val.
Name=mafb; Synonyms=valentino;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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"Isolation, characterization, and expression analysis of zebrafish
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J. Biochem. 129:139-146(2001).
-!- SIMILARITY: Belongs to the bZIP family.
EMBL; AB006322; BAB21102.1;
-.
HSSP; O54790; IKIV.
ZFIN; ZDB-GENE-980526-515; mafb.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR004827; TF_bZIP.
InterPro; IPR004826; TF_Maf.
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SEQUENCE FROM N.A.
MEDLINE=21064923; PubMed=11134968;
Kajihara M., Kawauchi S., Kobayashi M., Ogino H., Takahashi
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PROSITE; PS50217; BZIP; 1.
DNA-binding; Nuclear protein.
SEQUENCE 356 AA; 40243 MW; 07420DB0F6CD08F1 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Transcription factor MafB.
Name=mafb; Synonyms=mafB;
Brachydanio rerio (Zebrafish) (Danio rerio).
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Best Local Similarity 100.0.
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P33433;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein (Histidine-proline rich glycoprotein)
(HPRG) (Fragments).
Name=HRG;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                    .; Chordata; Craniata; Vertebrata; Euteleostomi;; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                       Length 356;
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SMART; SM00338; BRLZ; 1.
PROSITE; PS50217; BZIP; 1.
DNA-binding; Nuclear protein.
SEQUENCE 356 AA; 40233 MW; DE4C96B62C058865 CRC64;
                                                       100.0%; Score 37; DB 2; I
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5; Conservative
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Mammalia; Eutheria; C
Bovinae; Bos.
NCBI_TaxID=9913;
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Hahn M., Jackle H.;
"Drosophila goosecoid participates in neural development but not
body axis formation.";
EMBO J. 15:3077-3084(1996).
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                 100.0%; Score 37; DB 1; Length 396; 100.0%; Pred. No. 1.6e+02;
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MEDLINE=96202483; PubMed=8625850;
Goriely A., Stella M., Coffinier C., Kessler D., Mailhos
Dessain S., Desplan C.;
S -> Q.
H -> Y.
128A8223499DE6FC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSC_DROME STANDARD; PRT; 419 AA. P54366; Q9VPR9; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 25-JAN-2005 (Rel. 46, Last annotation update)
                                                                                                                                                                                                                                                     0; Mismatches
                                                                                       44470 MW;
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Name=Gsc; ORFNames=CG2851;
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Matches 5; Conservative
                                                                                396 AA;
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264 HHPHG 268
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ntry is copyright. It is produced through a collaboration s Institute of Bioinformatics and the EMBL outstation - nformatics Institute. There are no restrictions on its it institutions as long as its content is in no way statement is not removed. Usage by and for commercial a license agreement (See http://www.isb-sib.ch/announce/to license@isb-sib.ch).

systematic review.";
Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
-!- FUNCTION: Appears to regulate regional development of specific tissues. Can rescue axis polarity in UV-radiated Xenopus embryos.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: In early embryo development, expression confined to two regions; a horseshoe-like pattern across the dorsal side which is destined to form the brain hemispheres and a second domain which invaginates inside the stomodeum and which, is fated to form the foregut, ring gland and stomatogastric nervous system (SNS).

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                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Hisra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster euchromatic genome:
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50071; HOMEOBOX 2; 1.
11 protein; DNA-binding; Homeobox; Nuclear protein.
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EMBL; U52968; AAB17948.1; -.
EMBL; AE003589; AAF51473.1; -.
PIR; S70617; S70617.
HSSP; P06601; 1FJL.
INTACT; P54366; -.
TRANSFAC; T04041; -.
FlyBase; FBGN0010323; GBC.
INTERPO; IPR001356; Homeobox.
INTERPO; IPR009057; Homeodomain_like.
InterPro; IPR007104; Paired_homeo.
PFam; PF00046; Homeobox; 1.
PRODOM; PD000010; Homeobox; 1.
SMART; SM00389; HOX; 1.
PROSITE; PS00027; HOMEOBOX 1; 1.
PROSITE; PS50071; HOMEOBOX 2; 1.
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Poly-Ala.
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MEDLINE=99326148; PubMed=10395930; DOI=10.1016/S0167-4781(99)00066-4; Wang H., Gong Z.; "Characterization of two zebrafish cDNA clones encoding egg envelope
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Egg envelope protein ZP2.
Name=zp2.2; Synonyms=zp2;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                     Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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MEDLINE=21017556; PubMed=11144219;
DOI=10.1002/1098-2795(200101)58:1<4::AID-MRD2>3.0.CO;2-P;
Mold D.E., Kim I.F., Tsai C.-M., Lee D., Chang C.-Y., Huang F
"Cluster of genes encoding the major egg envelope protein of zebrafish.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428 AA; 46804 MW; 46E8825ACA17C6A7 CRC64;
                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                           proteins 2P2 and 2P3.";
Blochim. Blophys. Acta 1446:156-160(1999).
EMBL; AF095456; AAD49112.1; -.
ZFIN; ZDB-GENE-991129-5; Zp2.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR00519; P_trefoil.
Pfam; PF00100; Zona pellucida; 1.
Pfam; PF00100; Zona pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.
SMART; SM00241; ZP; 1.
PROSITE; PS00682; ZP_DOMAIN; 1.
Envelope protein.
SEQUENCE 428 AA; 46804 MW; 46E8825ACA17C
                                                                                                                                           Created)
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Matches 5; Conservative
                                                                                                                                                                                     Egg envelope protein ZP2 Name=zp2;
                                                                                                            PRELIMINARY;
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                            253 HHPHG 257
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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37 HHPHG 41
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NCBI_TaxID=7955;
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Q98SS0
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SEQUENCE FROM N.A.
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098SS1
1D 098SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   998SS3 PRELIMINARY; PRT; 430 AA.
998SS3;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Egg envelope protein ZP2 variant A.
Name=zp2.2; Synonyms=zp2;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11144219;
795(200101)58:1<4::AID-MRD2>3.0.CO;2-P;
', Tsai C.-M., Lee D., Chang C.-Y., Huang R.C.;
encoding the major egg envelope protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.0%; Score 37; DB 2; Length 430; Similarity 100.0%; Pred. No. 1.8e+02; 5; Conservative 0; Mismatches 0; Indels
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21017556; PubMed=11144219;
MEDLINE=21017556; PubMed=11144219;
DOI=10.1002/1098-2795(200101)58:1<4::AID
Mold D.E., Kim I.F., Tsai C.-M., Lee D.,
"Cluster of genes encoding the major egg
zebrafish.";
Mol. Reprod. Dev. 58:4-14(2001).
EMBL; AF331965; AAK16578.1; -.
ZFIN; ZDB-GENE-010622-1; Zp2.2.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR000519; P_trefoil.
Pfam; PF00100; Zona_pellucida; 1.
Pfam; PF00100; Zona_pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.
SMART; SM00241; ZP; 1.
ZFIN; ZDB-GENE-010622-1; zp2.2.
GO; GO:0019031; C:viral envelope; IEA.
InterPro; IPR001507; Endoglin/CD105.
InterPro; IPR000519; P_trefoil.
Pfam; PF00100; Zona_pellucida; 1.
Pfam; PF00100; Zona_pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.
SMART; SM0018; PD; 1.
SMART; SM00241; ZP; 1.
PROSITE; PS00682; ZP_DOMAIN; 1.
Envelope protein.
SEQUENCE 430 AA; 47124 MW; EC54C4EC0
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5, Conserv
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SEQUENCE 430 AA
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Q98SS2;
01-JUN-2001
01-JUN-2001
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Best Local S
Matches 5
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Q98SS2
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Q98SS3
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DE GREGORICO GUNCARELLO 26, LAND BE GREGORICO CONTRIBUTION CONTRIBU
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COFACTOR: Pyridoxal phosphate (By similarity)
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Best Local Similarity
Matches 5; Consera
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                1 ННРНС
                                                     family.
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Q9VIW0
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                                          Gape
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Nucleic Acids Res. 28:4317-4331(2000).

-!- FUNCTION: Catalyzes the formation of agmatine from arginine (By similarity).

-!- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2).
                                                                                                                                                                                                                                                                               STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
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,, Kuhara S.,
                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11058132; DOI=10.1093/nar/28.21.4317
e K., Takaki Y., Maeno G., Sasaki R., Masui
                                                                                                                                                                                                                                                                                                                                                                                                            Length 469;
                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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29-MAR-2004 (Rel. 43, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Arginine decarboxylase (EC 4.1.1.19).
Name=speA, OrderedLocusNames=BH2640;
Bacillus halodurans.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                      Length
 B985118D36ED5B8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        BECEIDSC4D18CC06 CRC64;
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Nakamura Y., Ogasawara N., Kuhara
                                                                                                                                                                   Last sequence update)
Last annotation update)
            Score 37; DB 2; L
Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 37; DB 2; L 100.0%; Pred. No. 1.9e+02; vative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            491 AA
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Submitted (JUL-2002) to the EMB
EMBL; AY128418; AAM75011.1; -.
FlyBase; FBgn0039647; CG14509.
SEQUENCE 469 AA; 51845 MW;
47343 MW;
                    100.0%;
                                                                                                                                               01-OCT-2002 (TrEMBLrel. 2:
01-OCT-2002 (TrEMBLrel. 2:
01-MAR-2003 (TrEMBLrel. 23
GH11945p.
                                                                                                                                    PRELIMINARY;
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                              Similarity 5; Conserv
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Fuji F., Hirama C.,
Horikoshi K.;
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Best Local Similarity
Matches 5; Conser
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432 AA;
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HHPHG 44
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MEDLINE=20512582;
                                                                                                                                                                                                 ORFNames=CG14509;
                                                            1 HHPHG 5
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Q8MQS2;
01-OCT-2002
01-OCT-2002
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Q9K9KS;
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                   Query Match
Best Local S
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SEQUENCE
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SPEA_BACHD
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EMBL; AP001510;

R PIR; H83979; H83979.

R InterPro; IPR000310; Decarbxylsel.

R InterPro; IPR008286; Decarbxylse_C.

DR InterPro; IPR011185; Lys_decarb.

DR Pfam; PF01711; OKR_DC_1; 1.

DR Pfam; PF03711; OKR_DC_1 C; 1.

DR PIRSF; PIRSF005938; Lys_decarb; 1.

DR PROSITE; PS00703; OKR_DC_1; 1.

KW Complete proteome; Decarboxylase; Lyase; Polyamine biosynthesis;

KW Complete proteome; Decarboxylase; Lyase; Polyamine biosynthesis;

KW Complete proteome; Decarboxylase; Lyase; Polyamine biosynthesis;

KW Putrescine biosynthesis; Pyridoxal phosphate; Spermidine biosynthesis;

TA449 MW; 3C2ACC55C3C57F5D CRC64;
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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PATHWAY: Putrescine biosynthesis from arginine, first step. PATHWAY: Spermidine biosynthesis from arginine, first step. SUBCELLULAR LOCATION: Cytoplasmic (Probable).
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 37; DB 1; Length 491; 100.0%; Pred. No. 2e+02; iive 0; Mismatches 0; Indels
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25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
CG10034-PA (Traffic jam).
ORFNames=CG10034;
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Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

Mount S.M., Moy M., Murphy L., Murphy L., Muzny D.M., Nelson D.L.,

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Pacleb J.M.,

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Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

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MEDLINE=22426065; PubMed=12537568;

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Ratel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.,
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MEDLINE=22954636; PubMed=14578908; DOI=10.1038/ncb1058;
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Nat. Cell Biol. 5:994-1000(2003).
EMBL; AE003663; AAF53804.2; -.
EMBL; AY325814; AAP88969.1; -.
HSSP; O54790; 1K1V.
IntAct; Q9VIW0; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster euchromatic genome: a
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                 Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"Murine histidine-rich glycoprotein: cloning, characterization and cellular origin.";
Immunol. Cell Biol. 78:280-287(2000).
EMBL; AF194029; AAG28417.1; -.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 2.
SEQUENCE 510 AA; 57581 MW; SOBEGEOGAA2ED5BE CRC64;
                                                                                                                                                                                                                                  ö
FlyBase; FBgn0000964; tj.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR008917; Euk transcr_DNA.
InterPro; IPR004826; TF_Maf.
InterPro; IPR004826; TF_Maf.
Ffam; PF03131; bZIP_Maf; 1.
SMART; SM00338; BRLZ; 1.
SEQUENCE 509 AA; 54043 MW; 0BD429AFB0BCCF38 CRC64;
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0
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                                                                                                                                                                                                                                0; Indels
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                           Score 37; DB 2; I
Pred. No. 2.1e+02;
; Mismatches 0;
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100.0%; Pred. No. 2.1e+02;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         510 AA
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SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Liver;
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MEDLINE=20307726; PubMed=10849117;
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                                                                                                                                                                                           100.0%;
                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
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nes 5; Conservative
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                                                                                                                                                                                                                                                                                           267 HHPHG 271
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                                                                                                                                                                                                                                                                  1 HHPHG 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Hrg;
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Q9ESB2
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Matches
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Q99PS7
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RESULT 34
HRG_HUMAN
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altschul S.F., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Mars J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Marsmann R.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Pakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
RA Generation and initial analysis of more than 15,000 full-length human
RY and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                            Gaps
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TISSUE=Eye;
Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: Belongs to the amiloride-sensitive sodium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                              ö
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S. Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AB055896; BAB33093.1; -. GO; GO:0004869; F:cysteine protease inhibitor activity; IEA. InterPro; IPR000010; Prot inh_cystat. Figm: PF00031; Cystatin; I. SMART; SM00043; CY; 2. SMART; SM00043; CY; 2.
                                                                                                                                                                                                                                  Length 515;
                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Accn4 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BCO46481; AAH46481.1; -.
MGD; MGI:2652846; Accn4.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005216; F:ion channel activity; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0006811; P:ion transport; IEA.
GO; GO:0006813; N:ion transport; IEA.
GO; GO:0006814; P:sodium ion transport; IEA.
InterPro; IPR001873; Na+channel_ASC.
Pfam; PF00858; ASC; 1.
                                                                                                                                                                                                                                Score 37; DB 2; I Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                100.0%;
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5; Conservative
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TISSUE=Eye;
MEDLINE=22388257;
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Q80XK4;
01-JUN-2003
01-JUN-2003
01-MAR-2004
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Best Local S
Matches 5
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Q80XK4
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"Plasma protein map: an update by microsequencing.";

Electrophoresis 13:707-714 (1992).

"In the physiological function is not yet known. It binds heme, dyes and divalent metal ions. It can inhibit rosette formation and is known to interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HMW kininogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood coagulation cascade.

--- SUBCELLULAR LOCATION: Secreted.

--- SUBCELLULAR LOCATION: Secreted.

--- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

--- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

--- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

--- SUBCELLULAR COATION: Secreted.

--- SUBCELLULAR LOCATION: Secreted.
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Koide T., Foster D.C., Yoshitake S., Davie E.W.;
"Amino acid sequence of human histidine-rich glycoprotein derived from
the nucleotide sequence of its cDNA.";
Biochemistry 25:2220-2225(1986).
                                                                                                                                                                                                                                                                                                                                                         Gaps
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Hennis B.C., Frants R.R., Bakker E., Vossen R.H., van der Poort E.W.,
Blonden L.A., Cox S., Khan P.M., Spurr N.K., Kluft C.;
"Evidence for the absence of intron H of the histidine-rich
glycoprotein (HRG) gene: genetic mapping and in situ localization of
HRG to chromosome 3q28-q29.";
Genomics 19:195-197(1994).
PRINTS; PR01078; AMINACHANNEL.
Ion transport; Ionic channel; Sodium channel; Sodium transport;
Transmembrane; Transport.
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20-MAR-1987 (Rel. 04, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich glycoprotein) (HPRG).
                                                                                                                                                                                                                                                             Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Plasma;
MEDLINE=93092937; PubMed=1459097;
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Wakabayashi S., Takahashi K., Tokunaga F., Koide T.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                       524 AA; 57469 MW; ADIB1991F9BB2FAF CRC64;
                                                                                                                                                                                                                                                             Score 37; DB 2; I
Pred. No. 2.2e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                100.0%;
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Best Local Similarity 100.
Matches 5; Conservative
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SEQUENCE
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P04196;
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Query Match
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Q99PS6
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STRAIN=FVB/N; TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Potential).
(Potential).
(Potential).
(Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R MIM; 142640; -.

R InterPro; IPR000010; Prot_inh_Cystat.

Pfam; PF00031; Cystatin; 1.

Direct protein sequencing; Glycoprotein; Heparin-binding;

Polymorphism; Repeat; Signal.

I SIGNAL 19 525 Histidine-rich glycoprotein.

T CHAIN 137 254 Cystatin-like 1.

DOMAIN 137 254 Cystatin-like 2.

DOMAIN 276 321 Pro-rich.

DOMAIN 350 497 His/Pro-rich.

DISULFID 24 504 By similarity.

DISULFID 203 417 By similarity.

DISULFID 203 417 By similarity.

DISULFID 203 417 By similarity.

DISULFID 218 241 By similarity.

CARBOHYD 63 63 N-linked (GlCNAC. ..) (Potentia CARBOHYD 87 87 N-linked (GlCNAC. ..) (Potentia 
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Cystatin-like 1.
Cystatin-like 2.
Pro-rich.
His/Pro-rich.
By similarity.
By similarity.
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By similarity.
N-linked (GlcNAc. . .) (Potent N-linked (GlcNAc. . .) (
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Tsuchida N., Wakabayashi S., Jahnen-Dechent W., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 37; DB 1; Length 52
100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0; Indels
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Histidine-rich glycoprotein.
Name=Hrg; Synonyms=MMHRG;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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EMBL; AB005803; BAA21613.1; -.
EMBL; Z17218; CAA78925.1; -.
PIR; A01287; KGHUGH.
SWISS-2DPAGE; P04196; HUMAN.
Genew; HGNC:5181; HRG.
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                                 between the Swigs Inthe European Bioinformuse by non-profit impositied and this state entities requires a lior send an email to li
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5; Conserv
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Liver;
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S., Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055897; BAB33094.1; -.
MGD; MGI:2146636; Hrg.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000010; Prot inh_Cystat.
Ffam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
SEQUENCE 525 AA; 59090 MW; AB3E93A439CFB3AC CRC64;
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STRAIN=FVB/N; TISSUE=Liver;
STRAIN=FVB/N; TISSUE=Liver;
Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055898; BAB33095.1; -.
R MGD; MGI:2146636; Hrg.
R MGD; MGI:2146636; Hrg.
R GO; GO:0005615; C:extracellular space; TAS.
R InterPro; IPR000010; Prot_inh_cystat.
R Pfam; PF00031; Cystatin; I.
R SMART; SM00043; CY; 2.
SEQUENCE 525 AA; 59162 MW; A83E93A439CFB126 CRC64;
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\A; 59090 MW; A83E93A439CFB3AC CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Histidine-rich glycoprotein.
Name=Hrg; Synonyms=MMHRG;
Mus musculus (Mouse).
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100.0%; Pred. No. 2.2e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2.2e+02;
ive 0; Mismatches 0;
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Matches 5, Conservative
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Best Local Similarity
Matches 5; Conserv
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HRG_RABIT
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HRG_RABIT
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; Chordata; Craniata; Vertebrata; Euteleostomi;
; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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rich glycoprotein: cloning, characterization and
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Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=Sprague-Dawley; TISSUE=Liver;
Wakabayashi S., Takahashi K., Hirokado Y., Togo Y., Izumi S.
Ohashi T., Sato N., Hirata D., Tsuchida N., Koide T.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055895; BAB33092.1; -.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot inh cystat.
Pfam; PF00031; Cystatin; I.
SMART; SM00043; CY; 2.
SEQUENCE 525 AA; 59049 MW; 38290A631FAC7777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 37; DB 2; Length 525; 100.0%; Pred. No. 2.2e+02; ative 0; Mismatches 0; Indels
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Pred. No. 2.2e+02;
Mismatches 0; Indels
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                                                                           099PS8;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Histidine-rich glycoprotein 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Histidine-rich glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=129;
MEDLINE=20307726; PubMed=10849117;
Hulett M.D., Parish C.R.;
Hulett M.D., Parish C.R.;
"Murine histidine-rich glycoprotein: cloning, cellular origin.";
Immunol. Cell Biol. 78:280-287(2000).
EMBL; AF194028; AAG28416.1; -.
MGD; MGI:2146636; Hrg.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; 1.
SMART; SM00043; CY; 2.
SEQUENCE 525 AA; 59132 WW; 6E55F2A439CFB1
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                                                       PRELIMINARY;
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Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                        Rattus norvegicus (F
Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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5; Conserv
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361 HHPHG 365
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                                                                                                                                                                                                                   Name=RNHRG1;
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Best Local S
Matches 5
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                                                    Q99PS8
RESULT 37
Q99PS8
ID Q99PS
AC Q99PS
DT 01-JU
DT 01-JU
DE Histi
GN Namma
OC BURAT
OC B
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Q9ESB3
ID Q9ESB
AC Q9ESB
DT O1-MADT
O1-MADT
OT-MADT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein.";
Elochemistry 35:1925-1934(1996).
Elochemistry in cand function is not yet known. It binds for interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HMW kininogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood coagulation cascade.
Elochemistry in plasma.
Elochemistry in addition to having a high His and Pro content, this protein has many internal repeats. 15 tandem repetitions of a 5-residue sequence (G[H/P][H/P]PH, consensus) form a His/Pro-rich
                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U32189; AAC48516.1; -.
InterPro; IPR000010; Prot_inh_cystat..
Pfam; PF00031; Cystatin; I.
Direct protein sequencing; Glycoprotein; Heparin-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich glycoprotein) (HPRG) (Fragment).
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 9-23; 301-313 AND 422-429. TISSUE=Serum;
MEDLINE=96229917; PubMed=8639676; DOI=10.1021/bi952061t;
Borza D.-B., Tatum F.M., Morgan W.T.;
"Domain structure and conformation of histidine-proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycoprotein
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Cleavage (by plasmin).
Cleavage (by plasmin).
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-1- SIMILARITY: Contains 2 cystatin-like domains.
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Histidine-rich g
Cystatin-like 1.
Cystatin-like 2.
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His/Pro-rich.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Potential.
N-linked (GlCN)
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QGYK32

ID QGYK32

ID QGYK32

DT GS-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

GN Name=Hrg;

OS Mus musculus (Mouse)

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TAXID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA HSU S.J., Balmain A.;

RA HSU S.J., Balmain A.;

RA Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.

DR Ffam; PF00031; Cystatin; 1.

DR SMART; SM00043; CY; 2.

SQ SEQUENCE 536 AA; 60439 MW; CCF14FC08DDS3D7C CRC64;
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Hsu S.J., Balmain A.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY137504; AAN27996.1; -.
GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.
InterPro; IPR000010; Prot inh_cystat.
Pf00031; Cystatin; I.
SMART; SM00043; CY; 2.
SEQUENCE 536 AA; 60439 MW; CCF14FC08DD53D7C CRC64;
Query Match 100.0%; Score 37; DB 1; Length 526; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 37; DB 2; Length 536; Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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Search completed: June 15, 2005, 14:21:24 Job time : 85.5 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein

June 15, 2005, 13:52:01; Search time 90 Seconds (without alignments) 21.487 Million cell updates/sec Run on:

US-10-074-225A-9 36 1 HPPHG 5 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

seqs, 386760381 residues 2105692 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003as:\*
7: geneseqp2003bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	line	HP :	je #	je #	in #	pou	bra	liv	bep	dinc	dinc	dinc	dinc	car	car	car	onib	onib	dinc	dinc	onib	onib	dinc	ner	dinc
uo	Histidine	Rabbit	Peptide	Peptide	Protein	Human bon	Human	Human	Human	Propioni	Propioni	Propioni	Propionib	Human car	Human	Human	Propionib	Propionib	Propionib	Propionib	Propioni	Propionib	Propionib	Human ner	Propionib
Description	Abb79810	Adh10417	Abb42309	Aam36117	Abb25810	Aam76009	Aam63195	Abg57735	Abg45414	Aau46033	Abm42552	Aau54374	Abm50893	Aau22059	Ade46027	Adj07445	Aau66176	Abm62695	Aau58530	Abm55049	Aau63724	Abm60243	Aau60014	Abb15846	Abm56533
QI	ABB79810	ADH10417	ABB42309	AAM36117	ABB25810	AAM76009	AAM63195	ABG57735	ABG45414	AAU46033	ABM42552	PAU54374	ABM50893	PAU22059	ADE46027	ADJ07445	AAU66176	ABM62695	AAU58530	ABM55049	PAU63724	ABM60243	AAU60014	ABB15846	ABM56533
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% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	36	36	36	36	36	36	36	36	36		36	36		36	36	36	36	36	36	36	36	36	36	36	36
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Adhl0412 Rabbit HP Aao13856 Human pol Abg70306 Human MDD Aau00910 Human can Aau40328 Propionib Abw36847 Propionib Aay29941 Zea mays Ada48350 Rice prot Aau87400 Novel cen Abo61857 Klebsiell Adi54715 Novel hum Abb66594 Drosophil Aau51225 Propionib Abw47744 Propionib Abw33219 Protein e	
ADH10412 AACH13856 ABG70306 AAU00910 AAU00910 AAV29941 AAV29941 AACH1850 AAU87400 AAU87400 AAU51225 ABB66594 AAU51225 ABM47744	ABC78053 ABB68243 ABC71042 ABB79805 ADH10410
<b>@404400047</b> @4400	74758
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## ALIGNMENTS

Histidine proline rich glycoprotein; HPRG; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian. Histidine proline rich glycoprotein pentapeptide. Plunkett ML, Mazar AP; ABB79810 standard; peptide; 5 AA 14-FEB-2002; 2002WO-US004336. 14-FEB-2001; 2001US-0268370P (first entry) (ATTE-) ATTENUON LLC Donate F, Harris S, WO200264621-A2 22-AUG-2002. 25-NOV-2002 Synthetic. ABB79810; RESULT 1 ABB79810 

WPI; 2002-666989/71

New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.

Claim 2; Page 67; 82pp; English.

The present sequence is a specific example of claimed anti-angiogenic pentapeptides of the invention. Claimed anti-angiogenic polypeptides or peptides comprise: the histidine-proline-rich (H/P) domain of human histidine proline rich glycoprotein (HPRG, see ABB79806); an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808, such as the present peptide, or its variant having an additional 1 to 4 amino acids comprising His, Pro or Gly at its Nor C-terminus. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or

multimer; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled polypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the HJP domain of human or rabbit HPRG, and which binds to HPRG or to any of the domains in a way which inhibits the anti-angiogenic activity of HPRG or the domains in a way which inhibits the anti-angiogenic activity of method for inhibiting call migration, cell invasion, cell proliferation or angiogenesis, a method for treating a consideration, provided in a subject; a method of subject having a disease or condition associated with undesired cell migration, proliferation, or angiogenesis; a method of stimulating or inhibiting angiogenesis in a subject; a method of etercting the presence of HPRG or its cleavage product or its peptide in a biological ample; isolated nucleic acids encoding the polypeptide, cell ample; isolated nucleic acids encoding the polypeptide, peptide or peptide multimer; an expression vector; transformed or transfected cells; a method of providing to a cell, tissue or organ and peptide multimer; an affinity ligand useful for the binding molecule, or the peptide multimer; an affinity ligand useful for binding to, or isolating, an HPRG-binding molecule, or isolating molecule, or isolating molecule, or isolating molecule, comprising the polypeptide, peptide or peptide compositions and methods are useful in diagnosing or treating a disease or condition associated with undestred cell migration, invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic compositions and methods are useful in inhibiting the growth of primary tumours or metastasces, and may also be used in treating neurodegenerative or elaboration of angiogenesis, and or condition associated with undestred cell migration, and in any and and an angional a ö peptide or peptide Gaps antiangiogenic receptor; rich glycoprotein; HPRG; cytostatic; antidiabetic; antiinflammatory; gynaecological; antiarthritic; rmatological; cardiant; vasotropic; vulnerary; e therapy; rabbit. iogenesis and are useful for promoting in pertinent disease states, and in various ; 0 100.0%; Score 36; DB 5; Length 5; 100.0%; Pred. No. 1.8e+06; vative 0; Mismatches 0; Indels beled anti-angiogenic polypeptide, protein H/P rich domain repeat fragment peptide; 5 AA. 17-MAR-2003; 2003WO-US008060 1-0364047P entry) (first ophthalmological; antipsoriatic; derm 15-MAR-2002; 2002US (ATTE-) ATTENUON LI angiogenesis; gene therapeutically la stimulators of ang neovascularization Query Match Best Local Similarity Matches 5; Conser Oryctolagus cunicu ADH10417 standard; Tpm; tropomyosin; histidine-proline WO2003077872-A2 HPPHG Ą; HPPHG Rabbit HPRG 11-MAR-2004 25-SEP-2003 Sequence 5 ADH10417; Н RESULT 2 ADH10417 ઠે 

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antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, of about 17 kDa and corresponds in its sequence to, or is a variant of, or an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide or variant has substantially the same blochemical cotivity of binding to the antiangiogenic polypeptide agents, as does the native Tpm internal fragment. The antiangiogenic polypeptide agent that corrivity of binding to the antiangiogenic polypeptide agent that corrivity of binding to the antiangiogenic polypeptide agent that corrivity of binding to the antiangiogenic polypeptide or peptide is buman histline-proline critical glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain or fragment of human or rabbit HPRG, two chain human kininogen (HK), the D5 domain of HK, or a Tpm-binding, the D5 domain or fragment of frhe HK or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antibodies and compositions are useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, for inducing conditions in compositions are useful for inhibiting such propressis, or for treating tumours or cancer, diabetic endothelial cell appoptosis, or for treating diseases or conditions in which correased angiogenesis, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease or promoting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease core fragment present in the rabbit HPRG protein His-Pro (H/P) rich domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                               New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer.
                                                                                                                                                                                                                                           The invention relates to an isolated tropomyosin (Tpm)-related antiangiogenic receptor polypeptide or peptide, which is a is a fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
 Mazar AP;
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Juarez J,
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
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Best Local Similarity 100.
Matches 5; Conservative
 Donate F,
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 Mccrae K,
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Sequence 20 AA;
                                                                                                                                  1 HPPHG
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                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
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                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single hearts.
                                                                                                                                                                             RESULT 5
ABB25810
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                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                       analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                      gene expression.
                                                                                                                                                                                                                                                    Gaps
                                                                                       probes useful for
                                                                                                                                                                                                                                                    ;
0
                                                                                                                  English
                                                                                                                                                                                                                                 100.0%; Score 36; DB 4; Length 20; 100.0%; Pred. No. 34;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      measuring placéntal
                                                                                                                                                                                                                                                                                                                                                                                                      human; placenta; antenatal diagnosis;
                                                                                                                 Claim 27; SEQ ID NO 34944; 639pp + Sequence Listing;
                                                                                       acid
                                                                                                                                                                                                                                                   Mismatches
                                                                                     ed single exon nucleic human fetal liver.
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                                                     Rank
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                                                                                                                                                                                                                                                                                                                                                                                     Peptide #10154 encoded by probe
                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                protein; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYNAMICS INC
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                    DYNAMICS INC
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                                                     Chen W,
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                    entry)
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gene expression in hu
                                                     Hanzel DK,
                                                                                       Human genome-derived
gene expression in hu
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                                                                     WPI; 2001-483447/52.
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                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                  AAM36117 standard;
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                                   (MOLE-) MOLECULAR
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                                                                                                                                                                                                                                                                                 HPPHG
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                                                                                                                                                                                                                 Sequence 20
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                                                                                                                                                                                                                                                                                                                                                  AAM36117;
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                                                             The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein #7809 encoded by probe for measuring heart cell gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                4; Length 20;
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Claim 27; SEQ ID NO 36386; 654pp; English
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                                                                                                                                                                                                                                                                                                                                                                                Score 36;
Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 5; Conservative
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HPPHG
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                                                                                  sapiens
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                         05-NOV-2001
                                         Human brain
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                                                                                                                  09-AUG-2001
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Best Local S
         AAM63195
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ABG57735
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                                                                                                                                                                                                                                                                                                                                                                                               Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancel such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                   Human bone marrow expressed probe encoded protein SEQ ID NO: 36315.
                                                                                                                                                                                    expression analysis; probe;
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                        4; Length 20;
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                                                                                                                                                                                    expressed exon; gene expressionaleukaemia; hymphoma; myeloma
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34;
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                        Score 36; DB Pred. No. 34; ; Mismatches
                                 34;
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Pred. No. 34;
; Mismatches
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                        100.0%;
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                                                                                                                                                  06-NOV-2001 (first
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488900/53
                      Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                   Human; bone marrow microarray; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
AAM63195
ID AAM63195 standard;
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Best Local Similarity
Matches 5; Conser
                                                                                                                  AAM76009 standard;
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                                                                      3 HPPHG 7
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         Sequence 20 AA;
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                                                                                                 RESULT 6
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                          Human; brain expressed exon; gene expression analysis; probe; microarray Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                     expressed single exon probe encoded protein SEQ ID NO:
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hypercholesterolaemia; coronary heart disease.
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Pred. No. 34;
; Mismatches
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100.0%; Pr
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                                                           2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG57735 standard; peptide;
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(first entry)
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5; Conservative
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us-10-074-225a-9.rag

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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for analyzing expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 36; DB 4; Length 20; 100.0%; Pred. No. 34; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                SEQ ID NO 36383; 658pp; English
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                                                                                                                                           Rank
                                                                                                                      DYNAMICS INC
                                     2000US-0180312P.
2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0234687P.
2000US-0234283.
                                                                                                                                          Hanzel DK, Chen W,
                   2001WO-US000664
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Best Local Similarity
Matches 5; Conser
                                                                                                                      MOLECULAR
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                                    04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                  30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20
09-AUG-2001
                                                                                                                                                                                                              Claim 27;
                                                                                                                                          Penn SG,
                                                                                                                     (MOLE-)
                                                                                                                                                                                  Human
                                                                                                                                                              WPI;
                                                                                                                                                                                             gene
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Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.

Rank DR;

Chen W,

Penn SG,

WPI; 2002-114183/15

(MOLE-) MOLECULAR DYNAMICS INC

03-AUG-2000; 2000US-00632366. 21-SEP-2000; 2000US-0234687P. 27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.

30-JAN-2001; 2001WO-US000665

2000US-0180312P

26-MAY-2000;

Claim 27; SEQ ID NO 35079; 634pp; English

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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from the probes for measuring gene expression in a sample derived from the 1214 to complements or the 1239 open reading frames derived from the 1214 probes. Also included are a microarray comprising the novel set of probes of the form the probes which phybridises at high stringency to a nucleic derived from human lung manauring gene expression in a sample derived from human lung comprising (a) contacting the arringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung mind, and (b) measuring the label derectably bound to each probe of the arringency identifying exons in a elkaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the early and (b) detecting specific hybridiaation of detectably labeled nucleic acids form early assigning exons to a single exon probe having a fragment identical to the predicted exon, the probe is included and the above mentioned microarray assigning exons to a single exon probe having a fragment identical to the predicted exon in several comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exons in a gene particularly using human lung derived mRNA and for the study of lung diseases such as assigned to a single gene, a peptide comprising concer, chronic obstructive pulmonary diseases (CODP), interstitial lung cancer, chronic obstructive pulmonary disease (CODP), interstitial lung cancer, chronic selected in disease, pulmonary diseases exon a single exon probes of present sequence is a specialed promoner of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Pred. No. 34;
; Mismatches
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Best Local Similarity
5; Conserva
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Gaps

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encoded by genome-derived single exon probe SEQ ID 35079.

peptide; 20 AA.

ABG45414 standard;

RESULT 9

(first entry)

19-AUG-2002

ABG45414

Human peptide

Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;

WO200186003-A2

Homo sapiens.

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ABM42552
ID ABM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, constructions) involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The sample polypeptides may be used as antigens in the production of antibodies and cherefore treat P. acnes proteins. These antibodies can be used to the expression and activity of P. acnes polypeptides and diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not format directly from WIPO at
                                                                                                                                                                            SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 36; DB 4; Length 53; 100.0%; Pred. No. 84; 0; Indels 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bhatia A;
                                                                                                                                              acnes immunogenic protein #6929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitcham JL, Wang S:
, Jen S, Carter D;
                                                                                                                                                                                                                                    dermatological; osteopathic; neuroprotectant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO 7228; 1069pp; English.
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                                       protein; 53 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 obtained in electronic format d
ftp.wipo.int/pub/published_pct_
                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                              20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Persing DH, Ne J, Zhang Y,
                                                                                                            entry)
                                                                                                                                                                                                                                                                       acnes
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N-PSDB; AASS9529.
                                                                                                        (first
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                                       standard;
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Best Local Similarity
Matches 5; Conser
                                                                                                                                              Propionibacterium
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                                                                                                                                                                                                                                                                                                                                          01-NOV-2001
                                                                                                         27-FEB-2002
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                                     AAU46033
                                                                        AAU46033
RESULT 10
                    AAU46033
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The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

cncoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; an invention; fusion proteins comprising a polypeptide of the invention; a comparising a polypeptide of the invention; a nation proteins comprising rels prepared to polymentiod a vaccine composition (comprising rels prepared to polymented and an isolated T cell population comprising T cells prepared to polymented and an isolated T cell population comprising rels method a vaccine composition (comprising T cells prepared to polymented a vaccine composition (comprising rels method and kit comprising the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the protein. The polymcleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymcleotides of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/published_pct_encoded pct_encoded pc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                  Propionibacterium acnes predicted ORF-encoded polypeptide #7228
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                                                                                                                                                                                 Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6; Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 36; DE 100.0%; Pred. No. 84; Ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 7228; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Persing DH,
Lodes MJ,
   A
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S
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Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2002; 2002WO-US032727.
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ABM42552 standard; protein;
                                                                                       (first entry)
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                     Propionibacterium acnes
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N-PSDB; ACF64458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                WO2003033515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53 AA;
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                                                                                       20-OCT-2003
                                            ABM42552;
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HPPHG

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7 HPPHG 11
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protein; 61 AA AAU54374 standard; AAU54374; RESULT 12 AAU54374

(first entry) 27-FEB-2002

acnes immunogenic protein #15270 Propionibacterium SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

acnes Propionibacterium

WO200181581-A2

01-NOV-2001

20-APR-2001; 2001WO-US012865

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP.

Bhatia A; L, Wang SS, Carter D; Persing DH, Mitcham JL, re J, Zhang Y, Jen S, C L'maisonneuve J, Skeiky YAW,

WPI; 2001-616774/71.

N-PSDB; AAS59564

rropionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.

NO 15569; 1069pp; English Example 1; SEQ ID

Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by polypeptides. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. To acnes is also involved in infections of bone, joints and the central pervenue system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies and specific for P. acnes proteins. These antibodies can be used to some specific for P. acnes infections. The acnes polypeptides and therefore treat P. acnes infections. The acnes polypeptides and charmed inmunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences 

Sequence 61 AA;

ö Gaps ; 0 4; Length 61; 0; Indels 100.0%; Score 36; DB 100.0%; Pred. No. 96; ive 0; Mismatches Similarity 100 5, Conservative Query Match Best Local S Matches 5

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ABM50893

ABM50893 standard; protein; 61 AA

ABM50893;

(first entry) 20-OCT-2003

Propionibacterium acnes predicted ORF-encoded polypeptide #15569.

Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine. 

Propionibacterium acnes.

WO2003033515-A1

24-APR-2003.

11-OCT-2002; 2002WO-US032727.

15-OCT-2001; 2001US-00978825

(CORI-) CORIXA CORP

Maisonneuve JL; Jones R, Carter D; Bhatia A, Benson DR, Persing DH, Lodes MJ, Mitcham JL, Skeiky YAW, Pers Zhang Y, Wang S, Jen S, Lod Barth B, Vallieve-Douglass J;

2003-381789/36 WPI; 2003-381789, N-PSDB; ACF64493

New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.

Example 1; SEQ ID NO 15569; 1481pp; English.

in through a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polypeptides of the invention; antibodies against polypeptides of the invention; antibodies against polypeptides of the invention; antibodies specific for a P. acnes polypeptide of the invention; an immune response specific for a P. acnes polypeptide and an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations or absence of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins, or for stimulating an immune response specific for a P. acnes protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. Immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymucleotides of the rimention. Note: The sequence data for this patent did not form part of invention, but was obtained pot encoded pot encoded by companies. invention relates to an isolated polynucleotide (ACF64435-ACF64733)

Sequence 61 AA;

Query Match

DB 6; 100.0%; Score 36;

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2000US-0229287P.
2000US-0229343P.
2000US-0229343P.
2000US-02293443P.
2000US-02293445P.
2000US-02293445P.
2000US-02293445P.
2000US-02293445P.
2000US-02293445P.
2000US-02293445P.
2000US-0229343P.
2000US-0239343P.
2000US-02312444P.
2000US-02312449P.
2000US-02312449P.
2000US-02312449P.
2000US-02312449P.
2000US-02312449P.
2000US-0231413P.
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2000US-0231413P.
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2000US-0231413P.
2000US-023141414P.
2000US-023141414
 30 - AUG - SEP - 2000 | 1 - SEP - 2000 |
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                                                                                                                                                                                                                                                                                                 Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat; chicken; sheep; immunosuppressive; antiarthritic; vasotropic; dog; antirheumatic; antiproliferative; cytostatic; cardiant; neuroprotective; cerebroprotective; nootropic; antibacterial; virucide; fungicide; cancer; ophthalmological; vulnerary; gene therapy; autoimmune disease; neoplasm; hyperproliferative disorder; breast; liver; cardiovascular disorder; hyperproliferation disorder; nervous system disorder; bacterial infection; fungal infection; viral infection; ocular disorder; endocrine disorder; gastrointestinal disorder; renal disorder; respiratory disorder; wound healing; skin aging; organ transplantation; tissue regeneration; anti-infertility.
                       Gaps
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N
                      IndelB
                                                                                                                                                                                                                                                                       polypeptide SEQ ID
                   0;
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Mismatches
                                                                                                                                                                                                                                                                        antigen
                                                                                                                                                                      protein; 63
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2000US-0180628P.
2000US-0184664P.
2000US-0186350P.
2000US-0189374P.
2000US-019076P.
2000US-019123P.
2000US-0209467P.
2000US-0216486P.
2000US-021643P.
2000US-021643P.
2000US-021643P.
2000US-0217486P.
2000US-0217486P.
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2000US-0217486P.
2000US-0217486P.
2000US-0217486P.
2000US-0225213P.
2000US-022573P.
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                                                                                                                                                                                                                                                                        system
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                                                                                                                                                                                                                                                                        Human cardiovascular
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  Similarity 5; Conserv
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04-FEB-2000;
24-FEB-2000;
16-MAR-2000;
11-MAR-2000;
11-MAR-2000;
19-MAY-2000;
07-JUN-2000;
07-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-AUG-2000;
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  Best Local
Matches
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AAU22059
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Human cardiovascular system related polypeptide #208

(first entry)

29-JAN-2004

ADE46027;

ADE46027 standard; protein; 63 AA

ADE4602

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Sequences AAU21852-AAU22466 represent the cardiovascular system antigen polypeptides of the invention. Cardiovascular system antigens and their associated polynucleotides are useful in the diagnosis, treatment and prevention of various types of disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. A pathological condition cardiovascular system antigen polynucleotide. The treatable disorders include autoimmune diseases such as rheumatoid arthritis, hyperproliferative disorders such as neoplasms of the breast or liver, cardiovascular disorders such as cardiac arrest, cerebrovascular disorders such as cardiac arrest, cerebrovascular disorders such as corneal infection, endocrine disorders such as of premature labour and infections caused by bacteria, viruses and fungi, coular disorders such as schema and pleurisy. The polypeptides can premature labour and infertility, gastrointestinal disorders such as corneal infection, endocrine disorders such as corneal infection, calconders such as corneal infection, calconders such as corneal infection, condition disorders such as corneal disorders such as set man and pleurisy. The polypeptides can respiratory disorders such as asthma and pleurisy. The polypeptides can calso be used to aid wound healing, to prevent skin aging due to sunburn, to maintain organs before transplantation, to regenerate tissues and in chemotaxis. Note: The sequence data for this patent did not form part of trom WIPO at ftp. WiPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New cardiovascular system related polynucleotides and polypeptides,
useful for diagnosing, treating and/or preventing disorders of the
cardiovascular system.
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2000US-0249211P.
2000US-0249213P.
2000US-0249213P.
2000US-0249214P.
2000US-0249214P.
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N-PSDB; AAS35333.
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    17-NOV-2000;
17-NO
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Human; cardiovascular system related polypeptide; cancer; proliferative disorder; foetal abnormality; developmental abnormality; haematopoietic disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; pregnancy-related disorder;
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2000US-0216443P.
2000US-0216480P.
2000US-0217486P.
2000US-0217496P.
2000US-0218290P.
2000US-0220964P.
2000US-0220964P.
2000US-0225213P.
2000US-0225214P.
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2000US-022575P.
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2000US-0184664P
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
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18-AUG-2000;
22-AUG-2000;
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22-AUG-2000;
23-AUG-2000;
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14-AUG-2000;
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2000US-0231414P

2000US-023198P

2000US-023239BP

2000US-023423PP

2000US-023423PP

2000US-023423PP

2000US-023423PP

2000US-023423PP

2000US-0234477P

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08-SEP-2000

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15-OCT-2000

16-NOV-2000

17-SEP-2000

18-SEP-2000

19-SEP-2000

11-SEP-2000

11-NOV-2000

11-NOV-2000
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The invention relates to human cardiovascular system related polypeptides and the polynucleotides encoding them. The polypeptides, polynucleotides and antibodies to the polypeptides are useful for diagnosing a and antibodies to the polypeptides are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, such as for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular system tissues, proliferative disorders, foetal and developmental abnormalities, haematopietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, etc. stherosclerosis, cardiovascular disorders, angiogenic disorders, atherosclerosis, cardiovascular disorders, pregnancy-calabetes, atherosclerosis, cardiovascular disorders, pregnancy-calabetes, atherosclerosis, cardiovascular disorders, pregnancy-calabetes, and disorders, gastrointestinal disorders, pregnancy-calabetes, endocrine disorders and infections. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and polymucleotides may also be used as food additives or preservatives to increase or decrease storage capabilities, fat content or other nutritional components. This sequence represents a human cardiovascular system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New cardiovascular system related polynucleotides and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer of cardiovascular tissues and cancer metastases.
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ADJ07445
ID ADJ07445 standard; protein; 63 AA.
XX
AC ADJ07445;
XX
DT 04-NOV-2004 (first entry)
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               17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0251988P.
06-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251999P.
11-DEC-2000; 2000US-0251999P.
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N-PSDB; ADE45412.
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autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasms; liver neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin aging; sunburn; organ transplantation; cell culture; tissue regeneration; chemotaxis; food additive; preservative; cardiovascular system associated antigen; nuclear factor kappaB; NFkappaB; promoter element; human.
            system associated polypeptide SeqID833
                                                                                                                                                                                                                                          2000US-019065P.
2000US-018064P.
2000US-0184664P.
2000US-0188350P.
2000US-019834P.
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2000US-022544P.
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2000US-0225468P.
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2000US-022546P.
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04-FEB-2000;
12-MAR-2000;
16-MAR-2000;
11-MAR-2000;
11-MAR-2000;
12-MAY-2000;
13-MAY-2000;
14-MU-2000;
11-JUL-2000;
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PR 14-58P-2000 2 000015-023339P
PR 14-58P-2000 2 000015-023339P
PR 14-58P-2000 2 000015-023339P
PR 14-58P-2000 2 000015-023339P
PR 21-58P-2000 2 000015-02333063P
PR 21-58P-2000 2 000015-023439B
PR 21-67P-2000 2 000015-02431B
PR 21-67P-2000 2 000015-02431B
PR 21-67P-2000 2 000015-02431B
PR 21-67P-2000 2 000015-02441B
PR 21-70P-2000 2 000015-02441B
PR 21-7
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Propionibacterium acnes
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ABM62695
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                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule encoding a fragment. Also included recombinant vectors, recombinant host cells, an isolated human cardiovascular system associated polypeptide (including isolated human cardiovascular system associated polypeptide (including its fragment, allelic variant, species homologue or epitope), an isolated antibody that binds specifically to a human cardiovascular system associated polypeptide, diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in human cardiovascular system associated mutation), identifying a binding partner to human cardiovascular system associated polypeptides, the gene corresponding to the human cardiovascular system associated cDNA sequence and identifying an activity in a biological assay comprising expressing the human cardiovascular system associated cDNA in a cell, isolating the numan cardiovascular system associated cDNA in a cell, isolating the cardiovascular system associated cDNA in a cell, isolating the human cardiovascular system associated cDNA; the cells assay and identifying the protein in the supernatant having the activity. The human cardiovascular system associated nucleic acids and polypeptides are used continuous mice, rabbits, goats, horses, cats, dogs, chickens or sheep), for the humans, mice, rabbits, goats, horses, dogs, chickens or sheep), for example autoimmune diseases such as rheumatoid arthritis, heat or
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                                                                                                                                                                                                                                                                         system-related nucleic acid molecule, useful for ting or treating diseases of the cardiovascular system, mapping, drug screening or in pharmacogenomics.
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          2000US-0251988P.
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2000US-0251868P.
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and in chromosome
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06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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11-DEC-2000;
05-JAN-2001;
17-JAN-2001;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by a cnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and choophhalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and characteries infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bhatia A;
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JL, Wang SS,
Carter D;
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                                                                                                                                                                                                                                                                        21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                            20-APR-2001; 2001WO-US012865
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e J, Zhang Y,
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Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating acne vulgaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccinating against
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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Best Local Similarity 100...
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                                                                        Propionibacterium acnes
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N-PSDB; AASS9592.
                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                    L'maisonneuve J,
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                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

cenceding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of F. acres polypeptides. The invention and to additionally encompasses expression vectors and host cells comprising a colymention; fusion proteins comprising a polypeptide of the invention; a immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, polymeleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or detecrining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polypucleotides, matibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne volgaris, or for stimulating an immune response specific for a P. acnes protein. The polymulation of an immune response against P. acnes, or for treating acne stimulation of an immune response against P. acnes, or for treating acne and the kit is useful for performing a diagnostic assay. The present and the kit is useful for performing a diagnostic assay. The present canding frame) contained within the P. acnes polymucleotides of the printed specification, but was obtained to be encoded by an ORF (open reading frame) contained which the P. acnes polymucleotides of the printed specification, when when an encoded the printed specification, which when the parternal directions and the kit was obtained the printed specification.
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                                                                                                                                                                                                                                                    New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                       Maisonneuve JL;
Jones R, Carter D;
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                                                                                                                                                       Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                      Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                            NO 27371; 1481pp;
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Wang S, Jen S, Lode
Vallieve-Douglass J;
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                                                                     11-OCT-2002; 2002WO-US032727.
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Best Local Similarity
Matches 5; Conserv
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N-PSDB; ACF64646.
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              WO2003033515-A1
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                                         24-APR-2003
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Barth B,
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                                                                                                                          (CORI-)
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AAUS8530
XEXTXEX
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The specific for P. acnes proteins in the production of antibodies specific for P. acnes proteins. These antibodies and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was
   osteomyelitis;
/stem; ELISA;
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
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obtained in electronic format directly from WIPO at
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Jen S, Carter D;
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(first entry)

27-FEB-2002

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The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

cocding a Propionibacterium acnes protein. The invention also relates to encoding a Propionibacterium acnes protein. The invention also relates to Dilypeptides encoded by the polynucleotides. The invention and to immunogenic fragments of P. acnes polypeptides. The invention; and additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; a comprising propertied of the invention; and propertied and an isolated T cell population comprising T cells prepared to polypeptide and an isolated T cell population comprising P. acnes polypeptides, autibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for dagnosing preventing or treating acne protein. The polymucleotides can also be used as probes or primers for uncleic acid hybridisation. The vaccine composition is useful for the expressent composition of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present creating frame) contained within the P. acnes polymericed to be encoded by an ORF (open reading frame) contained within the P. acnes polymericed to the printed specification, but was obtained in electronic format directly the printed pecification, but was obtained in electronic format directly contained protein patent and polymerices.
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Jones R, Carter
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iseborrhoeic; dermatological; antibacterial;
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Benson DR,
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100.0%; Pred. No. 1.4e+02;
Live 0; Mismatches 0;
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Acne vulgaris; antiseborrhoeic; dermatolo; immunostimulant; immune response; vaccine
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Lodes MJ,
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Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
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N-PSDB; ACF64521.
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polypeptide, usefu
or for stimulating
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Best Local Similarity
Matches 5; Conser
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                                                       Propionibacterium
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protein; 94 AA.

AAU63724 standard;

RESULT 21
AAU63724
ID AAU63
XX
AC AAU63

AAU63724

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lessons or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies and downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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                                   Propionibacterium acnes immunogenic protein #24620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 36; DB 4; L. larity 100.0%; Pred. No. 1.5e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 24919; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABM60243 standard; protein; 94 AA
                                                                                                                                                                                                                                                                                                                          21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US012865
                                                                                                                                                                                                                                                                                                                                                                                                                                           Skeiky YAW, Persing DH, M
L'maisonneuve J, Zhang Y,
                                                                                                                                                                      Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-616774/71.
N-PSDB; AAS59634.
                                                                                                                                                                                                                                                                                                                                                                                                      (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 94 AA;
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                                                                                                                                                                                                             WO200181581-A2
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes immunogenic protein #20910.

(first entry)

27-FEB-2002

AAU60014;

99 AA

AAU60014 standard; protein;

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concoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention, additionally encompasses expression vectors and host cells comprising a polynucleotide of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population (comprising P. acnes polypeptides, via this method; a vaccine composition (comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or absence of P. acnes in a cartigen-presenting cells that express the polypeptides; and method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the porteins, T cell populations or antigen-presenting cells that express the proteins. The polymucleotides or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne, rugaris, or for stimulations on mimune response appoint or for treating acne, and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polynucleotides of the reading frame) contained within the P. acnes polynucleotides of the reading frame) contained within the P. acnes polynucleotides of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_general patent and patent predicted to be encoded by an ORF (open reading frame) acroal published_pot_general patent and patent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l for diagnosing, preventing or treating acne vulgaris, an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tes to an isolated polynucleotide (ACF64435-ACF64733)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maisonneuve JL;
Jones R, Carter
                                                acnes predicted ORF-encoded polypeptide #24919
                                                                                               dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 36; DB 6; Length 94; 100.0%; Pred. No. 1.5e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO 24919; 1481pp; English.
                                                                                             Acne vulgaris, antiseborrhoeic, dermatoloç
immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitcham JL, Skeiky YAW, Pers
Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                            11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                             15-OCT-2001; 2001US-00978825
(first entry)
                                                                                                                                                                    acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-381789/36.
N-PSDB; ACF64563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA COR
                                                  Propionibacterium
                                                                                                                                                                    Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; SEQ ID
                                                                                                                                                                                                               WO2003033515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention
 20-OCT-2003
                                                                                                                                                                                                                                                               24-APR-2003
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Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for

Example 1; SEQ ID NO 21209; 1069pp; English.

treating acne vulgaris.

Bhatia A;

Mitcham JL, Wang SS, Jen S, Carter D;

Persing DH, M

L'maisonneuve J,

Skeiky YAW,

WPI; 2001-616774/71.

N-PSDB; AAS59607.

21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.

(CORI-) CORIXA CORP

20-APR-2001; 2001WO-US012865.

Propionibacterium acnes.

WO200181581-A2.

01-NOV-2001

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100.0%; Score 36; DB 4; Length 99; 100.0%; Pred. No. 1.5e+02; tive 0; Mismatches 0; Indels
                             Conservative
           Best Local Similarity
Matches 5; Conserv
                                                                                  61 HPPHG 65
                                                      1 HPPHG 5
   Query Match
                                                                                                                         RESULT 24
ABB15846
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                             ô
                              Gaps
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68 ß

RESULT 23 AAU60014

1 HPPHG 64 HPPHG

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Sequence 99 AA;

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Gaps

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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, practulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (BLISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at

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2000US-0232081P.
2000US-0232981P.
2000US-0232393P.
2000US-0232393P.
2000US-0232393P.
2000US-0232399P.
2000US-023499PP.
2000US-0244647PP.
2000US-024647PP.
2000US-024647PP.
2000US-024647PP.
2000US-024647PP.
2000US-024647PP.
2000US-024647PP.
2000US-024647PP.
2000US-0246611P.
2000U
 08 - SEP - 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2000; 2
    Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                            4503
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                                                                                           ΩI
                                                                                           SEQ
                                                                                           polypeptide
  protein; 99
                                                                                                                                                                                                                                                                                                                                                            2000US-019065P.
2000US-018664P.
2000US-0186550P.
2000US-0198123P.
2000US-0198123P.
2000US-0198123P.
2000US-0209467P.
2000US-0209467P.
2000US-0209467P.
2000US-0209467P.
2000US-020513P.
2000US-020513P.
2000US-0225268P.
2000US-0225264P.
2000US-0225264P.
2000US-0225264P.
2000US-0225268P.
2000US-0225268P.
2000US-0225268P.
2000US-0225268P.
2000US-0225268P.
2000US-0225268P.
2000US-0225757P.
2000US-0225759P.
2000US-0225769P.
2000US-0225769P.
2000US-0225769P.
2000US-0225769P.
2000US-0225769P.
2000US-0225769P.
2000US-0225769P.
2000US-0225769P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-0229343P.
2000US-0239343P.
2000US-0239343P.
2000US-0239343P.
2000US-0239343P.
2000US-0239343P.
2000US-0239343P.
2000US-0239448P.
                                                                                          related
                                                               entry
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                                                              ப
                                                                                          Human nervous syst
                                                              (firs
   standard;
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                                                                                                                                                                                                                                                                                                                                                             31-JAN-2000;
04-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-MAY-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-AUG-2000;
15-AUG-2000;
16-AUG-2000;
17-AUG-2000;
18-AUG-2000;
18-AUG-2000;
19-AUG-2000;
10-SEP-2000;
                                                                                                                                                                                                                                                                                                                                   17-JAN-2001;
                                                           23-JAN-2002
                                                                                                                                                                                                                                                                                                     16-AUG-2001
  ABB15846
                               ABB15846;
                                                                                                                                                                                                                                           Ношо
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Ω

Maisonneuve JL; Jones R, Carte

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The invention relates to an isolated polymuclectide (ACF64435-ACF64733)

cncoding a Propionibacterium acnes protein. The invention also relates to encoding a Propionibacterium acnes protein. The invention also relates to jumunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a comprising a polypeptide of the invention; an invention; antibodies against polypeptides of the invention; a polymention proteins comprising a polypeptide of the invention; a recipient a vaccine composition (comprising T cells prepared to polymentledies, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a proteins. T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne, polypeptides are useful for diagnosing, preventing or treating acne, protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridiastion. The vaccine composition is useful for performing a diagnostic assay. The present cut the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open creating frame) contained within the P. acnes polypucleded at a for this patent did not form part of invention. Note: The sequence data for this patent did not format directly and montained protein and polypeptide for performing a diagnositic assay. The present creating the printed specification, but was obtained in electronic format directly from the printed protein prot
                                                                                                                                                                                                                                                                                                             New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tpm; tropomyosin; antiangiogenic receptor;
histidine-proline rich glycoprotein; HPRG; cytostatic; antidiabetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 36; DB 6; Length 99; 100.0%; Pred. No. 1.5e+02;
                                                                                                                                                                             Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 21209; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                            Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rabbit HPRG protein H/P rich domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH10412 standard; protein; 101 AA
                                                                                                                                                                         Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                              11-OCT-2002; 2002WO-US032727.
                                                                                                   15-OCT-2001; 2001US-00978825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                      2003-381789/36
                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 HPPHG 65
                                                                                                                                                                                                                                                                      N-PSDB; ACF64536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADH10412;
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ADH10412
       ð
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (ABA11004-ABA21534) and proteins

(ABB14678-ABB18001) useful for preventing, treating or ameliorating
medical conditions e.g. by protein or gene therapy. The genes are
isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant) agonists are useful in
the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
covarian, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
cardiovascular disorders such as myocardial ischaemias; (d) wound healing
cardiovascular disorders such as wiral, bacterial, fungal and parasitic
infectious diseases such as viral, bacterial, fungal and parasitic
infections. Note: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format directly
trom WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acnes predicted ORF-encoded polypeptide #21209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iseborrhoeic; dermatological; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NO 4503; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 36; DB 4; Length 99; 100.0%; Pred. No. 1.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acne vulgaris; antiseborrhoeic; dermatologimmunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein; 99 AA
                                                                                                                                                                                                                                                                                                                              Ruben SM;
2000US-0249300P.
2000US-02513160P.
2000US-0251030P.
2000US-025198BP.
2000US-025198P.
2000US-025186P.
                                                                                                                                                                                                                                                                                         HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acnes
                                                                                                                                                                                                                                                                                                                              sc,
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-541565/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM56533 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium
                                                                                                                                                                                                                                                                                                                              Barash
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABA12172.
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 17-NOV-2000;
01-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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                                                                                                                                                                                                                                                                                                                              Rosen
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ABM56533
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RESULT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ઠે
                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated tropomyosin (Tpm) related antiangiogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antiangiogenic polypeptide agents; The isolated antiangiogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that bolypeptide, peptide or variant has substantially the same biochemical activity of binding to the antiangiogenic polypeptide agent that binds to the isolated polypeptide or peptide is human histidine-proline rich glycoprotein (HPRG), rabbit HPRG, a Tpm-binding, antiangiogenic polypeptide or peptide or rabbit HPRG, two chain human kininogen (HK), the D5 domain of HK, or a Tpm-binding, two chain human kininogen (HK), the D5 domain of HK, or a Tpm-binding, cantiangiogenic homologue, variant, domain of fragment of the HK or its D5 domain. The Tpm-related antiangiogenic receptor polypeptide or peptide, antibodies and compositions are useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for pronting wound healing, or for treating diseases or conditions in which increased angiogenesis is desired, e.g. coronary artery disease. The present sequence represents a rabbit HPRG protein His-Pro (H/P) rich domain.
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                                                                                                                                                                                                                                                         New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer.
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ophthalmological; antiinflammatory; gynaecological; antiarthritic; antipsoriatic; dermatological; cardiant; vasotropic; vulnerary; angiogenesis; gene therapy; rabbit.
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                                                                                                                                                                                                              Juarez J,
                                                                                                                               17-MAR-2003; 2003WO-US008060
                                                                                                                                                          15-MAR-2002; 2002US-0364047P
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5; Conserv
                                                     Oryctolagus cunicul
                                                                                                                                                                                                                                                                                                                                Claim 6; SEQ ID NO
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                                                                            WO2003077872-A2
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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100.0%; Pred. No. 1.7e+02;
tive 0; Mismatches 0;
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Human polypeptide SEQ ID NO 27748.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2001; 2001WO-US004927
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18-MAY-2000; 2000US-00577409
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N-PSDB; AAI93787.
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to the isolation of novel human molecules for disease detection and treatment (MDDT), and the polynucleotide sequences (mddt) encoding them. The MDDT polypeptides may be used to screen for molecules that bind to, or are bound by the encoded polypeptides, and to develop a transcript image of a tissue or cell type. Probes comprising at least 20 nucleotides of the mddt polynucleotide may be used to assess the toxicity of a test compound. The MDDT polypeptides and mddt polynucleotides are useful in the diagnosis, study, prevention and treatment of diseases associated with the expression of molecules for disease detection and treatment. Such disorders include cell proliferative disorders (e.g. arteriosclerosis, cirrhosis, or cancers), and autoimmune/inflammatory disorders (e.g. asthma, Crohn's disease, or multiple sclerosis). The mddt polynucleotides may also be used as molecule markers, in microarrays, and in somatic or germline gene therapy. ABG70306-ABG70311 represent the MDDT proteins of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer related protein; food additive; preservative; immunogen; antibody; bone cancer; adrenal cancer; bone marrow cancer; breast cancer; gastrointestinal cancer; liver cancer; lung cancer; urogenital cancer; immune disorder; Addison's disease; allergy; diabetes mellitus; autoimmune haemolytic anaemia; autoimmune thyroiditis; Crohn's disease;
                                                                                                                                                                                                                                                                                                              ion and treatment molecule (MDDT) polynucleotides and
il in diagnosing, studying, preventing or treating
with MDDT expression, e.g. autoimmune or inflammatory
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                                                                                                                                                                                                                      Jones
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                                                                                                                                                                                                           Length 117;
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V, Daffo A, Marwaha
David MH, Lewis SA;
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100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
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Dam TC, Liu TF, Harris B, Flores
Chang SC, Gerstin EH, Peralta CH,
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                                                                                                                                                                                                                                                                                                                                                                              ; 129pp; English
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                                                                                    16-JAN-2001; 2001US-0261865P.
17-JAN-2001; 2001US-0262208P.
17-JAN-2001; 2001US-0262209P.
17-JAN-2001; 2001US-026326P.
19-JAN-2001; 2001US-0263063P.
19-JAN-2001; 2001US-0263065P.
                                                 09-JAN-2002; 2002WO-US001008
                                                                           2001US-0261622P
                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC.
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                                                                                                                                                                                                                                                                                                            New disease detection polypeptides, useful diseases associated w disorders.
                                                                                                                                                                                                                                                                        WPI; 2002-590679/63.
N-PSDB; ABS51779.
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17 HPPHG 21
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WO200255738-A2
                                                                           12-JAN-2001;
                         18-JUL-2002
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Chang SC,
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Matches 5
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AC
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The sequence represents a novel Human cancer related protein. The polynucleotides and polypeptides are useful for preventing, treating or polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polynucleotide are useful for chromosome identification. The nucleic acids, protein, antibodies, agonists and antagonists are useful in the diagnosis, treatment and prevention of cancer (e.g. cancers of the adrenal gland, bone, bone marrow, breast, cancer (e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis, acquired immunodeficiency syndrome, AIDS), cardiovascular disorders such as myocardial ischaemias, wound healing, neurological diseases (e.g. Parkinson's disease, Alzheimer's disease, cerebral anoxia and epilepsy) and infectious diseases such as viral, bacterial, fungal and parasitic infections. Numerous examples of each type of disorder are given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Twenty nine nucleic acid molecules encoding human cancer associated proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
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multiple sclerosis; rheumatoid arthritis; ulcerative colitis; acquired immunodeficiency syndrome; AIDS; cardiovascular disorder; myocardial ischaemia; wound healing; neurological disorder; Parkinson's disease; Alzheimer's disease; cerebral anoxia; epilepsy; viral infection; bacterial infection; fungal infection; parasitic infection; agonist; antagonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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Pred. No. 1.8e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 422-423; 427pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  °
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                                                                                                                                                                                                                                                                                                                                                                                                                      2000WO-US023794.
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99US-0158003P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENOME SCI INC
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAS00851
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                                                                                                                                                                                                                                                                                          WO200118014-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specification
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                        15-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roschke V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU40328;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       acnes polypeptides and nucleic acids useful for it and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cnes predicted ORF-encoded polypeptide #1523.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 36; DB 4; Length 202; 100.0%; Pred. No. 3e+02; vative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                  Bhatia A;
                                                                                                                                                                                                                                                                                                                              Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO 1523; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 202 AA
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                 20-APR-2001; 2001WO-US012865
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s J, Zhang Y,
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                                                                             acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aris.
                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-616774/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccinating against
treating acne vulga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Propionibacterium a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acne vulgaris; anti
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Best Local Similarity
Matches 5; Conser
                                                                       Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                L'maisonneuve J,
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                                                                                                           WO200181581-A2
                                                                                                                                                                                                                                                                                                                              Skeiky YAW,
                                                                                                                                              01-NOV-2001
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The invention relates to an isolated polynuclectide (ACF64435-ACF64733)

C encoding a Propionibacterium acnes protein. The invention also relates to encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynuclectides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention; a additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; an invention; antibodies against polypeptide of the invention; a cinvention; an invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared to polypeptide and an isolated T cell population comprising T cells prepared to polymericlectides, antibodies, fusion proteins, T cell populations, or cantigen-presenting cells that express the polymericlectides and an exthod for inhibiting the development of P. acnes in a conting the presence or absence of P. acnes in a conting polypeptides, polymuclectides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the proteins, T cell populations or antigen-presenting cells that express the collypeptides are useful for idagnosing, preventing cells that express the proteins, T cell populations or antigen-presenting cells that express the collypeptides are useful for idagnosing, preventing cells that express the protein. The polymuclectides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence content of an immune response against P. acnes, or for treating acceptance and the kit is useful for performing a diagnositic assay. The present reading frame) contained within the P. acnes polymuclectides or primers of the printed specification, but was obtained in electronic format directly from WIPO at fip, wipo.int/published_pot_escrete presents a polypeptide predicted to be encoded by an ORF (from MIPO at fip, wipo.int/published_pot_escrete predicted acception or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptide, useful for diagnosing, preventing or treating acne vulgar or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Propionibacterium acnes polypeptides and polynucleotides encoding
                                                                                                                                                                                                                                                                                                                                      Carter D;
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                                                                                                                                                                                                                                                                                                                 Maisonneuve JL;
Jones R, Carte
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                                                                                                                                                                                                                                                                                                               Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 1523; 1481pp; English.
immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                               Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY29941 standard; protein; 231 AA.
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Zhang Y, Wang S, Jen S, Lode
Trrth B. Vallieve-Douglass J;
                                                                                                                                                                               11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                          15-OCT-2001; 2001US-00978825
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                                             Propionibacterium acnes
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Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 HPPHG 97
                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ACF64440.
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                                                                                          WO2003033515-A1
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AAY29941
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HPPHG 182
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                                                                                                                                           n,
                                                                                                                                        Glazebrook J
Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001;
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                                                                                                                                                                                                                                                                                                                      pathogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ21186 to AAZ21190 represents the nucleotide sequences for promoters isolated from a family of maize (Zea mays) genes encoding pathogenesis related (PR-1) proteins. The promoters are useful for expressing heterologous genes (including genes for disease resistance) in plants, especially dicots, or monocots i.e. maize. The promoters are useful for the genetic manipulation of plants to exhibit specific phenotypes, particularly enhanced resistance to pathogen-caused disease. Pathogens include viruses such as tobacco or cucumber mosaic virus, ringspot virus, necrosis virus, and maize dwarf virus, and viroids, bacteria, insects, nematodes and fungi. The present sequence represents a maize PR-1 protein given in the present invention
                                                     Zea mays; maize; pathogenesis-related class I; PR-1; promoter; regulation; expression; disease resistance; genetic manipulation; tobacco mosaic virus; cucumber mosaic virus; ringspot virus; neatode; necrosis virus; maize dwarf virus; viroid; bacterial; insect; nematode;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New promoter sequences from pathogenesis-related genes of
                     Zea mays pathogenesis-related class I PR-1#70 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                             (PION-) PIONEER HI-BRED INT INC
                                                                                                                                                                                                                                                                                              99WO-US003011
                                                                                                                                                                                                                                                                                                                                   98US-0076100P
98US-0079648P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-527621/44
N-PSDB; AAZ21192.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 69-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 HPPHG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 231 AA;
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                                                                                                                                                                                                                WO9943819-A1
                                                                                                                                                                                                                                                                                              11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                   26-FEB-1998;
27-MAR-1998;
                                                                                                                                                                                                                                                         02-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Crane VC;
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                                                                                                                                     fungal.
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ADA48350
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The invention relates to a novel isolated polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance or its fragment having substantially the same activity as the full-length polypeptide. The polynucleotide of the invention is useful for conferring resistance or tolerance to a plant pathogen. The present sequence represents a protein conferring disease resistance used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide comprising a plant nucleotide sequence having an open reading frame that encodes a polypeptide associated with disease resistance, useful for conferring resistance or tolerance to a plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; SEQ ID NO 420; 299pp; English.
                                                                                                                                                (SYGN ) SYNGENTA PARTICIPATIONS AG
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Kreps J, Provart N,
22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0352277P.
22-MAR-2002; 2002US-0366535P.
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04-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
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N-PSDB; ADA48349.
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Matches 5; Conserv
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2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
2000US-020467P.
2000US-0216880P.
2000US-0216880P.
2000US-0216880P.
2000US-0216880P.
2000US-0216880P.
2000US-0216880P.
2000US-022144P.
2000US-0225268P.
2000US-023299P.
2000US-02329P.
2000US-02
 17-MAR-2000;
19-MAY-2000;
19-MAY-2000;
19-MAY-2000;
107-JUN-2000;
30-JUN-2000;
11-JUL-2000;
11-J
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13 - OCT - 2000; 2000US - 0240960P.
20 - OCT - 2000; 2000US - 0241221P.
20 - OCT - 2000; 2000US - 0241221P.
20 - OCT - 2000; 2000US - 0241185P.
20 - OCT - 2000; 2000US - 0241186F.
20 - OCT - 2000; 2000US - 0241186F.
20 - OCT - 2000; 2000US - 0241180P.
20 - OCT - 2000; 2000US - 024180P.
20 - OCT - 2000; 2000US - 024180P.
20 - OCT - 2000; 2000US - 024618P.
20 - OCT - 2000; 2000US - 024618P.
20 - OCT - 2000; 2000US - 024617P.
20 - OCT - 2000; 2000US - 024617P.
20 - OCT - 2000; 2000US - 024652P.
20 - OCT - 2000; 2000US - 024652P.
20 - NOV - 2000; 2000US - 024651P.
21 - NOV - 2000; 2000US - 024652P.
21 - NOV - 2000; 2000US - 024652P.
21 - NOV - 2000; 2000US - 024921P.
22 - 2000; 2000US - 0249265P.
23 - 2000S - 2000US - 0249268P.
24 - 2000; 2000US - 0249268P.
25 - DEC - 2000; 2000US - 025198P.
26 - DEC - 2000; 2000US - 025198P.
26 - DEC - 2000; 2000US - 025198P.
27 - NOV - 2000; 2000US - 025198P.
28 - DEC - 2000; 2000US - 025198P.
29 - DEC - 2000; 2000US - 025198P.
20 - 2000US - 2000US -
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SCI INC GENOME HUMAN (HUMA-) S Ruben SC, Barash ð Rosen

WPI; 2001-581633/65 N-PSDB; ABK43730.

preventing, additives n for diagnosing, and used as food New isolated nucleic acid encoding a protein treating or ameliorating medical conditions a preservatives

918; 837pp; English Claim 9; SEQ ID NO encoding molecule (I) The invention describes an isolated nucleic acid

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convel central nervous system protein. (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include cautoimmune diseases e.g. rheumatoid arthritis, hyperproliferative autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease and amplogenesis, nervous system disorders e.g. Alzheimer's disease and amplotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. daysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary dwarfism, cancers and disorders e.g. malignancies, ceptiblitary dwarfism, cancers and disorders e.g. malignancies, ceptiblitary disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
preparing a vaccine composition against Klebsiella pneumoniae.
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Best Local Similarity
Matches 5; Conser
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ABO61857
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neuroprotective; nootropic; antiparkinsonian; anticonvulsant;

KW antidiabetic; antirheumatic; antiarthritic; dermatological;
antiinflammatory; immunosuppressive; antithyroid; antianemic; vasotropic;
KW antiinflammatory; immunosuppressive; antibacterial; fungicide;
antiinflammatory; immunosuppressive; antibacterial; fungicide;
antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
KW antiparasitic; muscular; gynaecological; gastrointestinal; respiratory;
KW nephrotropic; litholytic; cytostatic; gene therapy; neural disorder;
KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;
My Alzheimer's disease; Parkinson's disease; heumatoid arthritis;
anyotrophic lateral sclerosis; multiple sclerosis;
munue system disorder; diabetes; rheumatoid arthritis; haemolytic anaemia;
KW inflammatory bowel disease; crohn's disease; infection;
M Hougal infection; hepatitis infection; bacterial infection;
KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW renal disorder; acute glomerulonephritis; pyelonephritis;
KW renal lithiasis; proliferative disorder; cancerous diseases; human.
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                                                                                               Gaps
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0
                                                               Length 262;
                                                                                              Indels
 Klebsiella pneumoniae polypeptide of the invention
                                                            Score 36; DB 7; I
Pred. No. 3.8e+02;
; Mismatches 0;
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24-FEB-2000; 2000US-0180628P.
24-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-01998123P.
19-MAY-2000; 2000US-0205515P.
07-JUN-2000; 2000US-0214886P.
30-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0215135P.
07-JUL-2000; 2000US-021680P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
11-JUL-2000; 2000US-0217496P.
26-JUL-2000; 2000US-0217496P.
                                                                                                                                                                                                                                                                                                                                        Novel human protein seq id 918.
                                                              100.0%;
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                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                               Conservative
                                                              Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                            18 HPPHG 22
                                                                                                                             1 HPPHG 5
                                 Sequence 262 AA;
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ADI54715
ID ADI54
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JS - 0.22526479

JS - 0.2252689

JS - 0.2252689

JS - 0.22524709

JS - 0.2257579

JS - 0.2257579

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JS - 0.2257599

JS - 0.237999

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JS - 0.2370379

JS - 0.2370379
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IS-02418069
IS-02466179
IS-02464759
IS-02464769
IS-02464779
IS-02464789
IS-02465239
1144-AUG
114
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The invention describes an isolated polypeptide comprising an amino acid sequence at least 90% identical to: a polypeptide fragment, domain, epitope, or full-length protein of any one of 607 amino acid sequences (I) described in the specification; a polypeptide fragment of (I), or the encoded sequence contained in (II), having biological activity; or a variant, allelic variant, or a species homologue of (I). The polypeptides and nucleic acid molecules are useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating medical conditions such as neural disorders, e.g. Alzheimer's disease, Parkinson's disease, Huntington's chorea, amyotrophic lateral sclerosis or multiple sclerosis, immune system disorders, e.g. diabetes, rheumatoid arthritis, systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides and nucleic acid molecules, useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating mediconditions e.g. neural disorders, reproductive disorders or infectious
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08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-024652P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024920P.
17-NOV-2000; 2000US-024921P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025198P.
08-DEC-2000; 2000US-025199P.
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N-PSDB; ADI54117.
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RUBEN S M.
BARASH S C.
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Gaps

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Length 262 Indels

Score 36; DB 8; 1 Pred. No. 3.8e+02; Mismatches 0;

1 100.0%; 5 Similarity 100.0%; 1 5; Conservative 0;

Query Match Best Local S Matches 5

medical

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Propionibacterium acnes immunogenic protein #12121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                  Propionibacterium acnes
                                                                                                                                                                                                                                                                       vaccinating against and treating acne vulgaris.
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N-PSDB; AASS9551.
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Best Local Similarity
Matches 5; Conserv
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                                                                                     WO200181581-A2
                                                                                                                                                                                                    Skeiky YAW,
                                                                                                       01-NOV-2001
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ID ABM4
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AC ABM4
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DT 20-0
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                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                          acid detection reagent for detecting 1000 or more
a and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                  Drosophila, developmental biology; cell signalling; insecticide;
pharmaceutical.
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                                                                                                                                Orosophila melanogaster polypeptide SEQ ID NO 26574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 36; DB 4; L
100.0%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                            Myers EW
                                                                          protein; 311 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; 324
                                                                                                                                                                                                                                                                                                           Li PWD,
                                                                                                                                                                                                                                        23-MAR-2001; 2001WO-US009231
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11-JUL-2000; 2000US-00614150
                                                                                                               entry)
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                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic a
genes from Drosophila
interactions.
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N-PSDB; ABL10697.
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                                                                        ABB66594 standard;
                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 HPPHG 106
                                                                                                                                                                                                                                                                                                           Venter JC, Adams
                   |||||
17 HPPHG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU51225 standard;
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       1 HPPHG
                                                                                                                                                                                                  WO200171042-A2.
                                                                                                                                                                                                                    27-SEP-2001
                                                                                                             26-MAR-2002
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                                                                                           ABB66594;
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                                                      RESULT 37
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                                                                ABB66594
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indela
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100.0%; Pred. No. 4.7e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Wang SS,
Carter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABM47744 standard; protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2000; 2000US-0199047P. 02-JUN-2000; 2000US-0208841P. 07-JUL-2000; 2000US-0216747P.
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ABU33219

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conciding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention and the polymucleotides (ABM35624-ABM64536) and to additionally encompasses expression vectors and host cells comprising a dditionally encompasses expression vectors and host cells comprising a polymucleotide of the invention; antibodies against polypeptides of the invention; fusion proteins comprising a polypeptide of the invention; a method for stimulating an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising T cells prepared via this method; a vaccine composition (comprising T cells populations, or polymucleotides, antibodies, fusion proteins, T cell populations cells that express the polypeptides, and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence represents a polypeptide predicted to be encoded by an ORF (open creading frame) contained within the P. acnes polymucleotides of the invention. Note: The sequence data for this patent did not form part of the murant form with the proposition and the polymucleotides are obtained in the protection of the polymucleotide predicted to be encoded by an ORF (open creading frame) contained within the P. acnes polymucleotides of the invention. Note: The sequence data for this patent did not form part of the manner of the polymucleotides are determined by the polymucleotides of the protection of the polymucleotides are de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 es to an isolated polynucleotide (ACF64435-ACF64733)
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l for diagnosing, preventing or treating acne vulgar
an immune response specific for a P. acnes protein.
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                                                                                                                                                                                                                                                                                                                                                                                                Maisonneuve JL;
Jones R, Carter
scnes predicted ORF-encoded polypeptide #12420
                                           Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
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Benson DR,
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                         y YAW, Persi
Jen S, Lode
--Douglass J;
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                                                                                                                                                                                                                                                       11-OCT-2002; 2002WO-US032727
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Zhang Y, Wang S, S
Barth B, Vallieve-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Propionibacter;
polypeptide, useful
or for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-381789/30
N-PSDB; ACF64480.
                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA COR
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 Propionibacterium
                                                                                                               Propionibacterium
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                                                                                                                                                              WO2003033515-A1
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rom WIPO at
                                                                                                                                                                                                          24-APR-2003
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ö Gaps ; 0 DB 6; Length 324; Indels 5. 4.7e+02; ches 0; 100.0%; Score 36; DE 100.0%; Pred. No. 4.7 ive 0; Mismatches Query Match Best Local Similarity Matches 5; Conser 1 HPPHG 5

protein; 475 AA. 258 RESULT 40 ABU33219 ID ABU33219 standard; XX HPPHG 254 g

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Antisense; prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or e for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                              ¥¥
                                                                                                                                                                              Ohlsen |
Forsyth |
                            Protein encoded by Prokaryotic essential gene #18746
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                                                                                                                                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                              Malone C,
Carr GJ,
                                                                                                                  21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                    21-MAR-2002; 2002WO-US009107
              (first entry)
                                                                                                                                                               (ELIT-) ELITRA PHARM INC.
                                                          Legionella pneumophila
                                                                                                                                                                              Zamudio C,
Trawick JD,
                                                                                                                                                                                                   WPI; 2003-029926/02.
N-PSDB; ACA37089.
                                                                         WO200277183-A2
                                                                                       03-OCT-2002
              19-JUN-2003
                                                                                                                                                                              Wang L,
Wall D,
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screening

Claim 25; SEQ ID NO 61143; 1766pp; English.

The first series acquences given in the specification where expression of the 611 antisense acquences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway to proliferation or that thinbits cellular proliferation of the gene product or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies or gans on which the test compound that inhibits epoilferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound, s activity; (11) a culture comprising strains in which the gene or proliferation of an organism. The acides required for proliferation of an organism. The antisense nucleic acide are useful for proliferation of an organism. The antisense nucleic acide acide in the proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes nucleic acide acide required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WNPO at the sequence as the present in the present in the present sequence of the p The invention relates to an isolated nucleic acid comprising

Sequence 475 AA;

Gaps .. 0 Indels 100.0%; Score 36; DB 6; I ilarity 100.0%; Pred. No. 6.7e+02; Conservative 0; Mismatches 0; Query Match Best Local Similarity Matches 5; Conserv

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1 HPPHG 5 |||||| 412 HPPHG 416

Search completed: June 15, 2005, 14:15:50 Job time : 92 secs

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Sequence 22219, A Sequence 25194, A Sequence 16944, A Sequence 22093, A Sequence 22093, A Sequence 39233, A Sequence 20521, A Sequence 743, App Sequence 41815, A Sequence 8, Appli Sequence 8, Appli

US-09-248-796A-22219 US-09-252-991A-16944 US-09-252-991A-16944 US-09-489-039A-9494 US-09-252-991A-22093 US-09-270-767-39233 US-09-270-767-54450 US-09-270-767-54450 US-09-270-767-54450 US-09-270-767-54450 US-09-270-767-54450 US-09-270-767-41835 US-09-640-211A-743 US-09-640-21A-74 US-09-640-21A-74 US-08-451-947-8 US-08-451-947-8 US-08-451-947-8 US-08-451-947-8 US-08-451-947-8 US-08-451-947-8

Run on:

us-10-074-225a-9.rai

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Sequence 9, Appli
Sequence 8374, Ap
Sequence 26799, A
Sequence 2424, A
Sequence 24069, A
Sequence 25, Appl
Sequence 29, Appl
Sequence 24991, A
Sequence 24991, A
Sequence 2630, Ap
Sequence 2630, Ap
Sequence 2630, Appl
Sequence 2630, Appl
Sequence 2630, Appl
Sequence 29, Appl
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Sequence 59, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 59, Appl
Sequence 50, Appl
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n2_6/ptodata/1/jaa/5B_COMB.pep:*
n2_6/ptodata/1/jaa/6A_COMB.pep:*
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n2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
n2_6/ptodata/1/jaa/PCTUS_COMB.pep:*
n2_6/ptodata/1/jaa/backfiles1.pep:*
5.1.6
Compugen Ltd
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US-09-252-991A-19788
US-09-252-991A-19788
US-09-252-991A-24069
US-09-252-991A-24069
US-08-041-886-25
PCT-US94-05277-2
US-08-973-551-19
US-08-973-551-19
US-08-488-379-29
US-08-475-399A-29
US-08-475-399A-29
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US-08-475-399A-29
US-08-488-379-29
US-08-488-379-29
US-09-270-767-57079
US-09-248-796A-26393
US-09-252-9990-5250
US-08-481-985B-59
US-08-469-486-50
US-08-469-658-50
                                                                                                                                                                                                          tisfying chosen parameters:
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version 5
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Maximum Match 100%
Listing first 45 summaries
                                         protein search, using sw model
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GenCore
(c) 1993
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Perfect
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Sequence 8374, Application US/09489039A

Sequence 8374, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APELICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 8374

LENGTH: 262

LENGTH: 262
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                                          RESULT 1
US-09-257-583-9
; Sequence 9, Application US/09257583A
; Patent No. 6429362
; GENERAL INFORMATION:
; APPLICANT: Crane, Virginia
; TITLE OF INVENTION: Family Of Maize PR-1 Genes And Promoters
; FILE REFERENCE: 5718-32, 035718/175219
; CURRENT APPLICATION NUMBER: US/09/257,583A
; CURRENT FILING DATE: 1999-02-25
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 231
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100.0%; Pred. No. 59;
ative 0; Mismatches
ALIGNMENTS
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Best Local Similarity 100.
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US-09-489-039A-8374
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Result No.

2

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RESULT 6
US-09-252-991A-24069
; Sequence 24069, Application US/09252991A
; Patent No. 6551795
; General No. 6551795
; General No. 6551795
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR PELLING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-07-27
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24069
; LENGTH: 1003
APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22424
LENGTH: 613
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US-09-041-886-25
i Sequence 25, Application US/09041886
j Patent No. 6235872
j GENERAL INFORMATION:
j APPLICANT: Bredesen, Dale E.
j APPLICANT: Rabizadeh, Sharroz
j TITLE OF INVENTION: Proapoptotic Peptides, Dependence
j TITLE OF INVENTION: Polypeptides and Methods of Use
j NUMBER OF SEQUENCES: 72
correspondence Address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                     Score 36; DB 4; I
Pred. No. 1.3e+02;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 36; DB 4; I Best Local Similarity 100.0%; Pred. No. 2.1e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22424
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US-09-252-991A-24069
                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Best Local Similarity 100.
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                                                                                                                                RESULT 3
US-09-252-991A-26799
; Sequence 26799, Application US/09252991A
; Sequence 26799, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US 60/074,788
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26799
; TYPE: PRT

TYPE: PRT

TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gequence 1978, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 19788

LENGTH: 516

TYPE: PRI
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ches 0;
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100.0%; Pred. No. 1.1
ive 0; Mismatches
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US-09-252-991A-22424
; Sequence 22424, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 5; Conserv
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| HPPHG 362
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Best Local Similarity
Matches 5; Conserv
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HPPHG 22
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                             HPPHG 5
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US-09-252-991A-19788
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STREET: 300
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PCT-US94-05277-2
Sequence 2, Application PC/TUS9405277
GENERAL INFORMATION:
APPLICANT: Bruskin, Arthur
APPLICANT: Bruskin, Arthur
APPLICANT: Jarcez, David E.
APPLICANT: Jarcez, David E.
APPLICANT: Jarces, Raren
APPLICANT: Cabrecky, James R.
TITLE OF INVENTION: Antibodies Specific for DCC Gene Product
FITLE OF INVENTION: Antibodies Specific for DCC Gene Product
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington
COUNTRY: USA
ZIP: 20001
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLADES: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-DOS/MS-DOS
SOFTWARE: Patentin Re-DOS/MS-DOS
SOFTWARE: Patentin Re-DOS/MS-DOS
SOFTWARE: Patentin Re-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: PCT/US94/05277
FILING DATE:
CLASSIFTCANTER:
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ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/OCKET NUMBER: 31,815

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CLEAR STATE.
CLEAR STETCATION:
NAME: REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42709
TELECOMMUNICATION INFORMATION:
TELEFAX: 202.508.9100
TELEK: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1447 amino acids
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INFORMATION FOR SEQ II
SEQUENCE CHARACTERIS
LENGTH: 1447 amir
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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Best Local Similarity
Matches 5; Conser
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Projection and active to the content of the content
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Score 30; DB 2; Length 16; Pred. No. 42; 0; Mismatches 0; Indels
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; Sequence 29, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
    APPLICANT: Urban, Robert G.
    APPLICANT: Chicz, Roman M.
    APPLICANT: Vignali, Dario A.A.
    APPLICANT: Vignali, Dario A.A.
    APPLICANT: Stern, Lawrence J.
    APPLI
NUMBER OF SEQUENCES: 274

CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STREET: 225 Franklin Street
CITY: Boston
STREET: 35.4

ZIP: 02110-2804

COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION SYSTEM: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: AUGUST 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
RECISTRATION NUMBER: 30,162
ATTORNEY/AGENT INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
TELEPAX: (617) 542-8906
TELEPAX: 167
TELENCOMMUNICATION INFORMATION:
TELEPAX: 1617) 542-8906
TELERAX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE: Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 4; Conserv
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                           T: Robert G. Urban
T: Roman M. Chicz
T: Dario A. A. Vignali
T: Mary L. Hedley
T: Lawrence J. Stern
T: Jack L. Strominger
INVENTION: IMMUNOMODULATORY PEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB;
Pred. No. 42;
0; Mismatches
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US-08-488-379-29
; Sequence 29, Application
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Roman M.
; APPLICANT: Roman M.
; APPLICANT: Dario A.
; APPLICANT: Lawrence
; APPLICANT: Jack L. F
; APPLICANT: Jack L. F
; TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino ació
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Best Local Similarity
Matches 4; Conserv
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TOPOLOGY: linear
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Gaps

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Gaps
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                                                                                                                                        Length 16;
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                                                                                                                                                                                                                                                                                                                                             PCT-US93-07545-29
; Sequence 29, Application PC/TUS9307545
; GENERAL INFORMATION:
    APPLICANT: Robert G. Urban
    APPLICANT: Roman M. Chicz
    APPLICANT: Dario A. A. Vignali
    APPLICANT: Mary L. Hedley
    APPLICANT: Lawrence J. Stern
    APPLICANT: Lawrence J. Stern
    APPLICANT: Lawrence J. Strominger
    TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
    NUMBER OF SEQUENCES: 273
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fish & Richardson
    STREET: 225 Franklin Street
    CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%; Score 30; DB 5; 100.0%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 617) 542-8906
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TWORM OR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
                                                                                                                                     Score 30; DB ; Pred. No. 42; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 42
Mismatches
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                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS:
                                                                        ; TOPOLOGY: linear
US-08-077-255A-29
                                                                                                                                     Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                TYPE: amino STRANDEDNESS
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US-09-270-767-57079
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           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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US-08-077-255A-29
US-08-077-255A-29
US-08-077-255A-29
US-08-077-255A-29
US-08-077-255A-29
US-08-077-255A-29
US-08-078-255A-29
US-08-05-25 Application US/08077255A
Patent No. 669661
GENERAL INPORMATION:
MACAT:
MAPPLICANT: Roman M. Chicz
APPLICANT: Lawrence J. Stern
APPLICANT: Lawrence J. Stern
APPLICANT: Lawrence J. Stern
APPLICANT: Lawrence J. Strominger
TITLE OF INVENTION: INWUNMONDULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS: 274
CORRESPONDENCE ADDRESS: 274
CORRESPONDENCE ADDRESS: 274
COUNTRY: Boaton US-N.
STREET: Boaton US-N.
STREET: Assaachusetts
COUNTRY: Boaton US-N.
STREET: Assaachusetts
CONFUTER: Boaton US-N.
STREET: MASSachusetts
COMPUTER: Base PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFWARE: Wordeferfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: August 11, 1992
ATTORNEY/ARENT INVERMATION:
APPLICATION NUMBER: 30,162
RECERPENCE CHARACTENISTICS:
SEQUENCE CHARACTERISTICS:

INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     red. No. 42;
Mismatches
                                                                                                                                                                                              BER: 34,819
NUMBER: 00246/168003
INFORMATION:
542-507
        ER: US/08/475,399A -JUN-1995
APPLICATION NUMBER: US/08/475,399
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 00246/16
TELECOMMUNICATION INFORMATION:
TELEFAX: 617/542-890
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
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Best Local Similarity
Matches 4; Conser
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TOPOLOGY:
US-08-475-399A-29
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                                                                                                                                                                                                                                                                                                               Section 15.27. Section US/09107433
Section 05.00744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
NUMBER OF SEQUENCES: 5206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                     Length 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107, 433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
                                                                                                     Score 30; DB '; Pred. No. 1.600; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...69
SEQUENCE DESCRIPTION: SEQ ID NO: 2788:
                                                                                           83.3%; Scu.
100.0%; Pr
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                         ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26393
                                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
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          LENGTH: 64
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                                                                                                                                                                                                                                                                               RESULT 18
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US-09-248-796A-24991
; Sequence 24991, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; RIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ. ID NOS: 28208
; SEQ. ID NO 24991
; LENGTH: 60
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US-09-248-796A-26393

US-09-248-796A-26393

Sequence 26393, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26393
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Sequence 57079, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57079
LENGTH: 46
TYPE: PRT
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Pred. No. 1.1e+02;
0; Mismatches 0;
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100.0%; Pre
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Best Local Similarity 100.
Matches 4; Conservative
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US-09-270-767-57079
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Best Local Similarity
Matches 4; Conserv
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| HPPH 12
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; ORGANISM: Candid
US-09-248-796A-24991
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Gaps

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Length 74;

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83.3%; Score 30; DB 4; L6
100.0%; Pred. No. 1.8e+02;
ive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24698
LENGTH: 74
                                                                                                                    TYPE: PRT CORGANISM: Pseudomonas aeruginosa US-09-252-991A-24698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.3%; 2
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunner
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Best Local Similarity
                                                                                                                                                                                                                                                                                       9 HPPH 12
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STREET: 13
CITY: Wash
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NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
1196.136

NUMBER: US/09/252,991A
1999-02-18
                      RESULT 19
US-09-107-532A-5630
; Sequence 5630, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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100.0%; Pred. No. 1.7e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iniello, Pamela Deneke
TION NUMBER: 40,489
E/DOCKET NUMBER: GTC-012
TION INFORMATION:
E: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc feature
(B) LŌCATION 1...71
PTION: SEQ ID NO: 5630:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ION NUMBER: 60/085,598
ATE: 14 May 1998
ION NUMBER: 60/051571
ATE: July 2, 1997
T INFORMATION:
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US-09-252-991A-24698
; Sequence 24698, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMIN; TITLE OF INVENTION: AERUGINOSA FOR DIAGNO; FILE REPERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecium
                                                                                                                                                                                                                                                                                                      BLE FORM:
PE: CD/ROM ISO9660
                                                                                                                                                                                                                      00 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (781)893-8277
ID NO: 5630:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTERISTICS
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YES
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                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABI
MEDIUM TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATI
APPLICATIO
FILING DAT
APPLICATIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RMATION FOR SEQ
SEQUENCE CHARAC
LENGTH: 71
                                                                                                                                                                                                                   STREET: 10
CITY: Walt
STATE: Mas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL: )
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 4; Conserv
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US-09-107-532A-5630
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TELEPHONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY
                                                                                                                                                                                                                                                                         COUNTRY:
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RESULT 21
US-08-484-905-59
; Sequence 59, Application US/08484905
; Patent No. 5976551
; Patent No. 5976551
; APPLICANT: Mottez, Estelle
; APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
; TITLE OF INVENTION: An Altered Major Histocompatibility
; TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Usir
; TITLE OF INVENTION: Determinant
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 90; 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWAKE: Patencin Release #1.0, Version #1.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE-1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: POLLEY, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                % 1300 I Street, N.W., Suite 700 Washington
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Pred. No.
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RESULT 24
US-09-513-999C-5250
; Sequence 5250, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; Patent No. 6783961
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
                   APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.3%; Score 30; DB 3; Length 98; 100.0%; Pred. No. 2.3e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                  ADDRESSE: Finnegan, Henderson, Farabow, Garrett & ADDRESSE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/117,575
FILING DATE: 06-JUN-1993
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                              Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
Kourilsky, Phillipe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 10v.
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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31 HPPH 34
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do, Jean-Pierre
sky, Phillipe
: Altered Major Histocompatibility Complex
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 Indels
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                                                                                                                                                                                                                           COMPUTED TITLE OF INVENTION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: Do.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION ATS
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAWE: Mevers Kennerth J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
 Mismatches
                                                                                                                                                                                  on US/08481985B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Estelle
do, Jean-Pierre
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o acids
4; Conservative
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                                                                                                                                   RESULT 22
US-08-481-985B-59
; Sequence 59, Application
; Patent No. 6011146
; GENERAL INFORMATION:
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US-08-370-476-59
; Sequence 59, Application;
; Patent No. 6153408
; GENERAL INFORMATION:
; APPLICANT: Abastado,
;
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INFORMATION FOR SEQ IE
SEQUENCE CHARACTERIS
LENGTH: 98 amino
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XGY: linear
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202-408
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Best Local Similarity
Matches 4; Conser
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31 HPPH 34
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31 HPPH 34
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MOLECULE TYPE:

US-08-481-985B-59
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                                                                                                                                                                                                                                                                                              RESULT 25
US-08-469-486-50
; Sequence 50, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thoegersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
TITLE OF INVENTION: proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 119;
                                                                                                                                                   Length 109;
                                                                                                                                                DB 4; Les
2.6e+02;
hes 0;
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100.0%; Pred. No. 2.8e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Thoegersen, Hans Christian
APPLICANT: Holtet, Thor Las
APPLICANT: Etzerodt, Michael
TITLE OF INVENTION: Improved method for the r
TITLE OF INVENTION: Improved method for the r
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02110-2804
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: PatentIn Release #1.0, Version
SOFTWARE: PatentIn S30
PRELICATION NUMBER: US/08/469,486
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/192,060
FILING DATE: February 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
NAME: Paul T. Clark
NAME: Paul T. Clark
NAME: Paul T. Clark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 617 542 5070

TELEFAX: 617 542 8906

TELEFAX: 617 542 8906

TELEFAX: 617 542 8906

TELEFAX: 119 580 ID NO: 50:

SEQUENCE CHARACTERISTICS

TYPP
                                                                                                                                                83.3%;
  NOS: 36681
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TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
AOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vative
                                                                                             sapiens
; NUMBER OF SEQ ID NOS:
; SOFTWARE: Patent.pm
; SEQ ID NO 5250
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Homo sapie
US-09-513-999C-5250
                                                                                                                                             Query Match
Best Local Similarity
Matches 4; Conser-
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Best Local Similarity
Matches 4; Conser
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RELATING TO PSEUDOMONAS
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Sequence 9494, Application US/09489039A

Sequence 9494, Application US/09489039A

Sequence 9494, Application US/09489039A

Setent No. 6610836

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 9494

LENGTH: 147
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 147

TYPE: PRT

TYPE
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Pred. No. 3.5e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 83.3%; Score 30; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0;
        Pred. No. 3.4e+02;
                                           Mismatches
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US-09-252-991A-22093
; Sequence 22093, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 16944, Application US/09252991A; Patent No. 6551795
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16944
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        100.08;
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Best Local Similarity 80.0
                                           4; Conservative
  Best Local Similarity
Matches 4; Conserv
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                                                                                                                       1 HPPH 4
                                                                                                                                                                                                                                                                                                         RESULT 30
US-09-252-991A-16944
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US-09-248-796A-22219
i Sequence 22219, Application US/09248796A
j Patent No. 6747137
j GENERAL INFORMATION:
i TITLE OF INVENTION:
i TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
i TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
i TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
i CURRENT APPLICATION NUMBER: US/09/248,796A
i CURRENT FILING DATE: 1999-02-13
i PRIOR APPLICATION NUMBER: US 60/074,725
j PRIOR APPLICATION NUMBER: US 60/096,409
j PRIOR FILING DATE: 1998-08-13
i NUMBER OF SEQ ID NOS: 28208
j SEQ ID NO 22219
j TYPE: PRT
TYPE: PRT
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US-09-252-991A-25194
; Sequence 25194, Application US/09252991A
; Sequence 25194, Application US/09252991A
; Sequence 25194, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; ATTLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US 60/074,788
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25194
; LENGTH: 145
; TYPE: PRT

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Pred. No. 3.3e+02;
0; Mismatches 0;
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100.0%; Pred. No. 3.3e+02;
vative 0; Mismatches 0;
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US-09-252-991A-25194
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; SEQ ID NO 6561
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6561
                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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OTHER INFORMATION:
09-248-796A-22219
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HPPH 14
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FEATURE:
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us-10-074-225a-9.rai

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Score 30; DB (; Pred. No. 4e+0); Mismatches
                                                                ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-39233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-54450
         TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
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Best Local Similarity 100.0%;
Matches 4; Conservative 0
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity
Matches 4; Conserv
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76 HPPH 79
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22093
LENGTH: 162
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Nucleic acids and proteins of Drosophila melanogaster: Reference: 7326-094

NUMBER: US/09/270,767
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                                                                                                                                                                                                                                                                                                                                            Length 162;
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APPLICANT: Stanton, Lawrence A.
APPLICANT: Stanton, Lawrence A.
APPLICANT: Damm, Deborah L.
APPLICANT: Damm, Deborah L.
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: differentially expressed genes in d:
FILE REFERENCE: SCIOS.011A
CURRENT APPLICATION NUMBER: US/09/461,912A
CURRENT FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,008
PRIOR FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSEQ for Windows Version 4.0
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3.9e+02;
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US-09-270-767-39233
; Sequence 39233, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and pro; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39233
; LENGTH: 173
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100.0%;
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Best Local Similarity
Matches 4; Conserv
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Patent No. 6709855
GENERAL INFORMATION:
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Best Local Similarity
Matches 4; Conserv
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US-09-252-991A-22093
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US-09-461-912A-47
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LENGTH: 169
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Sequence 24810, Application US/09252991A

Sequence 24810, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                           US-09-270-767-54450

; Sequence 54450, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 54450
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
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Length 173;
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100.0%; Pred. No. 4.1e+02;
iive 0; Mismatches 0;
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                                                                                               ## Sequence 2820, Application US/09252991A
## Patent No. 6551795
## GENERAL INFORMATION:
## APPLICANT: Marc J. Rubenfield et al.
## TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
## TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## TILE REFERENCE: 107196.136
## CURRENT APPLICATION NUMBER: US/09/252,991A
## CURRENT FILING DATE: 1999-02-18
## PRIOR APPLICATION NUMBER: US 60/074,788
## PRIOR APPLICATION NUMBER: US 60/094,190
## PRIOR PILING DATE: 1998-07-27
## NUMBER OF SEQ ID NOS: 33142
## SEQ ID NO 28220
## LENGTH: 180
## TYPE: PRI
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US-09-252-991A-20521

i Sequence 20521, Application US/09252991A

j Patent No. 6551795

i GENERAL INFORMATION:

i TITLE OF INVENTION:

I TITLE OF INVE
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o. 4.2e+02;
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; Sequence 743, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CAGANISM: Pseudomonas aeruginosa
US-09-252-991A-20521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
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RESULT 37
US-09-252-991A-28220
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RESULT 40
US-09-270-767-41835
; Sequence 41835, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; TITLE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41835
; LENGTH: 203
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                      Length 200;
TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Modification of Gene Transcription FILE REFERENCE: 11000.1021C1U CURRENT APPLICATION NUMBER: US/09/640,211A CURRENT FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 2368 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 743 LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                      Query Match 83.3%; Score 30; DB 4; Lo Best Local Similarity 100.0%; Pred. No. 4.6e+02; Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 15, 2005, 14:24:20 Job time: 24.5 secs
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                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Eucalyptus grandis
US-09-640-211A-743
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GenCore version 5.1.6
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protein search, using sw model OM protein

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June 15 Run on:

, 2005, 14:21:52; Search time 79.75 Seconds (without alignments) 24.034 Million cell updates/sec

US-10-074-225A-9 36

1 HPPHG Title: Perfect score: Sequence: Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

seqs, 383334425 residues 1710399 Searched:

hits satisfying chosen parameters: of Total number

2000000000 seq length: seq length: Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

| cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/BCT\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
| cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Sequence 9, Appli Sequence 41108, A Sequence 338760, Sequence 833, App Sequence 833, App Sequence 833, App Sequence 345170, Sequence 6, Appli Sequence 149766, Sequence 149766, Description 14 US-10-074-225A-9 9 US-09-864-761-41108 16 US-10-425-115-338760 9 US-09-764-869-833 14 US-10-091-504-833 15 US-10-227-577-833 15 US-10-424-599-200189 16 US-10-424-599-149766 15 US-10-424-599-149766 15 US-10-424-599-149766 Length DB 520 200 533 63 63 76 92 101 112 Query Score 11098765432 Result No.

equence 137, connect 17951 equence 26174 equence 42907 equence 29311	Sequence 249025, Sequence 255234, Sequence 251226, Sequence 222089, Sequence 317091,	Sequence 11/204, Sequence 64276, A Sequence 918, App Sequence 64304, A Sequence 15548, Sequence 15548,	Sequence 70512, A Sequence 61143, A Sequence 106725, Sequence 3, Appli Sequence 200249, Sequence 19, Appl	Sequence 40555, A Sequence 47241, A Sequence 46, Appl Sequence 263123, Sequence 17944, A Sequence 17955, Sequence 17264, Sequence 129, App
.0-023-896-1 .0-437-963-1 .0-425-115-2 .0-425-114-4	0025 0024 001 001 001	US-10-43/-963-11/204 US-10-425-114-64276 US-09-76-875-918 US-10-425-114-64304 US-10-425-115-218724 US-10-437-963-175538	512 11143 6725 0249	US-U9-864-761-40555 US-09-864-761-47241 US-10-022-750-46 US-10-425-115-263123 US-10-424-599-159525 US-10-424-599-177264 US-10-415-383-9
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## ALIGNMENTS

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Sequence 9, Application US/10074225A
; Publication No. US20030082740A1
; GENERAL INFORMATION:
; APPLICANT: DONATE, Fernando
; APPLICANT: PLUNKETT, Maxian L
; APPLICANT: PLUNKETT, MAXIAN D
; TITLE OF INVENTION: ANTI-TUMOR AGENT
; TITLE OF INVENTION: ANTI-TUMOR AGENT
; TITLE OF INVENTION: ANTI-TUMOR AGENT
; TILLE OF INVENTION: ANTI-TONA AGENT
; TILLE OF INVENTION UNBER: US/10/074,225A
; CURRENT APPLICATION NUMBER: US 60/268,370
; FILE REFERENCE: 2001-02-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PATENTIN VEXBION 3.1
; FEATURE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Peptide US-10-074-225A-9
US-10-074-225A-9
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ö Indels Length 100.0%; Score 36; DB 14; 100.0%; Pred. No. 1.5e+06; rative 0; Mismatches 0; Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative

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Gaps

1 HPPHG 5 HPPHG ð g us-10-074-225a-9.rapb

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US-10-425-115-338760

i Sequence 338760, Application US/10425115

i Publication No. US20040214272A1

i GENERAL INFORMATION:

j APPLICANT: La Rosa, Thomas J.

i APPLICANT: Ea Nosa, Thomas J.

j APPLICANT: Ea Vorgwei

j TITLE OF INVENTION: Plants

j TITLE OF INVENTION: Plants

j TITLE OF INVENTION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: US/10/425,115

j CURRENT FILING DATE: 2003-04-28

j TYPE: PRT

j ORGANISM: Zea mays

j TYPE: PRT

j OTHER INFORMATION: Clone ID: MRT4577_72114C.1.pep
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-869-833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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LOCATION: (50)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
NAME/KEY: SITE
LOCATION: (55)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
NAME/KEY: SITE
LOCATION: (58)
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Sequence 833, Application US/09764869

Patent No. US20020061521A1

GENERAL INFORMATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC007

CURRENT APPLICATION NUMBER: US/09/764,869

CURRENT FILING DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper

NUMBER OF SEQ ID NOS: 2442

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 833

LENGTH: 63
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                       APPLICANT: Fent, Snarron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-00-04
PRIOR PELING DATE: 2000-00-04
PRIOR FILING DATE: 2000-00-04
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
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EXPRESSED IN PLACENTA, SIGNAL = 2.2
EXPRESSED IN HEART, SIGNAL = 1.5
EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
EXPRESSED IN BRAIN, SIGNAL = 1.3
EXPRESSED IN BONE MARROW, SIGNAL = 1.3
EXPRESSED IN LUNG, SIGNAL = 0.86
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NUMBER: PCT/USO1/00661

2001-01-30

NUMBER: PCT/USO1/00670

2001-01-30

VUMBER: US 60/234,687

2000-09-21

NUMBER: US 09/608,408

2000-06-30
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001-01-30
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:001-01-30
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:001-01-30
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                         RESULT 2
US-09-864-761-41108
; Sequence 41108, Application US/09864761
; Patent No. US20020048763A1
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                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
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5; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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APPLICATION NUM
FILING DATE: 20
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PRIOR FILING DATE: 20
NUMBER OF SEQ ID NOS:
SOFTWARE: Annomax Seq
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APPLICATION NU
FILING DATE: 2
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LENGTH: 20
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Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 833
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RESULT S
US-10-091-504-833

Sequence 833, Application US/10091504

Publication No. US20030059908A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC007C1

CURRENT APPLICATION NUMBER: US/10/091,504

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2442

Prior Application removed - See File Wrapper or Palm

SOFTWARE: PatentIn Ver. 2.0

SOFTWARE: PAT

LENGTH: 63

TYPE: PRT

ORGANISM: Homo sapiens
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Nucleic Acids, Proteins, and Antibodies
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PC007C2

CURRENT APPLICATION NUMBER: US/10/227,577

CURRENT FILING DATE: 2002-08-26

PRIOR FILING DATE: 2002-03-07

PRIOR FILING DATE: 2001-01-17

PRIOR FILING DATE: 2001-01-17

PRIOR PILING DATE: 2000-01-31

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-04

PRIOR PILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-02-04

PRIOR FILING DATE: 2000-06-28

PRIOR FILING DATE: 2000-06-28

PRIOR APPLICATION NUMBER: 60/217,487

PRIOR FILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-06-14

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-11

PRIOR PILING DATE: 2000-07-16

PRIOR PILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 60/220,963

PRIOR PILING DATE: 2000-07-26

PRIOR PILING DATE: 2000-07-26

PRIOR PILING DATE: 2000-07-17

PRIOR APPLICATION NUMBER: 60/225,758

PRIOR PILING DATE: 2000-07-17

PRIOR PILING DATE: 2000-07-26

PRIOR PILING DATE: 2000-07-17

PRIOR PILING DATE: 2000-07-17

PRIOR PILING DATE: 2000-07-17
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APPLICATION NUMBER: 60/225,447
FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (50)
OTHER INFORMATION: Xaa e
NAME/KEY: misc_feature
LOCATION: (55)
OTHER INFORMATION: Xaa e
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LOCATION: (58)
CTHER INFORMATION: Xaa
US-10-091-504-833
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26 HPPHG
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US-10-227-577-833
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and Other Molecules Associated With
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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LOCATION: (55)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
FEATURE:
NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (50)
OTHER INFORMATION: Xaa equals any of the naturally occurring
FEATURE:
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                                                                                                                                                                                                                                                                                                                       Length 63
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100.0%; Pred. No. 1.1e+02;
.ive 0; Mismatches 0; Indels
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US-10-424-599-200189
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 200189, Application US/10424599;
Publication No. US20040031072A1;
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and
TITLE OF INVENTION: Plants and Uses Thereof for F;
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(76)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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26 HPPHG 30
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040058365A1 LI:180252.16.orf2:2001JAN12
US-10-466-164-37
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APPLICANT: INCRNATION:
APPLICANT: LINCOLM, Stephen E; ALTUS, Christina M;
APPLICANT: LINCOLM, Stephen E; ALTUS, Christina M;
APPLICANT: DUFOCK, Gerard E; JACKSON, Jennifer L;
APPLICANT: JONES, Anisea L; DAM, Tam C;
APPLICANT: JONES, Anisea L; DAM, Tam C;
APPLICANT: LIU, Tommy F; HARIS, Bernard;
APPLICANT: FLORES, Vincent Z; DAFFO, Abel;
APPLICANT: GLANG, Simon C; GERSTIN, JT., Edward H;
APPLICANT: LERALTA, Careyna H; DAVID, Marie H;
APPLICANT: LONG MOBER: US 60/261,865
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-17
PRIOR PRIOR
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                                   OTHER INFORMATION: Clone ID: PAT_MRT3847_106260C.1.pep
                                                                                                           100.0%; Score 36; DB 15;
100.0%; Pred. No. 1.8e+02;
iive 0; Mismatches 0;
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/10466164 Publication No. US20040058365A1 GENERAL INFORMATION:
                                                                                                           Query Match
Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 5; Conserv
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                                         ; OTHER INFORMALLOW
US-10-424-599-149766
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US-10-466-164-37
          FEATURE:
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Sequence 6, Application US/10074225A

Publication No. US20030082740A1

GENERAL INFORMATION:

APPLICANT: DONATE, Fernando

APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

APPLICANT: HARRIS, Scott

TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC

TITLE REFERENCE: 38342-178463

TITLE REFERENCE: 38342-178463

TURRENT APPLICATION NUMBER: US/10/074,225A

CURRENT PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/268,370

PRIOR FILING DATE: 2001-02-14

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.1
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Sequence 149766, Application US/10424599
Sequence 149766, Application US/10424599
Sequence 149766, Application US/10424599
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 149766
LENGTH: 112
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Pred. No. 1.7e+02;
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100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
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; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 345170
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                              Similarity 100
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||||
|HPPHG 63
                                                                                                                                                                                                                                             OTHER INFORMATION:
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US-10-424-599-149766
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US-10-074-225A-6
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TYPE: PRT
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Best Local S
Matches 5
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Sequence 42907, Application US/10425114

Sequence 42907, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Bord Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Number and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 42907

LENGTH: 135
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; Sequence 203118, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)
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                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CORGANISM: Zea mays
FEATURE:
COTHER INFORMATION: Clone ID: MRT4577_170323C.1.pep
US-10-425-115-261744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 36; DB 16;
100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 36; DB 15;
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: 700570105_FLI.pep
US-10-425-114-42907
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.

Matches 5; Conservative
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US-10-425-115-293118
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Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Wu, Wei

APPLICANT: Buckharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Wu, Wei

APPLICANT: Buckharov, Andrey A.

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 179511

LENGTH: 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 118;
                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Victor Roschke
TITLE OF INVENTION: 29 Human Cancer Associated Proteins
FILE REFERENCE: PA004P1
CURRENT APPLICATION NUMBER: US/10/023,896
CURRENT APPLICATION NUMBER: US/10/023,896
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: PCT/US00/23794
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 2000-08-30
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 137
LENGTH: 118
TYPE: PRT
CORGANISM: Homo sapiens
US-10-023-896-137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone ID: PAT_MRT4530_76967C.1.pep
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100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0;
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US-10-425-115-261744
; Sequence 261744, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
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Best Local Similarity 100
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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96 HPPHG 100
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US-10-437-963-179511
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US-10-437-963-179511
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Sequence 26524, Application US/10425115
Sequence 26524, Application US/10425115
Sequence 26524, Application US/10425115
Sequence 265234
Sequence 265234, Application US/10425115
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Expon, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE OF INVENTION WIMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 265234
LENGTH: 168
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100.0%; Pred. No. 2.4e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Clone ID: MRT4577_30403C.1.pep
                                                                                                                                                                                                                                                                                                                                                unsure at all Xaa locations
     NUMBER: US/10/425,115
2003-04-28
3: 369326
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thomas J., David K.
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CURRENT APPLICATION NC
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 293118
LENGTH: 150
TYPE: PRT
ORGANISM: Zea maye
                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(150)
OTHER INFORMATION: ur
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Best Local Similarity
Matches 5; Conserv
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HPPHG 55
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Best Local S
Matches 5
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RESULT 20
US-10-424-599-222089

i) Sequence 222089, Application US/10424599

j) Publication No. US20040031072A1

j) Rublication No. US20040031072A1

j) APPLICANT: La Rosa Thomas J

j) APPLICANT: Cao Yongwei

j) APPLICANT: Cao Yongwei

j) TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

j TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

j FILE REFERENCE: 38-21(53223)B

j) CURRENT APPLICATION NUMBER: US/10/424,599

j) CURRENT FILING DATE: 2003-04-28

j) NUMBER OF SEQ ID NOS: 285684

j) SEQ ID NO 222089

j) LENGTH: 181

m. LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
US-10-425-115-251226

Sequence 251226, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

CURRENT APPLICANTON: Plants

CURRENT APPLICANTON: Plants

CURRENT APPLICANTON: Sea mays

FEATURE:

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 251226

LENGTH: 170

LENGTH: 170

TYPE: PRT

CREATURE:

NAME/KEX: unsure

LOCATION: (1) .. (170)

COTHER INFORMATION: Unsure at all Xaa locations

FEATURE:

FEATURE:

COTHER INFORMATION: Unsure at all Xaa locations

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COTHER INFORMATION: Unsure at all Xaa locations

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                                                                                                                                                                                                                                                                Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_160703C.1.pep
US-10-425-115-251226
                                                                                                                                                                                                                                                             100.0%; Score 36; DB 16;
100.0%; Pred. No. 2.6e+02;
iive 0; Mismatches 0;
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_1734C.1.pep
US-10-425-115-265234
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Best Local Similarity 100.
Matches 5; Conservative
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Matches 5; Conserv
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us-10-074-225a-9.rapb

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Conservative
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ORGANISM: Oryza sativa
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Best Local Similarity
Matches 5; Conserv
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ORGANISM: Zea mays
FEATURE:
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US-10-425-115-317091

i Sequence 317091, Application US/10425115

j Publication No. US20040214272A1

j GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yongwei
    TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants
    TITLE OF INVENTION NUMBER: US/10/425,115
    CURRENT FILING DATE: 2003-04-28
    NUMBER OF SEQ ID NOS: 369326
    SEQ ID NO 317091

LENGTH: 230
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US-09-840-479-9
i Sequence 9, Application US/09840479
j Patent No. US20010025380A1
j GENERAL INFORMATION:
i APPLICANT: Crane, Virginia
i TITLE OF INVENTION:
i FILE REFERENCE: 5718-32, 035718/175219
i CURRENT APPLICATION NUMBER: US/09/840,479
i CURRENT FILING DATE: 2001-04-23
j PRIOR FILING DATE: 1999-02-25
i NUMBER OF SEQ ID NOS: 37
i SOFTWARE: Patentin Ver. 2.0
i LENGTH: 231
i TYPE: PRT
i ORGANISM: Zea mays
    Length 181;
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100.0%; Pred. No. 3.4e+02;
:ive 0; Mismatches 0; Indels
                                     Indels
  Score 36; DB 15;
Pred. No. 2.7e+02;
); Mismatches 0;
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100.0%; Pred. No. 3.4e+02;
vative 0; Mismatches 0;
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    100.0%;
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Best Local Similarity 100.
Matches 5; Conservative
Query Match
Best Local Similarity 100
Matches 5; Conservative
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; OTHER INFORMATION: un
; FEATURE:
; OTHER INFORMATION: C1
US-10-425-115-317091
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Best Local Similarity
Matches 5; Conserv
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|HPPHG 27
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US-09-840-479-9
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ORGANISM: Zea mays
                                                                      1 HPPHG 5
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Sequence 64276, Application US/10425114
; Sequence 64276, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Rosen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313) B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; LENGTH: 260
; LENGTH: 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
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US-10-437-963-117204
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US-10-425-114-64276
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TYPE: PRT
ORGANISM: Zea mays
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 64304
LENGTH: 264
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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                                                                   al.
Nucleic Acids, Proteins, and Antibodies
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                                                       APPLICANT: Rosen et al.

APPLICANT: Rosen et al.

ITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ02

CURRENT APPLICATION NUMBER: US/09/764,875

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALI

NUMBER OF SEQ ID NOS: 1249

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 918

LENGTH: 262

TYPE: PRT

ORGANISM: Homo sapiens

US-09-764-875-918
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Publication No. US20040034888A1
GENERAL INFORMATION:
Sequence 918, Application US/09764875 Publication No. US20040018969A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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HPPHG 21
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
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US-10-425-115-218724
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Sequence 155484, Application US/10437963

Sequence 155484, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rovalic, David K.

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Wu, Wei

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 155484

LENGTH: 313
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
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US-10-437-963-155484
                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: MRT4577_131068C.1.pep
US-10-425-115-218724
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100.0%; Pred. No. 3.8e+02;
ative 0; Mismatches 0;
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100.0%; Pred. No. 4.4e+02;
:ive 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 218724
LENGTH: 265
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US-10-437-963-173538
; Sequence 173538, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Oryza sativa
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us-10-074-225a-9.rapb

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TYPE: PRT
ORGANISM: Oryza sativa
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i Sequence 70512, Application US/10425114

j Publication No. US20040034888A1

j Publication No. US20040034888A1

j Publication No. US2004003488BA1

j Publicant: Invormation:

j APPLICANT: Liu, Jingdong

j APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E

j APPLICANT: Tabaska, Jack E

j APPLICANT: Tabaska,
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
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                                                                                                                                                                                                                                                                                                                                           Length 346;
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                                                                                                                                                                                                                                   Clone ID: PAT_MRT4530_71566C.1.pep
                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 36; DB 16; Best Local Similarity 100.0%; Pred. No. 4.8e+02; Matches 5; Conservative 0; Mismatches 0;
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2003-05-14
: 204966
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Chlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS
SEQ ID NO 173538
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                   ; OTHER INFORMATION: US-10-437-963-173538
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US-10-282-122A-61143
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Bi, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 106725
LENGTH: 517
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US-10-437-963-106725
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100.0%; Pred. No. 6.7e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 36; DB 15;
100.0%; Pred. No. 6.3e+02;
iive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-09
PRIOR FILING DATE: 2001-02-09
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US-10-282-122A-61143
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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CTHER INFORMATION: determining region of Fv region of an;
CTHER INFORMATION: immunoglobulin
US-10-417-895A-39
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Sequence 39, Application US/10417895A

Publication No. US20040033569A1

GENERAL INFORMATION:
APPLICANT: Crea, Roberto
APPLICANT: Cappuccilli, Guido
TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
FILE REFERENCE: 1551.2002-001

CURRENT APPLICATION NUMBER: US/10/417,895A

CURRENT APPLICATION NUMBER: 60/373,686

PRIOR FILING DATE: 2002-04-17

NUMBER OF SEQ ID NOS: 86

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 39

LENGTH: 15

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.3%; Score 30; DB 10; I Best Local Similarity 100.0%; Pred. No. 1.5e+06; Matches 0; Mismatches 0;
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ORGANISM: Artificial Sequence
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US-10-417-895A-39
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                                                                           Sequence 3, Application US/10074225A;
Publication No. US20030082740A1
GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: PLUNKETT, Marian L
APPLICANT: PLUNKETT, MATIAN L
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC
TITLE OF INVENTION: ANTI-TUMOR AGENT
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT FILING DATE: 2002-02-14
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LINGTH: 526
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APPLICANT: Kovalic, David K.
APPLICANT: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Applicant: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 200249
LENGTH: 1498
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Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.8e+02;
tive 0; Mismatches 0;
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Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT CORGANISM: Lepus americanus US-10-074-225A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 5; Conserv
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|HPPHG 357
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; OTHER INFORMATION:
US-10-437-963-200249
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                                              RESULT 33
US-10-074-225A-3
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US-09-827-345-19
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| Sequence 47241, Application US/09864761 |
| Sequence 47241, Application US/0266311 |
| Septiconn: Barbar David N. |
| APPLICANN: Barbar David N. 
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EXPRESSED IN LUNG, SIGNAL = 0.47
EXPRESSED IN ADULT LIVER, SIGNAL = 0.41
EST_HUMAN HIT: H23753.1, EVALUE 8.00e+00
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  4; Conservative
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: EXPRE;
OTHER INFORMATION: EXPRE;
OTHER INFORMATION: EXPRE;
OTHER INFORMATION: EST H
US-09-864-761-47241
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N: EXPRESSED IN LUNG, SIGNAL = 1.7

N: EXPRESSED IN PLACENTA, SIGNAL = 2.8

N: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6

N: EXPRESSED IN HELA, SIGNAL = 4.6

N: EXPRESSED IN HEART, SIGNAL = 2.9

N: EXPRESSED IN FETAL LIVER, SIGNAL = 3.8

N: EXPRESSED IN BRAIN, SIGNAL = 2.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 3.6

N: EXPRESSED IN BONE MARROW, SIGNAL = 3.6

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N: EXPRESSED IN BONE MARROW, SIGNAL = 3.6
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2001-01-30
10MBER: PCT/USO1/00661
2001-01-30
10MBER: PCT/USO1/00670
2001-01-30
10MBER: US 60/234,687
2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TUMBER: PCT/US01/00664
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UMBER: PCT/US01/00669
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Pred. No.
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001-01-30
MBER: PCT/USO1/00667
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MMBER: PCT/US01/00668
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001-01-30
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JMBER: US 09/632,366
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IMBER: US 60/236,359
1000-09-27
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001-01-29
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IMBER: GB 24263.6
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ORGANISM: Homo sapiens
FEATURE:
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NUMBER OF SEQ ID NOS:
SOFTWARE: Annomax Sequised ID NO 40555
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RESULT 40
US-10-425-115-263123
; Sequence 263123, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Royalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NOS: 369326
; SEQ ID NO 263123
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Zea mays
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                                                                                                                                   Sequence 46, Application US/10092750
; Sequence 46, Application US/10092750
; Publication No. US20030032157A1
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Alpin, Julia
; APPLICANT: Wright, Martin C.
; TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
; FILE REFERENCE: 50036/05002
; CURRENT FILING DATE: 2002-03-07
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/274,526
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-46
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Job time : 80.75 secs
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| HPPH 22
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34 HPPH 37
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GenCore version 5.1.6
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- protein search, using sw model OM protein

June 15, 2005, 14:04:57; Search time 17.5 Seconds (without alignments) 27.491 Million cell updates/sec Run on:

US-10-074-225A-9 36 1 HPPHG S

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

SUMMARIES	Description	4 hypothetical prote		pathogenesis					tumor Bu	early	hypotheti	hypothetical	hypothetical	hypothetical		1 hypothetical prote				hypothetical	conserved hyp	hypothetical	proline-rich	conserved hyp		0	9 peripheral benzoda		5 peripheral benzodi	
SOS	ID	F72674		T06168	G72454	T46814	B95419	151669	A54100	ERAD64	H71311	T47876	A03861	B72629	866936	T17301	MGMSB2	B72546	T46369	A05160	B69320	F71070	839206	A99226	C84299	A97760	JE0149	138724	I38105	
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	Length	118	176	235	251	470	470	1427	1447	61	73	107	112	113	113	115	119	121	122	125	126	141	148	157	159	167	169	169	169	
dip	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	83.3	83.3	83.3	83.3	83.3	83.3	83.3	83.3			•	m	m	m	•	щ	m	83.3		n	
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RESULT 2
F82478
hypothetical protein VCA0284 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Accession: F82478
C;Accession: F82478
C;Accession: F82478
C;Accession: F82478
C;Accession: F82478
C;Accession: F82478
C;Accession: PG2478
C;Accession: PG2478
C;Accession: D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P. I. Neture 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82478
A;Genetics: UNIPROT:Q9KMPO; GB:AE004368; GB:AE003853; NID:g9657677; FIDN:AAF96193
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0284
A;Map position: 2

glycine/proline-ri uclacyanin II [imp formylmethionine d conserved hypothet hypothetical prote hypothetical prote hypothetical prote protein T24A6.3 [i conserved hypothet hypothetical prote eHAND - mouse calf thymus ribonu CHT28 protein - ch conserved hypothet hypothetical prote hypothetical prote	ALIGNMENTS	PRESULT 1  PY2674  Pypothetical protein APE0819 - Aeropyrum pernix (strain K1)  C; Sgecies: Aeropyrum pernix  C; Sgecies: Aeropyrum pernix  C; Sgecies: Aeropyrum pernix  C; Sgecies: Aeropyrum pernix  C; Accession: F72674  F; Kiawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha A.; H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kudoh, Y.; Yamazaki,
T51469 T52409 B97784 AC2903 H69937 B84315 D75004 C89005 AF2901 H97676 AF3100 AF310 AF31	ALIC	No de la
0000000000000000		- Ae HO: S , S , S , S , S , S , S , S , S , S
1144 2003 2003 2003 2004 2009 2000 2000 2000		APE0819 - Aer  pernix  sequence_rev' ino, Y.; Horr i Masuda, S.; 999 come sequence 72450; MUID:9 WA MIPROT:Q9YDUS :: strain K1 rum pernix hy rum pernix hy ty 100.0%; ervative (
$\begin{array}{c} \mathbf{c} & $		RESULT 1  F72674 hypothetical protein APE0819 - Aeropyrum per C; Species: Aeropyrum pernix C; Species: Aeropyrum pernix C; Date: 20-Aug-1999 #sequence_revision 20-Au C; Accession: F72674 R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; awa, H.; Takamiya, M.; Masuda, S.; Funahashi DNA Res. 6, 33-101, 1999 A; Title: Complete genome sequence of an aero A; Reference number: A72450; MUID:99310339; EA; Accession: F72674 A; Reference number: A72450; MUID:99310339; EA; Accession: F72674 A; Reference number: A72450; MUID:99310339; EA; Residues: 1-118 < KAW> A; Residues: 1-118 < KAW> A; Experimental source: strain K1 C; Genetics: C; Genetics: C; Superfamily: Aeropyrum pernix hypothetical
		ical property of the control of the
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		RESULT 1 F72674 hypothetical protein C; Species: Aeropyrum C; Date: 20-Aug-1999 # C; Accession: F72674 A; Reference number: A A; Accession: F72674 A; Complete gen A; Reference number: A A; Accession: F72674 A; Cossion: F72675 A; Cossion: F72

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A; Accession: B95419
A; Status: preliminary
A; Ratus: preliminary
A; Ratus: preliminary
A; Ratus: preliminary
A; Molecule type: DNA
A; Residues: 1-470 < KUR>
A; Cross-references: UNIPROT: Q923R2; GB: AE006469; PIDN: AAK65916.1; PID: g14524429; GSPDB: GA
A; Experimental source: strain 1021, megaplasmid pSymA
A; Experimental source: strain 1021, megaplasmid pSymA
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
Bela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 23, 668-672, 2001
A; Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidher, S.; Wells, D.H.; Wong, K.; Yeh, K.C
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diaminobutyrate-pyruvate transaminase (EC 2.6.1.46) RhbA [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Species: Sanorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: B95419
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
:; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tumor suppressor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51669
R;Pierceall, W.E.; Reale, M.A.; Candia, A.F.; Wright, C.V.; Cho, K.R.; Fearon, B.R. Dev. Biol. 166, 654-665, 1994
A;Title: Expression of a homologue of the deleted in colorectal cancer (DCC) gene in the
                                      A; Accession: T46814
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-470 <LYN>
A; Cross-references: UNIPROT:Q9Z3R2; EMBL:AF110737; PIDN:AAD09412.1
A; Experimental source: strain 2011
C; Genetics:
A; Gene: rhbA
C; Function:
A; Pathway: siderophore biosynthesis
C; Superfamily: beta-alanine-pyruvate transaminase
C; Keywords: aminotransferase
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A,Genome: plasmid
C,Superfamily: beta-alanine-pyruvate transaminase
C,Keywords: aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 36; DB
100.0%; Pred. No. 40;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 5; Conservative
            A; Reference number: Z24097
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406 HPPHG 410
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IS1669
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C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C; Accession: G72454
R; Amarabayasi, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Recession: G72454
A; Recession: G72454
A; Accession: G72454
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-251 «KAW>
A; Residues: 1-251 «KAW>
A; Residues: 1-251 «KAW>
A; Experimental source: strain K1
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: probable phosphoesterase MTH1882; phosphoesterase core homology
                                                                                                                                                                                                                                                                                                                                                                    pathogenesis related protein - barley
C;Species: Hordeum vulgare (barley)
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06168
R;Scott, K.J.
submitted to the EMBL Data Library, June 1994
A;Reference number: 215503
A;Reference number: 215503
A;Accession: T06168
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-235 <SCO>
A;Cross-references: UNIPROT:P16273; EMBL:X16648; NID:g499073; PIDN:CAA34641.1; PID:g4990
A;Experimental source: cv. Psakon 4
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C;Species: Rhizobium meliloti
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: T46814
R;Lynch, D.; O Connell, M.; O Brien, J.
R;Lynch, D.; O Connell, M.; O Brien, J.
Submitted to the EMBL Data Library, December 1998
A;Description: Cloning and sequence analysis of the Sinorhizobium meliloti 2011 rhizobad
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          100.0%; Score 36; DB 100.0%; Pred. No. 15;
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100.0%; Pred. No. 20;
tive 0; Mismatches
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                                                                             Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
Query Match
Best Local Similarity
Matches 5; Conser
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51 HPPHG 55
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C;Superfamily: adenovirus early E3 6.4K protein
C;Keywords: early protein
                                                                                                      Query Match
Best Local Similarity 80.0%;
Matches 4; Conservative
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NyAlternate names: colorectal cancer suppressor DCC
C;Species: Homo sapiens (man)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
A;Reference DCC gene product in cellular differentiation and colorectal tumorigenesis.
A;Reference number: A54100; MUID:95011532; PMID:7926722
A;Reference number: A54100; MUID:95011532; PMID:7926722
A;Reference submober: A100
A;Redidues: 1-147 **HED>
A;Cross-references: UNIPROT:P43146; EMBL:X76132; NID:9453209; PIDN:CAA53715.1; PID:94533
B;Redidues: UNIPROT:P43146; EMBL:X76132; NID:9453209; PIDN:CAA53715.1; PID:94533
B;Redidues: 10-147 **HED>
A;Reference number: A40098; MUID:90100559; PMID:2294591
A;Reference number: A40098; MUID:90100559; PMID:2294591
A;References: GB:M32292; NID:9181492; PIDN:AAA35751.1; PID:9181493
A;Cross-references: GB:M32292; NID:9184492; PIDN:AAA35751.1; PID:91840403
A;Cross-references: GB:M32292; NID:9184406
A;Cross-references: GB:M32392; NID:9184406
A;Cross-references: GB:M324406
A;Cross-references: GB:M32292; NID:9184406
A;Cross-references: GB:M324406
A;Cross-r
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early E3 6.4K protein - human adenovirus 35
C; Species: Mastadenovirus h35 (human adenovirus 35)
A; Note: host Homo sapiens (man)
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C; Accession: B31162
R; Flomenberg, P.R.; Chen, M.; Horwitz, M.S.
J. Virol. 62, 4431-4437, 1988
A; Title: Sequence and genetic organization of adenovirus type 35 early region 3.
A; Reference number: A93039; MUD:89012230; PMID:3172347
A; Reference number: B31162
A; Molecule type: DNA
A; Residues: 1-61 < FLO>
A; Residues: 1-61 < FLO>
A; Cross-references: UNIPROT:P17591; GB:M23195; NID:g516584; PIDN:AAA42436.1; PID:g516586
                             A; Accession: I51669
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1427 <PIE>
A; Cross-references: UNIPROT: Q91562; EMBL: U10986; NID: g606873; PIDN: AAA70168.1; PID: g6068
C; Genetics:
A; Genetics:
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668; MUID:95113183; PMID:7813784
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100.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 0;
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100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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  151
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A; Reference number:
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hypothetical protein TP0539 - syphilis spirochete
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C; Accession: H71311
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinr rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDon they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Accession: H71311
A; Accession: H71311
A; Accession: H71311
A; Accession: H71311
A; Coll.
A; Coll.
A; Cost references: UNIPROT: 083550; GB: AE001229; GB: AE000520; NID: g3322827; PIDN: AAC6553(A; Experimental source: strain Nichols
C; Genetics:
A; Genetics:
A; Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47876
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; San. W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A;Reference number: 224479
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     Length 61;
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-107 < CHO>
A; Cross-references: UNIPROT: Q9LZZ8; EMBL; AL162295
A; Experimental source: cultivar Columbia; BAC clone T4C21
C; Genetics:
A; Map position: 3
A; Note: T4C21.60
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       <u>ب</u>
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Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches
Score 30; DB :
Pred. No. 60;
1; Mismatches
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Metale names: class I histocompatibility antigen beta chain C;Species: Mus musculus (house mouse)
N;Alternate names: class I histocompatibility antigen beta chain C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1981 #sequence revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A90822; A93889; B93889; A12344; I79322; I58971; I63179; I63180; I63178; Sparnes, J.R.; Seidman, J.G.
Cell 29, 661-669, 1982
A;Title: Structure of wild-type and mutant mouse beta-2-microglobulin genes.
A;Reference number: A90822; MUID:83001942; PMID:6180834
A;Reference number: A90822
A;Molecule type: DNA
A;Residues: 1-119 <PRN>
A;Residues: 1-119 <PRN>
A;Residues: 1-119 <PRN>
A;Residues: 1-119 <PRN>
A;Residues: 1-110 <PRN>
A;Residues:
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T17301
hypothetical protein DKFZp564B147.1 - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T17301
R; Bloecker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A; Reference number: Z18724
A; Reference number: Z18724
A; Residues: Preliminary
A; Molecule type: mRNA
A; Residues: 1-115 <BLO>
A; Cross-references: UNIPROT: Q9UFN1; EMBL: AL117556
A; Experimental source: fetal brain; clone DKFZp564B147
C; Genetics:
A; Note: DKFZp564B147.1
C; Superfamily: human hypothetical protein DKFZp564B147.1
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           A; Experimental source: strain $288C
R; Landt, O.; Hiesel, R.; Unseld, M.
submitted to the Protein Sequence Database, July 1996
A; Reference number: $66907
A; Accession: $66927
A; Molecule type: DNA
A; Residues: 1-8 <LAN>
A; Cross-references: EMBL: Z74961; MIPS: YOR053w
A; Experimental source: strain $288C
C; Genetics:
A; Cross-references: $GD:$0005579
A; Map position: 15R
C; Keywords: transmembrane protein
F; 3-19/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 83.3%; Score 30; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 4; Conservative 0; Mismatches 0;
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ilarity 100.0%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 4; Conserv
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MGMSB2
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B72629
hypothetical protein APE1490 - Aeropyrum pernix (strain K1)
C; Species: Aeropyrum pernix
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C; Accession: B72629
K; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Jamazaki, J.; K DNA Res. 6, 83-101, 1999
A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A: Reference number: A72450; MUID:99310339; PMID:10382966
A; Reference number: A72450; MUID:99310339; PMID:10382966
A; Accession: B72629
A; Ratus: preliminary
A; Molecule type: DNA
A; Residues: 1-113 < KAW>
A; Roberimental source: strain K1
C; Genetics:
A; Experimental source: strain K1
C; Genetics:
A; Genetics:
C; Superfamily: Aeropyrum pernix hypothetical protein APE1490
hypothetical protein F-112 - human adenovirus 2
C; Species: Mastadenovirus h2 (human adenovirus 2)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C; Accession: G92351; G92352; A03861
R; Gingeras, T.R.; Sciaky, D.; Gelinas, R.E.; Bing-Dong, J.; Yen, C.E.; Kelly, M.M.; Bull
J; Biol. Chem. 257, 13475-13491, 1982
A; Reference number: A92351; MUID:83056843; PMID:7142161
A; Reference number: A92351
A; Residues: 1-112 <GIN>
A; Residues: 1-112 <GIN>
A; Residues: 1-112 <GIN>
A; Residues: 1-12 <ALE>
A; Residues: 1-112 <ALE>
A; Residues: 1-112 <ALE>
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NyAlternate names: hypothetical protein 02799
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S66936; S66927
R;Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, N.; Bohn, C.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Dang, D.V.; Valens, N.; Reference number: S66929
A;Reference number: S66929
A;Accession: S66936
A;Molecule type: DNA
A;Residues: 1-113 <BOH>
A;Cross-references: UNIPROT:Q08428; EMBL:Z74961; NID:g1420188; PID:e252336;
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100.0%; Pred. No. 1.1e+02;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 1.1e+02;
.ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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S66936
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RESULT 17
B7246
hypothetical protein APE1654 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Decies: Aeropyrum pernix
C;Decies: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: B72546
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Vamazaki, J.; K.
DNA Res. G, 83-101, 1999
A,Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr.
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72546
A;Accession: B72646
A;Accession: B72646
A;Accession: B72646
A;Accession: B7266
A;Accessi
                        A; Molecule type: protein
A; Residues: 'X',22-30,'X',32-44 <SEU>
A; Residues: 'X',22-30,'X',32-44 <SEU>
A; Note: this protein was found as a minor contaminant during the purification of prote C; Genetics:
A; Introns: 23/1; 116/1
C; Complex: heterodimer with MHC class I histocompatibility antigen alpha chain
C; Function:
A; Description: necessary for the expression of MHC class I histocompatibility antigen C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: heterodimer
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-119/Product: beta-2-microglobulin #status experimental <MAT>
F; 21-110/Domain: immunoglobulin homology <IMM>
F; 45-100/Disulfide bonds: #status predicted
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C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_chan
C;Accession: T46369
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber,
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23031
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <AAA>
A;Cross-references: UNIPROT:Q9NT54; EMBL:AL137525
A;Experimental source: adult testis; clone DKFZp43410118
C;Genetics:
A;Note: DKFZp43410118.1
C;Superfamily: human hypothetical protein DKFZp43410118.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 30; DB 1; Le
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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100.0%; Pred. No. 1.2e+02;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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A Rocession: B3189

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Seubert, P.; Vigo-Pelfrey, C.; Esch, F.; Lee, M.; Dovey, H.; Davis, D.; Sinha, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 359, 325-327, 1992
A,Title: Isolation and quarkReference number: S29076
A,Accession: S29077
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DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic as A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Reference number: A71070
A;Residue: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-141 <KAW>
A;Residues: 1-141 <KAW>
A;Experimental source: strain OT3
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1258
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ABSOLI 23

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CONSErved hypothetical protein [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus

C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C;Accession: A99226

R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-V Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P. arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.

Submitted to GenBank, April 2001

A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139

A;Reference number: A99139

A;Reference number: A99139

A;Reference number: A99126

A;Reference number: A99126

A;Reference number: A99126

A;Residues: 1-157 < KUR>

A;Residues: 1-157 < KUR>

A;Cross-references: UNIPROT:Q9UXF4; GB:AE006641; NID:g13813940; PIDN:AAK41064.1; GSPDB:GR
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: A53118; S39206
R;Courty, Y.; Rosinski-Chupin, I.; Rougeon, F.
J. Biol. Chem. 269, 520-527, 1994
A;Title: A new proline-rich protein precursor expressed in the salivary glands of A;Reference number: A53118; MUID:94103265; PMID:8276845
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                                                                                                                                                                                                                                                                                                                                                                                                                               Length 141,
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0;
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A;Status: translated from GB/EMBL/DDBJ
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C;Species: Discorting C; Accession: B69320
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Recession: B69320
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-126 <KLE>
A;Cross-references: UNIPROT:029691; GB:AE001066; GB:AE000782; NID:g2689389; PIDN:AAB9067
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C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Accession: F71070
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
                                                                                                                                                                                                                                                                                                                                                         hypothetical protein 49 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Feb-1997
C;Accession: A05160
R;O'Connell, P.; Rosbash, M.
Nucleic Acids Res. 12, 5495-5513, 1984
A;Title: Sequence, structure, and codon preference of the Drosophila ribosomal protein A;Reference number: A93527; MUID:84272233; PMID:6087289
A;Accession: A05160
A;Molecule type: DNA
A;Residues: 1-125 <OCON>
C;Genetics:
A;Gene: FlyBase:M(3)99D
A;Cross-references: FlyBase:FBgn0002626
A;Map position: 3R, 99D
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              Length 122;
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            83.3%; Score 30; DB 2; Le
100.0%; Pred. No. 1.2e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0;
            Query Match
Best Local Similarity
Matches 4; Conser
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| HPPH 35
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RESULT 27

138724
mitochondrial benzodiazepine receptor - human
C;5pecies: Homo sapiens (man)
C;5pecies: 29-May-1998 #sequence_revision 29-May-1998 #text_change 12-Jul-2004
C;0ate: 29-May-1998 #sequence_revision 29-May-1998 #text_change 12-Jul-2004
C;Accession: 138724
R;Yakovlev, A.G.; Ruffo, M.; Jurka, J.; Krueger, K.E.
Gene 155, 201-205, 1995
A;Title: Comparison of repetitive elements in the third intron of human and rodent mitoch
A;Reference number: 138724
A;Reference number: 138724
A;Reference number: 138724
A;Reference number: 138724
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-169 <RES
A;Cross-references: UNIPROT:P30536; EMBL:U12421; NID:g529945; PIDN:AAA83252.1; PID:g52994
A;Genetics:
C;Genetics:
A;Genetics:
A;
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138105
peripheral benzodiazepine receptor - human
C;Species: Homo sapiens (man)
C;Species: Amono sapiens (man)
C;Superfamily: peripheral benzodiazepine receptor gene: cloning and characterization
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: D
                                   peripheral benzodaizepine receptor - human
c;Species: Homo sapiens (man)
C;Date: 10-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 12-Jul-2004
C;Accession: JE0149
R;Xu, G.H.; Hu, B.R.; Luo, C.Q.; Chen, R.Z.; Qiu, P.X.
Chinese Biochem. J. 13, 423-427, 1997
A;Title: Cloning of the cDNAs encoding human peripheral benzodaizepine receptor and its
A;Reference number: JE0149
A;Accession: JE0149
A;Molecule type: mRNA
A;Residues: 1-169 <XUA>
C;Superfamily: peripheral-type benzodiazepine receptor/signal transduction protein TspO
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100.0%; Pred. No. 1.7e+02;
:ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 4; Conservative
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C; Species: Halobacterium sp. NRC-1
C; Species: Halobacterium sp. NRC-1
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C; Accession: C84299
R; NG; W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: C84299
A; Accession: C84299
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-159 <STO>
A; Cross-references: UNIPROT:Q9HPV8; GB:AE004437; NID:g10580949; PIDN:AAG19759.1; GSPDB:GCGGenetics:
A; Genetics:
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A97760
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Accession: A97760
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; RC
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97760
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-167 <KUR>
A;Residues: 1-167 <KUR>
A;Residues: 1-167 <KUR>
A;Gene: nuoE
C;Gene: nuoE
C;Superfamily: NADH dehydrogenase (ubiquinone) I chain E; NADH dehydrogenase (ubiquinone
C;Keywords: oxidoreductase; NAD
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80.0%; Pred. No. 1.6e+02;
vative 1; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0;
                                                                                               hypothetical protein ybhB
C,Genetics:
A,Gene: SSO0767
C,Superfamily: conserved
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Best Local Similarity
Matches 4; Conser
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98 HPPH 101
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25 YPPHG 29
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DB 2;

Score 30;

26

RESULT

4:51

13:0

Thu Jun 16

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C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52409
R;Nersissian, A.M.; Mehrabian, Z.B.; Nalbandyan, R.M.; Hart, P.J.; Fraczkiewicz, G.; Czen Protein Sci. 5, 2184-2192, 1996
A;Title: Cloning, expression, and spectroscopic characterization of Cucumis sativus stell A;Reference number: Z17046; MUID: 97084803; PMID: 8931137
A;Accession: T52409
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-181 <NER>
A;Cross-references: UNIPROT: O80517; EMBL: U76299; PIDN: AAC32039.1
C;Superfamily: stellacyanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              formylmethionine deformylase (BC, 3.5.1.31) - Rickettsia conorii (strain Malish 7)

c; Species: Rickettsia conorii

C; Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C; Accession: B97784

R; Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Rot Science 293, 2093-2098, 2001

A; Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.

A; Reference number: A97700; MUID:21442074; PMID:11557893

A; Accession: B97784

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-183 < KUR>
A; Residues: 1-183 < KUR>
A; Cenetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: peptide deformylase
C; Superfamily: peptide deformylase
C; Keywords: hydrolase
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AC2903
Conserved hypothetical protein Atu2660 [imported] - Agrobacterium tumefaciens (strain C56 C; Species: Agrobacterium tumefaciens (c; Accession: AC2903 R; Mood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClelle; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2332, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F ster, E.W.
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, F ster, E.W.
A; Accession: AC2903
A; Accession: AC2903
A; Accession: AC2903
A; Accession: AC2903
A; Accession: Liss ACMR>
A; Molecule type: DNA
A; Molecule type: DNA
A; Coss-references: UNIPROT: OBUC38; GB: AE008688; PIDN: AAL43641.1; PID: G17741163; GSPDB: G)
C; Genetics: Accession: Accessio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.3%; Score 30; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0;
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nes 4; Conser
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Best Local S
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                                                                                                                                                                                                                                                                                                    RESULT 29
S14257
benzodiazepine receptor, peripheral-type - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 18-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 12-Jul-2004
C;Date: 18-Reb-1994 #sequence_revision 10-Nov-1995 #text_change 12-Jul-2004
C;Accession: S14257
R;Riond, J.; Mattei, M.G.; Kaghad, M.; Dumont, X.; Guillemot, J.C.; le Fur, G.; Caput, L
Eur. J. Biochem. 195, 305-311, 1991
A;Title: Molecular cloning and chromosomal localization of a human peripheral-type benzo
A;Accession: S14257
A;Status: preliminary
A;Accession: S14257
A;Status: preliminary
A;Accession: S14257
A;Catus: preliminary
A;Accession: S14257
A;Catus: UNIPROT:P30536; GB:M36035; NID:g184333; PIDN:AAA03652.1; PID:g306883
A;Cross-references: UNIPROT:P30536; GB:M36035; NID:g184333; PIDN:AAA03652.1; PID:g306883
A;Cross-references: GDB:127347; OMIM:109610
A;Map position: 22q13.31-22qter
C;Superfamily: peripheral-type benzodiazepine receptor/signal transduction protein TspO
C;Keywords: mitochondrion; transmembrane protein
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NyAlternate names: protein K10A8_130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51469
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mew submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Reference number: Z25394
A;Atatus: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <SAT>
A;Residues: 97/1
A;Map position: S
A;Introns: 97/1
A;Note: K10A8_130
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80.0%; Pred. No. 1.7e+02;
ive 1; Mismatches 0; Indels
                                                                Indels
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100.0%; Pred. No. 1.7e+02;
:ive 0; Mismatches 0;
                            red. No. 1.7e+02;
Mismatches 0;
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thaliana (mouse-ear cress)
                              Pred. No.
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                              100.08;
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Best Local Similarity 80.0
Matches 4; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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                      Best Local Similarity
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25 YPPHG 29
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HPPH 46
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TS1469
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T52409
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RESULT 36
D75004
hypothetical protein PAB1037 - Pyrococcus abyssi (strain Orsay)
N;Alternate names: yafJ homolog
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D75004
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A;Reference number: A75001
A;Accession: D75004
A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1-208 <KAW>
A;Cross-references: UNIPROT:Q9UYDB; GB:AJ248288; GB:AL096836; NID:g5458960; PIDN:CAB50474;
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1037
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Cispecies: Caenorhandins elegans
Cispecies: Caenorhandins elegans
Cispecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
Cispecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
Cispecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
Cispecies: 282, 2012-2018, 1998
Aintle: Genome sequence of the nematode C. elegans: a platform for investigating biology
Airtle: Genome sequence of the nematode C. elegans: a platform for investigating biology
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C;Genetics:
A;Gene: T24A6.3
A;Map position: 5
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AF2901
conserved hypothetical protein Atu2647 [imported] - Agrobacterium tumefacies C; Species: Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                      Score 30; DB 2; Le
Pred. No. 2e+02;
); Mismatches 0;
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Pred. No. 2.1e+02;
0; Mismatches 0;
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches
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83.3%; Scc.
100.0%; Pre
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Best Local Similarity 100.
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Best Local Similarity 100.
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                                                                                                                                                                           1 HPPH 4
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A; Residues: 1-209 <S'
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                         Query Match
Best Local S
Matches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ypjp - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: Ob-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: H69937
R;Kunst, F:; Ogasawara, N:; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Broulilet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chic
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Naturors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Athors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, K.; Lapidus, A.; Lardinois
A;Athors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Liu, H.; Masuda, S.; Maucel
A;Authors: Lauber, J.; Bazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucel
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Tosafo, V.; Sekowska, A.; Setonion,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Attle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A65580; MUID:98044033; PMID:9384377
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Cross-references: UNIPROT:P54172; GB:299115; GB:AL009126; NID:92634478; PIDN:CAB14102.
A;Experimental source: strain 168
C;Genetics:
A;Gene: Ypjp
C;Superfamily: Bacillus subtilis hypothetical protein ypjp
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B84315
hypothetical protein Vng1625h [imported] - Halobacterium sp. NRC-1
C; Species Halobacterium sp. NRC-1
C; Species Halobacterium sp. NRC-1
C; Species Halobacterium sp. NRC-1
C; Accession: B84315
R; NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc, Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: B84315
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-207 <STO>
A; Cross-references: UNIPROT:Q9HFI1; GB:AE004437; NID:g10581098; PIDN:AAG19886.1; GSPDB:C
C; Genetics:
A; Genetics:
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                                                                                           Score 30; DB 2; L
Pred. No. 1.8e+02;
0; Mismatches 0;
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2e+02;
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                                                                                  Query Match 83.3%;
Best Local Similarity 100.0%;
Matches 4; Conservative 0
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Best Local Similarity 100.
Matches 4; Conservative
                      A; Map position: circular
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H97676
hypothetical protein AGR_C_4799 [imported] - Agrobacterium tumefaciens (strain C58, Cere c) Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: H97676
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Reseasion: H97676
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <KUR>
A;Cross-references: UNIPROT:Q8UC51; GB:AE007869; PIDN:AAK88369.1; PID:g15157854; GSPDB:GCGenetics:
A;Genetics:
A;Gene: AGR_C_4799
A;Map position: circular chromosome
C;Accession: AF2901
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romerco, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Accession: AF2901
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2901
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <KURN>
A;Residues: 1-214 <KURN>
A;Residues: 1-214 <KURN>
A;Residues: 1-214 <KURN>
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu2647
A;Map position: circular chromosome
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153100
eHAND - mouse
C; Species: Mus sp. (mouse)
C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C; Accession: 153100
R; Cserjesi, P.; Brown, D.; Lyons, G.E.; Olson, E.N.
Dev. Biol. 170, 664-678, 1995
A; Title: Expression of the novel basic helix-loop-helix gene eHAND in neural crest deriv A; Reference number: 153100; MUID:95377552; PMID:7649392
A; Accession: 153100
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-216 <RES>
A; Accession: 15360; NID:g1086931; PIDN:AAB35104.1; PID:g1086932
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Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0;
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Query Match
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps

2y 1 HPPH 4
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Ob 17 HPPH 20

Search completed: June 15, 2005, 14:22:49 Job time: 19.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 15, 2005, 13:53:11 ; Search time 83.5 Seconds (without alignments) 30.663 Million cell updates/sec Run on:

US-10-074-225A-9 36 1 HPPHG 5 Title: Perfect score: Sequence: Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	O15952 homo sapien	oryza	aeropy				2719 rhodobacter	Q8pqu3 xanthomonas	Q7usz6 rhodopirell	P16273 hordeum vul	Q9xhx3 oryza sativ	Q9xhx6 oryza sativ	09y9k5 aeropyrum p		Q9yjn5 equid herpe					Q9z3r2 r diaminobu	mycol						•	Q7mmdl vibrio vuln	-		Q6c276 yarrowia li
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Result No.	-	8	m	4	ഗ	9	7	œ	σ	10	11	12	13	14	15	16			19	20	21	22	23	24	25	56	27	28		30	31

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Query Match 100.0%; Score 36; DB 2; Length 62; Best Local Similarity 100.0%; Pred. No. 33; Matches 5; Conservative 0; Mismatches 0; Indels

1 HPPHG S

ò g 0655P3 PRELIMINARY; PRT; 108 AA.
0655P3;
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein B1011A07.27.
Name=B1011A07.27;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae.

RESULT 2 Q655P3 ID Q655 AC Q655 DT 25-0 DT 25-0 DT 25-0 DT 25-0 DT 25-0 OC SPEX OC SPEX OC SPEX

Q95r83 drosophila Q86bb9 drosophila Q6xli4 ciona intes Q91562 xenopus lae Q63155 rattus norv P43146 homo sapien P70211 mus musculu Q6s1e5 cochliobolu Q9s8a0 pinus monti Q9v2v2 methanobact Q71yr7 plasmid pme Q8km82 mycoplasma Q9ndz7 leishmania P17591 human adeno		date) update)	ebrata; Euteleostomi; minidae; Homo.	, Francke U., Scheller R.; the mammalian agrin gene.";	B CRC64;
Q95R83 Q86BB9 Q6XL14 Q91562 Q63155 DCC_HUMAN DCC_MOUSE Q6SLE5 Q9SBA0 Q9V2V2 Q7LYR7 Q8KM82 Q9NDZ7	ALIGNMENTS	PRT; 62 AA. Created) Last sequence update) Last annotation update)	a; Craniata; Vertebrata; Butel 8; Catarrhini; Hominidae; Homo	; Peterson K. ization of	C:basal lamina; TAS. P:synaptic transmission; NAS. 645; FO1 N. 350; Prot_inh_Kazal. 2azal_1; 1. FOLN; 1. KAZAL; 1. 6344 MW; 4CD1653E6B8F09E8
100.0 773 2 100.0 938 2 100.0 1075 2 100.0 1447 2 100.0 1447 1 100.0 1447 1 100.0 2013 2 83.3 30 2 83.3 30 2 83.3 55 2 83.3 55 2		PRELIMINARY; (TrEMBLrel. 01, (TrEMBLrel. 24, ent).	(Human). etazoa; Chordata; theria; Primates; 606;	MEDLINE=92407628; PubMed=1326608; MEDLINE=92407628; PubMed=1326608; Rupp F., Ozcelik T., Linial M., P "Structure and chromosomal localid. Neurosci. 12:3535-3544(1992). EMBL; S44195; AAB23327.1; HSSP; P21674; 1LR7.	GO; GO:0005605; C:basal lamina; TAS GO; GO:0007268; P:synaptic transmis InterPro; IPR003645; Fol N. InterPro; IPR002350; Prot_inh_Kazal Pfam; PF00050; Kazal 1; 1. SMART; SM00274; FOLN; 1. SMART; SM00280; KAZAL; 1. NON TER 62 62 SEQUENCE 62 AA; 6344 MW; 4CD165
333 334 335 335 336 337 337 337 337 337 337 337 337 337	1.	15952 15952; 1-NOV-1996 1-JUN-2009 1-JUN-2009 grin (Fragm	Homo sapinan) Fukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;	MEDLINE=92407628; Rupp F., Ozcelik T. "Structure and chr J. Neurosci. 12:35 EMBL; S44195; AAB2	GO; GO:0005605; C:ba GO; GO:0007268; P:sy InterPro; IPR003645; InterPro; IPR002350; Pfam; PF00050; Kazal SMART; SM00280; KAZA NON TER 62
	RESULT	015952 1D 00 AC 00 DT 00 DT 00 DT 00	80000 X	R R R R R R R R R R R R R R R R R R R	80

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FROM N.A
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                                            Q7PG70
Q7PG70;
01-MAR-2004
01-MAR-2004
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RX SEQUENCE FROM N.A.

RX Saaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayoun RA, Saaki T., Matsumoto T., Nagamura Y., Antonio B.A., Kanamori H., RA, W. J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H., RA, Hosokawa S., Masukawa M., Arikawa K., Hamada M., Harada C., RA, Hjishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M., RA Isasawa W., Itoh Y., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K., Rarasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I., RA, Machita K., Makehara T., Mizuno H., Mizubayashi T., Mukai Y., Nakamura M., Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M., RA, Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K., RA, Maki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., RA, Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K., RA, Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y., Vann M., Jiang J., Gojobori T.;
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A Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
A Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; APO00060; BAA79798.1; -.
R PIR; F72674; F72674.

R Complete proteome; Hypothetical protein.
SEQUENCE 118 AA; 12953 MW; 6134441D6406CDB0 CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE0819.
OrderedLocusNames=APE0819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 36; DB
100.0%; Pred. No. 57;
tive 0; Mismatches
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Yano M., Jiang J., Gojobori T.;
"The genome sequence and structu
Nature 420:312-316(2002).
EMBL, AP003722; BAD45462.1; -.
Hypothetical protein.
SEQUENCE 108 AA; 11886 MW; 6:
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NCBI_TaxID=56636;
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5; Conserv
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Archaea; Crenarcha
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MEDLINE=99310339;
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                                                                                                01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGP0000002414 (Fragment).
Name=ENSANGG00000020585;
Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L., Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
                                                                                                                                                                                                                                                                                                                                                                    Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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InterPro; IPR008727; PAAR.
Pfam; PF05488; PAAR motif; 2.
Complete proteome; Hypothetical protein.
SEQUENCE 176 AA; 18431 MW; 79A633E68C447515 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 171 171 171 171 AA; 18450 MW; 1A135D70C5F14B67 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein VCA0284.
OrderedLocusNames=VCA0284;
                                               (TrEMBLrel. 26, Created)
(TrEMBLrel. 26, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 90;
tive 0; Mismatches
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100.0%; Pred. No. 93;
iive 0; Mismatches
  171 AA
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PRT;
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EMBL; AAAB01008847; EAA45048.1; -.
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EMBL; AE004368; AAF96193.1; -.
PIR; F82478; F82478.
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Best Local Similarity 100.
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PRELIMINARY;
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Best Local Similarity
Matches 5; Conserv
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Query Match
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"The nucleotide sequence of a flavodoxin-like gene which precedes two ferredoxin genes in Rhodobacter capsulatus.";
Nucleic Acids Res. 18:5284-5284 (1990).
                                                                                                                                                                                                                                                                    .
D
                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=06:H1 / CFT073 / ATCC 700928 / UPEC;

MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schatt E., Jouanneau Y., Vignais P.M.; "Molecular cloning and sequence analysis of the structural gene of ferredoxin I from the photosynthetic bacterium Rhodobacter
                                                                                                 Ol-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein c0967.
OrderedLocusNames=c0967;
Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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052719;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Orf10 (Fragment).
Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacteraceae; Rhodobacter.
Rhodobacteraceae; Rhodobacter.
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                                                                                                                                                                                                                                                                                                                                                             21398 MW; B3EAEC5743D88D3D CRC64;
                                                                                                                                                                                                                                                                                                                          U.S.A. 99:17020-17024(2002)
                                                                                                                                                                                                                                                                                                               of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:1705
EMBL; AE016758; AAN79440.1; -.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=2402451;
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MEDLINE=90036712;
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MEDLINE=90384835;
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STRAIN=306 / ATCC 13902 / XV 101;

STRAIN=306 / ATCC 13902 / XV 101;

STRAIN=306 / ATCC 13902 / XV 101;

MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

A cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos M.V.F.,

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Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

A Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

A Setubal J.C., Kitajima J.P.,

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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein XAC0228.
OrderedLocusNames=XAC0228;
Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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NCBI_TaxID=92829;
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EMBL; AE011647; AAM35120.1; -.
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176 HPPHG 180
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28-FEB-2003 (Rel. 41, Last annotation update)
Pathogen-related protein.
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100; Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T., Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R., Schlesner H., Amann R., Reinhardt R.; "Complete genome sequence of the marine planctomycete Pirellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv. Psakon 4; TISSUE=Leaf;
MEDLINE=90067951; PubMed=2587271;
Jutidamrongphan W., Mackinnon G., Manners J.M., Scott K.J.;
"Sequence of a near-full length cDNA clone for a mRNA of barley induced by fungal infection.";
Nucleic Acids Res. 17:9478-9478 (1989).
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Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
Planctomycetaceae; Pirellula.
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Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     strain 1.";
Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).

EMBL, BX294140; CAD73646.1; -,
Complete proteome, Hypothetical protein.

SEQUENCE 234 AA; 26924 MW; 03A974166BAA3FEC CRC64;
                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
OrderedLocusNames=RB4213;
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Best Local Similarity
Matches 5; Conserv
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P16273;
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PRPX_HORVU
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Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
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Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
A Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
M. Yano M., Jiang J., Gojobori T.,
M. Yamana H., Kim H.I., Eun M.Y.,
M. Yano M., Jiang J., Gojobori T.,
M. Yamana H., Kim H.I., Eun M.Y.,
M. Yano M., Jiang J., Gojobori T.,
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative pathogenesis related protein.
Name=OSJNBa0049B20.20; Synonyms=P0034C11.23;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
NCBI_TaxID=39947;
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Buell R., Benito M.-I., Lin X., Mason T.M., Umayam L., Shea T.P.
Fujii C.Y., Shen M., Fraser C.M.,
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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Nature 420:312-316(2002).
EMBL; AC007789; AAD38293.1; -.
EMBL; AP002865; BAB18332.1; -.
Gramene; Q9XHX3; -.
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SEQUENCE 235 AA; 26293 MW; 995136DD24A9CD3C CRC64;
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240 AA; 27196 MW; 4ABC7B300FAFEBD6 CRC64;
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Pred. No. 1.3e+02;
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 5; Conservative
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STRAIN=KI;
MEDLINE=99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Kawarabayasi Y., Hino Y., Horikawa H.,
Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Hosoyama A., Fukui S., Funahashi T., Tanaka T., Kudoh Y.,
Takamiya M., Masuda S., Funahashi T., Aoki K.-I., Kubota K.,
Namazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative pathogenesis related protein.
Name=OSJNBa0049B20.17; Synonyms=P0034C11.20;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                     Shea T.P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and structure of rice chromosome 1.";
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Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcaceae; Aeropyrum.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Buell R., Benito M.-I., Lin X., Mason T.M., Umayam L., &
Fujii C.Y., Shen M., Fraser C.M.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27146 MW; 86C7D7A6F409AD7E CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein APE2283.
OrderedLocusNames=APE2283;
 240 AA
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 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The genome sequence and str
Nature 420:312-316(2002).
EMBL; AC007789; AAD38290.1;
EMBL; AP002865; BAB18330.1;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XHX6; -.
240 AA;
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182
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SEQUENCE
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09хнх6
09хнх6;
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Q9Y9K5
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vereecke D.M.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Y09820; CAA70950.1; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR009057; Homeodomain_like.
InterPro; IPR000005; HTHAraC.
Pfam; PF00165; HTH AraC; 2.
PRINTS; PR00032; HTHARAC.
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STRAIN=D188;
MEDLINE=20461232; PubMed=11004184;
DOI=10.1128/JB.182.20.5832-5840.2000;
Temmerman W., Vereecke D., Dreesen R., Van Montagu M., Holsters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterineae, Nocardiaceae, Rhodococcus.
                                                                                                                                                                                                                                                                                  100.0%; Score 36; DB 2; Length 251; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
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genome sequence of an aerobic hyper-thermophilic
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                    crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; AP000064; BAA81295.1; -.
PIR; G72454; G72454.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR004843; M-pesterase.
Pfam; PF00149; Metallophos; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 251 AA; 27075 MW; 9C30FE5292F51B60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1124; HTH ARAC FAMILY 2; 1.
Transcription; Transcription regulation.
77 AA; 30866 MW; 071DB9DEFC11E113 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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100.0%; Pred. No. 1.4e+02;
ive 0; Mismatches 0;
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Best Local Similarity 100...
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                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 5; Conservative
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DNA-binding, Transcrit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhodococcus fascians
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NCBI_TaxID=5085;
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Q6MYV5,
05-JUL-2004 (
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99292766; PubMed=10364242; DOI=10.1074/jbc.274.25.17946; Srinivasula S.M., Ahmad M., Lin J.H., Poyet J.L., Fernandes-Alnemri T., Tsichlis P.N., Alnemri E.S.; "CLAP, a novel caspase recruitment domain-containing protein in the tumor necrosis factor receptor pathway, regulates NF-kappaB activation
                                                                                                                                                                                      willis T.G., Jadayel D.M., Du M.Q., Peng H., Perry A.R., Abdul-Rauf M., Price H., Karran L., Majekodunmi O., Wlodarska I., Pan L., Crook T., Hamoudi R., Isaacson P., Dyer M.J.; "Bcllo is involved in t(1;14) ($22;q32) of MALT B-cell lymphoma and mutated in multiple tumor types."; Cell 96:35-45(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
0
        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (CARD-like apoptotic protein) (V-CARMEN).
Name=CLAP; Synonyms=E10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 36; DB 2; Length 311; 100.0%; Pred. No. 1.6e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Willis A.G.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32602 MW; 04EC68C7353D723B CRC64;
                                                                                                                              Viruses, dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
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QBFT73
ID QBFT73;
AC QBFT73;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DF O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Equine herpesvirus-2 E10 gene product, but not in homologue, activates NF-kappaB transcription fact terminal kinase.";
J. Biol. Chem. 274:9962-9968(1999).
EMBL; AJ006410; CAA07016.1; -.
EMBL; AF134394; AAD39146.1; -.
EMBL; AF100340; AAD16430.1; -.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005515; F:protein binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and apoptosis.";

J. Biol. Chem. 274:17946-17954(1999).
[4]
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9; DEATH_like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein.
311 AA; 32
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InterPro; IPR011029
Pfam; PF00619; CARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=99292766; I Srinivasula S.M., Fernandes-Alnewri 7
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Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                   NCBI_TaxID=12657;
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SEQUENCE 31
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MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
Nishio Y., Nakamura Y., Kawarabayasi Y., Usuda Y., Kimura E.,
Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
Gojobori T.;
"Comparative complete genome sequence analysis of the amino acid
replacements responsible for the thermostability of Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible bhlh transcription factor.
ORFNames=AfA28D10.070;
Aspergillus fumigatus (Sartorya fumigata).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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EMBL; AE017242; AAS06857.1; -.
InterPro; IPR001865; Ribosomal_S2.
PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
Complete proteome; Hypothetical protein.
SEQUENCE 355 AA; 38394 MW; A97DDD1B43A5797D CRC64;
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCM _ TaxID=152794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                       321 AA; 34772 MW; 2278243DEDD90920 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Hypothetical protein.
OrderedLocusNames=MAP4307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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100.0%; Pred. No. 1.7e+02;
cive 0; Mismatches 0;
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05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
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                                                                                                                                                                                                                                                                                                                                       Genome Res. 13:1572-1579(2003).
EMBL; AP005219; BAC18507.1; -.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome sequence of Clostridium tetani, the causative agent of tetanus disease.";

I tetanus disease.";

Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).

Rembl; AE015939; AA035605.1; -.

RO; GO:0016020; C:membrane; IEA.

GO; GO:000518; F:electron transporter activity; IEA.

GO; GO:000518; P:electron transport; IEA.

GO; GO:0006118; P:electron transport; IEA.

RO; GO:0006118; P:electron transport; IEA.

InterPro; IPR001450; 4Fe48_ferredoxin.

R InterPro; IPR011538; Complex1_51K_dom.

InterPro; IPR010208; RnfC.

R InterPro; IPR01054; Rudmnt_hyb_motif.

R Ffam; PF01512; Complex1_51K; 1.

R Pfam; PF00037; Fer4; 1.
                     Pubmed=1499827; DOI=10.1016/j.fgb.2003.12.003;
Pubmed=1499827; DOI=10.1016/j.fgb.2003.12.003;
Pubmed=1499827; DOI=10.1016/j.fgb.2003.12.003;
Pubmed=1499827; DOI=10.1016/j.fgb.2003.12.003;
Posker N., Fraser A., Harris D., Larke N., Murphy L., Humphray S., O'Neil S., Pertea M., Price C., Rabbinowitsch E., Rajandream M-A., Salzberg S., Saunders D., Seegar K., Sharp S., Warren T.,
A Denning D.W., Barrell B., Hall N.;
Insight into the genome of Aspergillus fumigatus: analysis of a 922 region encompassing the nitrate assimilation gene cluster.";
Fungal Genet. Biol. 41:443-453(2004).
C-1-SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
RMBL; BX649605; CAB47904.1; -.
RITERPRO; IPR001092; HLH_basic.
R Ffam; PF00010; HLH; 1.
RMART; SM00353; HLH; 1.
RMART; SM00353; HLH; 1.
RPOSITE; PS50888; HLH; 1.
ROSITE; PS50888; HLH; 1.
                                       Collins M.,
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                                                                                                             a 922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium tetani.
Bacteria, Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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; 4FE4S_FERREDOXIN; 2.
proteome; Iron; Iron-sulfur; Metal-binding.
A; 49052 WW; 6F98DC0B98F52C78 CRC64;
                                                                                                                                                                                                                                                               Length 399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 100.0%; Score 36; DB 2; Length 449; Local Similarity 100.0%; Pred. No. 2.3e+02; nes 5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                            Indels
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
RnfC/ngrF.
                                                                                                                                                                                                                                                              100.0%; Score 36; DB 2; I
100.0%; Pred. No. 2.1e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=CTC01019;
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PS00198; 4F
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SEQUENCE FROM N.A.
STRAIN-Massachusett:
MEDLINE=22457253; Pi
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E 449 AA;
          SEQUENCE FROM N.A.
Pubmed=14998527; I
Pain A., Woodward
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Q89615;
01-JUN-2003
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Q89615
ID Q8
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MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;

Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,

Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,

Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,

Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;

"Nucleotide sequence and predicted functions of the entire

C.!- CATALYTIC ACTIVITY: L-2,4-diaminobutyrate + 2-oxoglutarate = L-

Glutamate + L-aspartic 4-semialdehyde.

C.!- CATALYTIC ACTIVITY: L-2,4-diaminobutyrate + 2-oxoglutarate = L-

Glutamate + L-aspartic 4-semialdehyde.

C.!- CATALYTIC ACTIVITY: Belongs to the class-III pyridoxal-phosphate-dependent

C.!- PATHWAY: Siderophore biosynthesis; rhizobactin biosynthesis.

C.!- SIMILARITY: Belongs to the class-III pyridoxal-phosphate-dependent

aminotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Generation of the region encoding regulation, biosynthesis, and transport of rhizobactin 1021, a siderophore produced by Sinorhizobium meliloti.";
J. Bacteriol. 183:2576-2585(2001).
                                                                                                                                                                                                                                                                                                         MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
25-MAY-2004 (Rel. 45, Last annotation update)
Diaminobutyrate--2-oxoglutarate aminotransferase (EC 2.6.1.76) (L-diaminobutyric acid transaminase) (Diaminobutyrate transaminase) aminotransferase (BC 2.6.1.76) (AB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=rhbA; Synonyms=rhsA; OrderedLocusNames=RA1258; ORFNames=SMa2400; Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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STRAIN=RCR2011 / SU47;
MEDLINE=21172875; PubMed=11274118;
DOI=10.1128/JB.183.8.2576-2585.2001;
Lynch D., O'Brien J., Welch T., Clarke P., Cuiv P.O., Crosa J.H., O'Connell M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSEPP P12995; 1003.

HSEPPCO IPRO04637; Dat.

InterPro; IPR004637; Dat.

Pfam; PF00202; Aminotran 3; 1.

TIGRFAMS; TIGR00709; dat; 1.

TIGRFAMS; TIGR01885; Orn aminotrans; 1.

PROSITE; PS00600; AA TRANSFER CLASS 3; 1.

Aminotransferase; Complete proteome; Iron transport; Plasmid; Pyridoxal phosphate; Transferase.
                                                                                                                                                                                                                               470 AA
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                                                                                                                                                                                                                           STANDARD;
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PIR; T46814; T46814.
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25 HPPHG 29
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493 AA;
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X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                          Gaps
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Catarrhini; Hominidae; Homo.
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EMBL; AE017240; AAS06271.1; -. Complete proteome.
SEQUENCE 491 AA; 54266 MW; 442E24F9A831D8E0 CRC64;
 Pyridoxal phosphate (Potential). 0377B3BBBBA09049 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                          Score 36; DB 1; Length 470;
Pred. No. 2.4e+02;
Mismatches 0; Indels
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Pred. No. 2.5e+02;
Mismatches 0; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                               073TJ7;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
OrderedLocusNames=MAP3721;
                                                                                                                                                                                                                                                                                             491 AA
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Mammalia; Eutheria; Primates;
 304 E
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Best Local Similarity 100.
Matches 5, Conservative
                                                                                 Similarity 100
5; Conservative
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 304
470 AA;
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Matches 5
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SEQUENCE
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RAdams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beson K.Y., Benos P.V., Bernal B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriera S., Fleischmann W.,

RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibbegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibbegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum R.
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 36; DB 2; Length 493;
; Pred. No. 2.5e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062581; AAH62581.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003598; Ig.cl.
InterPro; IPR003598; Ig.cl.
InterPro; IPR003596; Ig.v.
R InterPro; IPR003596; Ig.v.
R SMART; SM00409; IG; 4.
SMART; SM00409; IGc1; 2.
SMART; SM00406; IGv; 2.
R PROSITE; PS50835; IG_LIKE; 4.
HYpothetical protein.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CG13506-PA.
                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Best Local Similarity 100.
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244 HPPHG 248

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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Melson D.R., Spittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
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Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R. Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster euchromatic genome: a
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Pred. No. 2.6e+02;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG LIKE; 3. 57072 MW; 8B37EE13309A511E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003457; AAF46839.2; -. FlyBase; FBgn0034723; CG13506. InterPro; IPR003599; Ig. InterPro; IPR007110; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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SMART; SM00409; IG;
PROSITE; PS50835; IC
SEQUENCE 503 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein.";

Elycoprotein.";

Slockemistry 35:1925-1934(1996).

Slockemistry and divalent metal ions. It can inhibit rosette formation and is known to interact with heparin, thrombospondin, and the lysine-binding site of plasminogen. On the basis of its homology with HMW kininogen, the His-rich region of this protein may mediate the contact activation phase of intrinsic blood coagulation cascade.

Slockemistry and secreted in plasma.

Slockemistry and secreted in plasma.
                                                                                                                                                                                                                                                               Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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(Potential).
(Potential).
(Potential).
(Potential).
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InterPro; IPR000010; Prot_inh_cystat.
Pfam; PF00031; Cystatin; I.
Direct protein sequencing; Glycoprotein; Heparin-binding; Repeat; Signal.
NON_TER 1 1
SIGNAL <1 8 Potential.
                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Histidine-rich glycoprotein precursor (Histidine-proline rich glycoprotein) (HPRG) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 9-23; 301-313 AND 422-429
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Serum;
MEDLINE=96229917; PubMed=8639676; DOI=10.1021/bi952061t;
Borza D.-B., Tatum F.M., Morgan W.T.;
"Domain structure and conformation of histidine-proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Potential.
Histidine-rich glycoprotein.
Cystatin-like 1.
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Pro-rich.
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N-linked
Cleavage
                                                       STANDARD;
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CARBOHYD
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NCBI_TaxID=672;
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Q87RZ6
ID Q87RZ
AC Q87RZ
DT O1-JU
DT O1-MA
DE HYPOT
OS VIBEL
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OX VIBEL
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RR SEQUE
RR SEQUE
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X TISSUE=Embryo;

X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

X Altschul S.F., Zeeberg B., Buetow K.H., Scheetz T.E.,

X Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

X Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

X Robark S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Robards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X Nillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

X Raha Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

X Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

X Zonner A., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
HMG-box transcription factor (Transcription factor 7-like 1a) (T-cell
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Zebrafish) (Danio rerio).
; Chordata; Craniata; Vertebrata; Euteleostomi;
opterygii; Teleostei; Ostariophysi; Cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AF097410; AAC64609.1; -.

EMBL; BC053135; AAH53135.1; -.

HSSP; P27782; 2LEF.

ZFIN; ZDB-GENE-980605-30; tcf711a.

GO; GO:0003677; F:DNA binding; IEA.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPR009071; HMG-box.

InterPro; IPR00910; HMG_12_box.

Pfam; PF00505; HMG_box; 1.

SMART; SM00398; HMG_12.
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"Function of zebrafish beta-catenin and TCF-3 in dorsoventral
                                                                                                      100.0%; Score 36; DB 1; Length 526; 100.0%; Pred. No. 2.7e+02; ive 0; Mismatches 0; Indels
Cleavage (by plasmin).
810F23D367D93D42 CRC64;
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422 C
58877 MW;
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Name=tcf7lla; Synonyms=TCF-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patterning.";
Mech. Dev. 77:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (S
Eukaryota, Metazoa,
Actinopterygii, Neor
Cyprinidae, Danio.
  421
526 AA;
                                                                                                                                                  Similarity
5; Conserv
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TISSUE=Embryo;
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STRAIN=RIMD 2210633 / Serotype O3:K6;
STRAIN=RIMD 2210633 / Serotype O3:K6;
MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
                                                                                                                  Gaps
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=VP0628;
Vibrio parahaemolyticus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Predicted metal-dependent hydrolase with the TIM-barrel fol OrderedLocusNames=VV13145;
Vibrio vulnificus.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP005075; BAC58891.1; -.
GO; GO:0016787; F:hydrolase activity; IEA.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR011550; Amidohydro_like.
InterPro; IPR011059; Metalo_hydrolase.
Pfam; PF01979; Amidohydro_1; 1.
ProDom; PD001248; Amidohydro_like; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 581 AA; 64511 MW; 292D0C34F2159F9E CRC64;
61459 MW; DC35C50EA4D61232 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein VP0628.
                                                      100.0%; Score 36; DB 2; I 100.0%; Pred. No. 2.9e+02;
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100.0%; Pred. No. 3e+02;
ive 0; Mismatches 0
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Predicted metal-dependent hydrolase.
OrderedLocusNames=VV1141;
Vibrio vulnificus (strain YJ016).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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                                                                                                                                                                                                       100.0%; Score 36; DB 2; Length 583; 100.0%; Pred. No. 3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                  64278 MW; 64AF798F8DCE69A6 CRC64;
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Last annotation update)
EMBL; AE016807; AA011465.1; -. GO; GO:0016787; F:hydrolase activity; IEA. InterPro; IPR006680; Amidohydro 1. InterPro; IPR011550; Amidohydro 1. InterPro; IPR011059; Metalo hydrolase. Pfam; PF01979; Amidohydro 1; 1. ProDom; PD001248; Amidohydro 1; 1. Complete proteome; Hydrolase. SEQUENCE 583 AA; 64278 MW; 64AF798F8DCE6
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InterPro; IPR011550; Amidohydro 1.
InterPro; IPR011059; Metalo hydrolase.
Pfam; PF01979; Amidohydro 1; 1.
ProDom; PD001248; Amidohydro 1; 1.
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Q75HV8;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last anno
Hypothetical protein OSJNBb0092G21.7;
Name=OSJNBb0092G21.7;
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|HPPHG 352
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Complete proteome,
SEQUENCE 587 AA,
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01-MAR-2004
01-MAR-2004
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RESIDENCE FROM N.A.

2. SEQUENCE FROM N.A.

2. Chord T.-Y. Idang S.-U. C., Chen C.-S., Chen H.-H., Liu S.-M.,

2. Chord T.-Y. Chang S.-U. C. Chen C.-S., Chen H.-H., Liu S.-M.,

2. Chord T.-Y. Idang S.-U. Chang S.-U. Chen S.-Y. Chen S.-Y. Yu S.-W.,

2. Chen T.-Y. Idang S.-U. Lin Y.-C., Ang S.-W. Yu C.-Y. Yu S.-W.,

2. Lin Y.-P. Lin S.-J. Lin Y.-C., Ang S.-W. Yu C.-Y. Yu S.-W.,

2. Submitted MAY-2004 to the Resulcheank/DDBJ databases.

3. Submitted MAY-2004 to the Resulcheank/DDBJ databases.

3. Submitted MAY-2004 to the Resulcheank/DDBJ databases.

3. Submitted MAY-2004 to the Resulcheank/DDB databases.

3. Characteristic MAY-2004 to the Resulcheank/DDB databases.

3. Characteristic MAY-2004 to the Resulcheank/DDB databases.

3. Submitted MAY-2004 to the Resulcheank/DDB databases.

3. Submitted MAY-2004 (TERBERA) 3. Latt sequence update)

3. Submitted MAY-2004 (TERBERA) 3. Latt
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Query Match
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Q95R83
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    Zheng L.,
Zhu X., Smith H.O.,
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MEDLINE-21426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         elements of the Drosophila melanogaster euchromatin:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Svirskas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaste
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to tr|Q873A0 Neurospora crassa B24N11.240.gene.
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Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195 (2000).
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100.0%; Pred. No. 3.7e+02;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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78778 MW;
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Eukaryota, Fungi, Asc
Saccharomycetales, Di
NCBI_TaxID=284591;
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Submitted (MAR-2004)
EMBL; AE003840; AAO:
FlyBase; FBgn0050492
SEQUENCE 723 AA;
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5; Conserv
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SEQUENCE FROM N.A.
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Submitted (SEP-200)
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ORFNames=YALIOF101.
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                                                                                                                                                                                         SEQUENCE FROM
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Best Local S
Matches 5
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Q6C276;
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Q6C276
ID Q6C27
AC Q6C27
DT 25-OC
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                STRAIN—CLIB99;
Genolevures;
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
Dujon B., Sherman D., Fischer G., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Roszul R., Lemaire M., Joyet P., Kachouri R.,
Rerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Seniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
"Thierry A., "Charle J.L.;
"Genome evolution in yeasts.";
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY061574; AAL29122.1; -.
FlyBase; FBgn0050492; CG30492.
SEQUENCE 773 AA; 84486 MW; 674466ECDC7B0FFF CRC64;
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 36; DB 2; Length 736; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382132; CAG78043.1; -.
SEQUENCE 736 AA; 79795 MW; A63EAAE2BA4CE2A2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Name=BcDNA:GH02712; ORFNames=CG30492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 430:35-44(2004)
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nes 5; Conser
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FROM N.A
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RESULT 35
Q91562
ID 09156
      REPRESENTATIONS OF SERVICE SER
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RR PEDIJNE-20196006; Pubwed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D. Cellniker S.E., in Puw. Hoskins R.A., Galle R.F.

RA George R.A., Lewis B.E., Richards S., Ashburnar M., Henderson S.N., Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Batter E.G., Helt G., Nelson C.R., Baldwin D., Abril J.F., Agbayani A., Barter B.G., Helt G., Nelson C.R., Baldwin D., RA Ballew R.M., Basu A., Bayarkataroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolahakov S., Borchan M.R., Bouck J., Borcktein P., Brottier P., Cawley S., Dahlke C., Davenport L.B., Davises P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davises P., Borchan M.R., Bouck J., Borcktein P., Brottier P., Brottier P., Borden S., Dalike C., Davenport L.B., Davises P., Borson K.Y., Bouck J., Borden S., Dalike C., Davenport L.B., Davises P., Borners M.D., Davises P., Gorger S., Gorle L. Mays B., Dalike C., Davenport L.B., Davises P., Bourel J.H., Gu Z., Gelbart, M.M., Classer K., A. Godge P., Gorrell J.H., Gu Z., Gelbart, M.M., Classer K., A. Godge P., Gorrell J.H., Gu Z., Gelbart, M.M., Classer K., A. Godge P., Gorrell J.H., Ke Z., Kennison J.A., Retchum K.A., Hostinn D., Houston K.A., Hewland T.J., Mei M.H. Ibegwan C., Martei B., Molincoh T.C., McLeod M.P., McPhartis M., Milshins N.W., Molandor J.M., Molandor J., Lia Z., Liang Y., Lin X., Martei B., McIncoh T.C., Molandor J., Munny D.M., Nelson D.L., Ranket B. M. Milshins N.W., Molandor J., Pull S., Pan S., Pollard J., Wosherei J., Shon H., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Santh T., Shien B.C., Stapleton M., Skupski M.P., Shien H., Shien B.C., Stapleton M., Skupski M.P., Shien B., Shiens S., Man WoodageT, Worley K.C., Wu D., Yang S., Zhon X., Santh H., Rang X.H., Zaveri J.S., Zhon M., Weinstern D., Weille S., Shien K., Remigner C., Phill M., Weinster D., Shiens B., Shiens B., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22426065; Pubmed=12537568;
MEDLINE=22426065; Pubmed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams R.A., Laverty T., Muzny D.M., Nelson C.R., George R.A., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Pacleb J.M., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C. Svirskas R., Tabor P.E., Myers E.W., Gibbs R.A., Rubin G.M.; Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                    Last sequence update)
Last annotation update)
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EARCH0079-RESEARCH0079(2002)
                          938 AA
                                                                           Created)
                            PRT;
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                                                                       (TrEMBLrel. 24, (TrEMBLrel. 24, 1 (TrEMBLrel. 26, 1
                          PRELIMINARY;
                                            QB6BB9;
01-JUN-2003 (TrEMB)
01-JUN-2003 (TrEMB)
01-MAR-2004 (TrEMB)
CG30492-PE.
ORFNames=CG30492;
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3:RESE
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melanogaster e
Genome Biol. 3
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                                                                    MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                                                                                                                                                                        Annotation of the Drosophila melanogaster euchromatic genome:
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY226102; AAP48572.1; -.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; RRM 1; 3.
SMART; SM00360; RRM; 6.
PROSITE; PS50102; RRM; 3.
SEQUENCE 1075 AA; 120486 MW; 24A993DB6F4BCBD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0050492; CG30492.
InterPro; IPR011011; FYVE PHD ZnF.
InterPro; IPR011009; Kinase lTke.
SEQUENCE 938 AA; 102954 MW; 9984B6D579A1EA14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 36; DB 2; L
100.0%; Pred. No. 4.8e+02;
ive 0; Mismatches 0;
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002)
                                                                                                                                                                                                                                                                                                                                    systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729 HPPHG 733
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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05-JUL-2004
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Q6XLI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase
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PRT; 1427 AA.

PRELIMINARY;

091562

us-10-074-225a-9.rup

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DCC_HUMAN
P43146;
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DCC_HUMAN
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MEDLINE=97015074; PubMed=8861902; DOI=10.1016/S0092-8674(00)81336-7;

MEDLINE=97015074; PubMed=8861902; DOI=10.1016/S0092; PubMed=870094; PubMed=8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                             the deleted in colorectal cancer (DCC) developing Xenopus embryos.";
                                                                                                                                                                                                                                                                                              MEDLINE=95113183; PubMed=7813784; DOI=10.1006/dbio.1994.1345; WEDLINE=95113183; PubMed=7813784; DOI=10.1006/dbio.1994.1345; WAEDLINE=95113183; PubMed=7813784; DOI=10.1006/dbio.1994.1345; WAEDLINE=95113183; PubMed=7813784; DOI=10.1006/dbio.1994.1345; RT Rearon E.R.; Reale M.A., Candia A.F., Wright C.V., Cho K.R., Rearon E.R.; Rearon e.R.; Rearon of a homologue of the deleted in colorectal cancer (DC RT gene in the nervous system of developing Xenopus embryos."; DR EMBL; U10986; AAA70168.1; -.. DR EMBL; U10986; AAA70168.1; -.. DR Pfam; PF00041; fin3; 6. DR Pfam; PF00047; ig; 1. DR Pfam; PF0583; Neogenin C; 1. DR Pfam; PF0583; Neogenin C; 1. DR Pfam; PF0583; RG.2; 3. DR PROSITE; PS50835; IG_LIKE; 4. BROSITE; PS50835; IG_LIKE; 4. BROSITE; PS50835; IG_LIKE; 4.
                                                                                                         Tumor suppressor.
Name=XDCCa;
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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0
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                            Created)
Last sequence update)
Last annotation update)
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01,
26,
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Best Local Similarity 100.
Matches 5; Conservative
Q91562;
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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Q63155
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MEDLINE=90100559; PubMed=2294591;
Fearon E.R., Cho K.R., Nigro J.M., Kern S.E., Simons J.W.,
Ruppert J.M., Hamilton S.R., Preisinger A.C., Thomas G., Kinzler K.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a chromosome 18q gene that is altered in colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE=91121517; PubMed=1991322; DOI=10.1016/0092-8674(91)90244-S;
Nigro J.M., Cho K.R., Fearon E.R., Kern S.E., Ruppert J.M.,
Oliner J.D., Kinzler K.W., Vogelstein B.;
"Scrambled exons.";
Cell 64:607-613(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Genes Dev. 8:1174-1183(1994).
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MEDLINE=94245241; PubMed=8188295;
Cho K.R., Oliner J.D., Simons J.W., Hedrick L., Fearon E.R.,
Preisinger A.C., Hedge P., Silverman G.A., Vogelstein B.;
"The DCC gene: structural analysis and mutations in colorectal carcinomas.";
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PubMed=9334332;
Hu G., Zhang S., Vidal M., Baer J.L., Xu T., Fearon E.R.;
"Mammalian homologs of seven in absentia regulate DCC via the
                                                                                                                                                                                                                                                                                                                                                     Length 1445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Netrin receptor DCC precursor (Tumor suppressor protein DCC)
(Colorectal cancer suppressor).
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MEDLINE=95011532; PubMed=7926722;
Hedrick L., Cho K.R., Fearon E.R., Wu T.-C., Kinzler K.W.,
Vogelstein B.;
SMART; SM00060; FN3; 6.
SMART; SM00408; IGC2; 3.
PROSITE; PS50853; FN3; 6.
PROSITE; PS50835; IG_LIKE; 4.
SEQUENCE 1445 AA; 157940 MW; 084F625954481988 CRC64;
                                                                                                                                                                                                                                                                                                                                            100.0%; Score 36; DB 2; 1
100.0%; Pred. No. 7.3e+02;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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Science 247:49-56(1990).
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                                                                          REM VARIANT CARCINOWA THR-168, AND VARIANT GLY-201.

REM MEDLINE-94243822; PubMed-8187090;

RA Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;

Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;

Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;

Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;

Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;

Miyake S., Nagai K., Yoshino K., Oto M., Endo M., Yuasa Y.;

Recaptor mutations and allelic deletion of tumor suppressor gene of the system upon ligand binding. Its association with UNC5 proteins may trigger signaling for axon requision. It also acts as a dependence receptor required for apoptosis induction when not associated with netrin ligand. Implicated as a tumor suppressor gene.

C. SUBUMAT: Interact with the cytoplasmic part of UNC5A, UNC5B, UNC5C and probably UNC5D (By similarity).

C. SUBUMAT: Interact with the cytoplasmic part of UNC5A, UNC5C.

INCSC and probably UNC5D (By similarity).

C. SUBCELLULAR LOCATION: Type I membrane protein.

C. SUBCELLULAR LOCATION of DCC due to allelic deletion and/or differentiate into mucus producing cells uniformly lack DCC expression. Inactivation of DCC due to allelic deletion and/or metastasis of esophageal squamous cell carcinomas.

C. SIMILARITY: Contains 6 fibronectin type III domains.

C. SIMILARITY: Contains 6 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PROSITE; PS50835; IG LIKE; 4.
Anti-oncogene; Apoptosis; Developmental protein; Disease mutation; Glycoprotein; Immunoglobulin domain; Polymorphism; Receptor; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transmembrane receptor activity; TAS
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EMBL; M32286; AAA52174.1; --
EMBL; M32286; AAA52176.1; --
EMBL; M32289; AAA52176.1; --
EMBL; M32290; AAA52176.1; --
EMBL; M32290; AAA52176.1; --
EMBL; M63696; AAA52177.1; --
EMBL; M63700; AAA52180.1; --
EMBL; M63702; AAA52180.1; --
EMBL; M63702; AAA52180.1; --
EMBL; M63698; AAA52181.1; --
EMBL; M63698; AAA52181.1; --
EMBL; M63698; P: transmembrane receptor activity
Go, GO:000409; P: axonogenesis; TAS.
GO, GO:000409; P: axonogenesis; TAS.
GO, GO:000409; P: axonogenesis; TAS.
InterPro; IPR003961; FN III-like.
InterPro; IPR003961; FN III-like.
InterPro; IPR003962; Fn III subd.
InterPro; IPR003963; Rogenin C.
Emmi; PF00041; En3; 6.
Emmi; PF00041; En3; 6.
Emmi; PF00041; En3; 6.
Emmi; PF00041; En3; 6.
Emmi; PF00691; ISB A.
Emmi; PF00041; En3; 6.
Emmi; PF00691; ISB A.
Emmi; PF00041; En3; 6.
Emmi; PF00691; ISB A.
Emmi; PF0069
ubiquitin-proteasome pathway.";
Genes Dev. 11:2701-2714(1997).
[7]
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Cooper H.M.;
Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor for netrin required for axon guidance. Mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cooper H.M., Armes P., Britto J., Gad J., Wilks A.F.; "Cloning of the mouse homologue of the deleted in colorectal cancer gene (mDCC) and its expression in the developing mouse embryo."; Oncogene 11:2243-2254(1995).
                                      Netrin raceptor DCC.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Ig-like C2-type 1.
Ig-like C2-type 2.
Ig-like C2-type 3.
Ig-like C2-type 4.
Fibronectin type-III 1.
Fibronectin type-III 2.
Fibronectin type-III 5.
Fibronectin type-III 6.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. .) (Potential).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Netrin receptor DCC precursor (Tumor suppressor protein DCC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sing (in Ref. 3).
sing (in Ref. 3).
sing (in Ref. 3).
4A8612766ED0471F CRC64;
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STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=96112625; PubMed=8570174;
                           Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missing
Missing
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939
1041
   Transmembrane;
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233 32
421 42
1447 AA;
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Best Local Similarity
Matches 5; Conser
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DCC_MOUSE
ID DCC_MOUSE
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operan terracion of internon growth comes to the developmentary concerns attraction than the internol operan upon ligand binding lies association with NGS procedum and trigger signaling for acon reputation. It is the acts as a dependency concern ligant. Implicated as a tunne support of NGS, NGCS, NG
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Cochliobolus heterostrophus (Drechslera maydis).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; Cochliobolus.
NCBI_TaxID=5016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         'FTId=VSP_002501.
                 Fibronectin type-III 4.
Fibronectin type-III 5.
Fibronectin type-III 6.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC...) (N-linked (GlCNAC...) (Missing (in isoform C)...)
    6 4 10 4
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Putative histidine kinase HHK2p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 36; DB 1; I
100.0%; Pred. No. 7.3e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2013 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158298 MW;
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Best Local Similarity 100.
Matches 5; Conservative
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                       814
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fam; PF00989; PAS;
fam; PF00072; Respo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1447 AA;
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Q9SBAO;
Q9SBAO;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Ribulose BIPHOSPHATE carboxylase small subunit (Fragment).
Pinus monticola (Western white pine).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
NCBI_TaxID=3345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE.
MEDLINE=96213005; PubMed=8665095;
Ekramoddoullah A.K., Taylor D.W.;
Ekramoddoullah A.K., Taylor D.W.;
"Seasonal variation of western white pine (Pinus monticola D. Don)
foliage proteins.";
foliage proteins.";
Plant Cell Physiol. 37:189-199(1996).
SEQUENCE 16 AA; 1803 MW; 27D4934C881717DE CRC64;
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                                                                                                                                                                                                                             100.0%; Score 36; DB 2; Length 2013; 100.0%; Pred. No. 1e+03; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 16;
                                                                                                                                                                   RESPONSE REGULATORY; 1.
ation; Sensory transduction.
1; 219997 MW; E4B99CFCC9D57065 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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PRINTS; PR00344; BCTRLSENSOR.
ProDom; PD000039; Response_reg; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HiskA; 1.
SMART; SM00086; PAC; 2.
SMART; SM00091; PAS; 2.
SMART; SM00091; PAS; 2.
SMART; SM00448; REC; 1.
TIGRFAM8; TIGR00229; sensory_box; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50113; PAC; 2.
PROSITE; PS50112; PAS; 2.
PROSITE; PS50110; RESPONSE_REGULATORY; Kinase; Phosphorylation; Sensory trans SEQUENCE 2013 AA; 219997 MW; E4B99
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HPPHG |||:| HPPYG

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Search completed: June Job time : 86.5 secs

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Thu Jun 16 13:0

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- protein search, using sw model OM protein

June 15, Run on:

2005, 13:52:01; Search time 90 Seconds (without alignments) 21.487 Million cell updates/sec

US-10-074-225A-10 35 1 PPPHG 5

Title: Perfect score:

Scoring table:

Sequence:

0.0 , Gapext 0.5 BLOSUM62 Gapop 10 seqs, 386760381 residues 2105692 Searched: Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: ( Maximum DB seq length: 2

Match 0% Match 100% first 45 summaries Post-processing: Minimum Maximum Listing

Database :

A\_Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
4: geneseqp2001s:\*
5: geneseqp2001s:\*
6: geneseqp2003s:\*
7: geneseqp2003s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		þ				
Result		Query				
No.	Score	Match	Match Length DB	DB	σı	Description
-	35	100.0	5	5	ABB79811	Abb79811 Histidine
~	35	100.0	S	α	ADH10416	Adh10416 Rabbit HP
ო	35	100.0	17	m	AAB39278	Aab39278 Human sec
4	35	100.0	53	4	ABB70178	Abb70178 Drosophil
ហ	35	100.0	55	4	AAM15229	Aam15229 Peptide #
9	35	100.0	52	4	ABB34219	Abb34219 Peptide #
7	35	100.0	55	4	AAM27690	Aam27690 Peptide #
œ	35	100.0	55	4	ABB29058	Abb29058 Peptide #
σ	35	100.0	55	4	ABB19655	Abb19655 Protein #
10	35	100.0	52	4	AAM67398	Aam67398 Human bon
11	35	100.0	55	4	AAM55013	Aam55013 Human bra
12	35	100.0	52	4	ABG49057	Abg49057 Human liv
13	35	100.0	52	4	AAM02972	Aam02972 Peptide #
14	35	100.0	52	ស	ABG37025	Abg37025 Human pep
15	35	100.0	57	4	AAU54664	
16	35	100.0	57	9	ABM51183	Abm51183 Propionib
17	35	100.0	9	4	AAU43160	Aau43160 Propionib
18	35	100.0	9	9	ABM39679	
19	35	100.0	61	4	AAM37888	Aam37888 Peptide #
20	35	100.0	61	4	AAM77682	Aam77682 Human bon
21	35	100.0	61	4	AAM64953	Aam64953 Human bra
22	32	100.0	61	4	ABG59329	Abg59329 Human liv
	35	100.0	75	4	AAU32380	
24	35	100.0	77	4	AAU41116	Aau41116 Propionib
25	32	100.0	77	4	AAU43934	Aau43934 Propionib

Propionib Human 5' Drosophil Human ORF Protein e Novel hum Klebsiell Rabbit HP Klebsiell Human gly Glycosyl Arabidops Arabidops Human pol Human pol Human nov Human con Propionib	
Abm40453 Abm37635 Aby12827 Abb611024 Abb10412 Abc63515 Adc6179 Aag67890 Aag67890 Aag67890 Aag16967 Aac01973 Aac01253 Adc32845 Adc32845 Adc32845 Adc32845 Adc4880 Abm41399	
ABM40453 ABM37635 AAY12827 ABB61183 ABB11024 ABB224494 ABG24494 ABG24494 ABG6179 AAG67890 AAG67890 AAG67890 AAG67890 AAG67890 AAG67890 AAG67890 AAG67890 AAG67890 AAG67890 AAG67890	
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## ALIGNMENTS

ABB79811 standard; peptide; 5 AA RESULT 1 ABB79811

(first entry) 25-NOV-2002 Histidine proline rich glycoprotein pentapeptide.

Histidine proline rich glycoprotein; HPRG; antiangiogenic; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; gynaecological; antiarthritic; antiulcer; osteopathic; antitumour; ophthalmological; nootropic; neuroprotective; antiparkinsonian. 

Synthetic

WO200264621-A2.

22-AUG-2002.

14-FEB-2002; 2002WO-US004336

14-FEB-2001; 2001US-0268370P

(ATTE-) ATTENUON LLC.

Mazar AP; Plunkett ML, Harris S, Donate F,

WPI; 2002-666989/71.

New histidine-proline rich glycoprotein (HPRG) polypeptide, useful for diagnosing or treating diseases associated with undesired cell migration, invasion, proliferation, or angiogenesis, e.g. cancer, atherosclerosis.

Claim 2; Page 67; 82pp; English

The present sequence is a specific example of claimed anti-angiogenic pentapeptides of the invention. Claimed anti-angiogenic polypeptides or peptides comprise: the histidine-proline-rich (H/P) domain of human histidine proline rich glycoprotein (HPRG, see ABB79806); an H/P domain of rabbit HPRG (see ABB79807); a variant of these that is capable of inhibiting angiogenesis, endothelial cell proliferation or endothelial tube formation in vitro or in vivo; or a pentapeptide having the generic sequence given in ABB79808, such as the present peptide, or its variant having an additional 1 to 4 amino acids comprising His, Pro or Gly at its No or C-terminus. Also claimed are: chemically synthesised or recombinantly produced peptide multimers; a diagnostically or

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multimer; a diagnostically useful HPRG-related composition, comprising the diagnostically labeled polypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the diagnostically labeled polypeptide, peptide or peptide multimer and a carrier; an antibody specific for an epitope of HPRG that is present in the HPR domain of human or rabbit HPRG, and which binds to HPRG or to any of the domains in a way which inhibits the anti-angiogenic activity of HPRG or the domain, or an antigan-binding fragment of the antibody; a method for inhibiting call migration, cell invasion, cell proliferation or angiogenesis, a method for treating a medical migration, invasion, proliferation, or angiogenesis; a method of stimulating or inhibiting angiogenesis in a subject; a method of estimulating or inhibiting angiogenesis in a subject; a method of stimulating or inhibiting angiogenesis in a subject; a method of estimulating or inhibiting angiogenesis in a subject; a method of stimulating or inhibiting angiogenesis in a subject; transfected cells; a method of providing to a cell, tissue or organ andial peptide multimer; an affinity ligand useful for transfected cells; a method of providing to a cell, tissue or organ and peptide multimer; an affinity ligand useful for the binding molecule, comprising the polypeptide, peptide or peptide multimer; and anthod of conjudical support or carrier; and a method of soluting molecule, or isolating or enriching cells captions and methods are useful in diagnosing or treating a disease or condition associated with undesired cell migration, invasion, proliferation, or angiogenesis, such as cancer, atherosclerosis, diabetic cells and methodes are useful in inhibiting the growth of primary cumours or metastases, and may also be used in treating neurodegenerative ethical processes into and may also be used in treating neurodegenerative ethical processes and may also be used in treating are ethical processes.
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 peptide or peptide
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rich glycoprotein; HPRG; cytostatic; antidiabeticantiinflammatory; gynaecological; antiarthritic;
rmatological; cardiant; vasotropic; vulnerary;
therapy; rabbit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
therapeutically labeled anti-angiogenic polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein H/P rich domain repeat fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 35; DB 5; I
100.0%; Pred. No. 1.8e+06;
vative 0; Mismatches 0;
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histidine-proline rich glycopro
ophthalmological; antiinflamma(
antipsoriatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAR-2003; 2003WO-US008060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cunicu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stimulators of ang
neovascularization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADH10416 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO2003077872-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPPHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit HPRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADH10416;
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ADH10416
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The invention relates to an isolated tropomyosin (Tpm)-related
antiangioganic receptor polypeptide or peptide, which is a is a fragment
of a full-length native Tpm protein expressed on the surface of
a full-length native Tpm protein expressed on the surface of
of a full-length native Tpm protein expressed on the surface of
c andothelial cells, or a variant of the fragment. It has a molecular mass
of about 17 kDa and corresponds in its sequence to, or is a variant of,
an internal fragment of a native Tpm its sequence to, or is a variant of,
of applyeptide peptide or variant has substantially the same biochemical
activity of binding to the antiangiogenic polypeptide agent that
protein to the isolated polypeptide or peptide is human histidine-proline
c native Tpm internal fragment. The antiangiogenic polypeptide agent that
binds to the isolated polypeptide or peptide is human histidine-proline
c rich glycoprotein (HRRG), rabbit HPRG, a Tpm-binding, antiangiogenic homologue, variant, domain of fragment of the HRR or its D5
c human kininogen (HK), the D5 domain of HK, or a Tpm-binding,
c companion. The Tpm-related antiangiogenic receptor polypeptide or peptide
antiangiogenic homologue, variant, domain or fragment of the HR or its D5
c antiangiogenic homologue, variant, domain or fragment of the HR or its D5
c antiangiogenic homologue, variant, domain or fragment of the HR or its D5
c antiangiogenic pomologue, variant, domain or fragment of the HR or its D5
c antiangiogenic pomologue, variant, domain or angiogenesis, for inducing
migration, invasion, proliferation or angiogenesis, for inducing
c endothelial cell apoptosis, or for treating tumours or cancer, diabetic
c retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis,
c psoriasis, or scleroderma. The antibody may be also used for detecting
the presence of a Tpm polypeptide or peptide in a biological sample,
c promoting wound healing, or for treating diseases or conditions in which
increased angiogenesis is desired engangenesis.
c fragment present i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; neoplasm; opthalmalogical; autoimmune disease; rheumatoid arthritis; angiogenesis; hyperproliferative disorder; cardiovascular disorder; infection; cerebrovascular disorder; nervous system disorder; ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; immunosuppressive; antiarthritic; antirheumatic;
                                                                                     New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein sequence encoded by gene 31 SEQ ID NO:158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
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Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0;
Mazar AP;
                                                                                                                                                                                                                       Example 5; SEQ ID NO 30; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB39278 standard; protein; 17 AA.
Juarez J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chemotaxis.
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Donate F,
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Mccrae K,
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11-JUL-2000; 2000US-00614150
                                                                                  N-PSDB; ABL14281
                                                                                                                                                                                                                                                                                                               Sequence 53 AA;
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Best Local S
Matches 5
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 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The polymucleotide sequences given in AAC74223-C74279 encode the human secreted proteins represented in AAB39179-B39226. Sequences AAB39227-C78939308 are alternative proteins encoded by the genes, and also protein sequences with which they share homology. The proteins have activities bequences with which they share homology. The proteins have activities cardinate immunosuppressive, antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; cortropic; neuroprotective; antibacterial; virucide; fungicide; and coptialmalogical. The human secreted proteins, polymucleotides; and optialmalogical. The human secreted proteins, polymucleotides; and agonists of the invention may be useful in the treatment, prevention, and/or diagnosis of various disease, disorders and conditions such as autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative cisorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound chealing and epithelial cell proliferation, to regenerate tissues, maintain organs before transplantation, in chemotaxis and as a food additive or preservative e.g. to increase storage capabilities. Sequences characterisation of the genes of the invention
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                                                                                                                                        Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               developmental biology; cell signalling; insecticide;
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100.0%; Pred. No. 71;
ive 0; Mismatches
                                                                                Komatsoulis G;
                                                                                                                                                                           Disclosure; Page 52; 434pp; English
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16-MAR-2000; 2000WO-US006792
                       99US-0125362P
99US-0169980P
                                                         SCI INC
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                                                                                 Ruben SM,
                                                        (HUMA-) HUMAN GENOME
                                                                                                      WPI; 2000-579483/54.
N-PSDB; AAC74253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17 AA;
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                     19-MAR-1999;
10-DEC-1999;
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                                                                                 Rosen GA,
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                         New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide #1663 encoded by probe for measuring cervical gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 37326; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 4; Length 53; 100.0%; Pred. No. 2e+02; ive 0; Mismatches 0; Indels
                                                               Myers EW;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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                                                            PWD,
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5; Conservative
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                                                            Venter JC, Adams M,
                                                                                                                              2001-656860/75
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(PEKE ) PE CORP NY.
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(first entry)
                                                        Conservative
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5; Conserv
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                                                                                                                                                                                                                                                               genetic disorder
            Sequence 55 AA;
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                                                                                                                                                                                                                                                                                       Homo sapiens
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                                Query Match
Best Local S
Matches 5
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Matches 5
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ABB29058
ID ABB2
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                                         The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Human; foetal liver; gene expression; single exon nucleic acid probe
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                                                                                                                                                                                            Length 55;
                                                                                                                                                                                                                   Indels
human cervical epithelial cells
                                                                                                                                                                                            Score 35; DB 4; I
Pred. No. 2.1e+02;
Mismatches 0;
                       English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rank
                       487pp;
                                                                                                                                                                                                                                                                                                                       peptide; 55 AA
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
                                                                                                                                                                                          100.0%;
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2000US-0207456P.
2000US-00608408.
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                     SEQ ID NO 20055;
                                                                                                                                                                                                                                                                                                                                                                    entry
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                                                                                                                                                                                                                                                                                                                                                                   (first
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gene expression in
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                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                      PPPHG
                                                                                                                                                                       Sequence 55 AA;
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
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                      Claim
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ABB34219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP: see AAI3131315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                         expression.
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #1727 encoded by probe for measuring placental gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 55;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 35; DB 4; 1
100.0%; Pred. No. 2.1e+02;
:ive 0; Mismatches 0;
                    . 2.1e+02;
                                                0; Mismatches
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  Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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100.0%;
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from manA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                    New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                           single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                     Peptide #1709 encoded by breast cell single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                           Rank
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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                                                                                                                                                                          2001WO-US000662
                                 t entry)
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5; Conservative
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                                                                                                                                                                                                                                                                                                                               WPI; 2001-496933/54.
                                                                           microarray;
                                (firs
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11111
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                           Homo sapiens
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                                01-FEB-2002
                                                                                                                                                    09-AUG-2001
           ABB29058;
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Best Local S
Matches 5
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                                                                                      cancer.
                                                                          Human;
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ID ABB1
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AC ABB1
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                                                       Protein #1654 encoded by probe for measuring heart cell gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
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                                                                                                                 Human; gene expression; heart; microarray; vascular system;
cardiovascular disease; hypertension; cardiac arrhythmia;
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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(first entry)
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                                                                                                                                                                           congenital heart disease.
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Best Local Similarity 100.
Matches 5; Conservative
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                                                                                                                                             cardiovascular
                                                                                                                                                                                                                                                                                             WO200157274-A2
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23-JAN-2002
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27-SEP-2000; 2000US-0236359P 04-OCT-2000; 2000GB-00024263
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                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression in human
                                                                                                                                                                                                                    Conservative
                                                                                       ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived
                           ΩK,
                                                                                                                                                                                                                                                                                                                                                     Human liver peptide,
                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                              exon nucleic
                                           WPI; 2001-483446/52
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                           Hanzel
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                          SG,
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                                                              Single
brains.
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                           Penn
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ABG49057
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                                                                                                                                                                                                                                           The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                ed single exon nucleic acid probes useful for analyzing human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ssed exon; gene expression analysis; probe; microarray; e; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoded protein SEQ ID NO: 27118
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                                                                                                                                                                                                                           + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                           100.0%; Score 35; DB 4; Length 55; 100.0%; Pred. No. 2.1e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probe
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                                                                                                                                                              Rank
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                                                                     04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0234687P.
2000US-0234589F.
                                                                                                                                                              Chen W,
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                                                    30-JAN-2001; 2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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Alzheimer's disease; mu
                                                                                                                                                              Penn SG, Hanzel DK,
                                                                                                                                                                                                 Human genome-derived
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                                                                                                                                                                                                         gene expression in
                                                                                                                                                                               WPI; 2001-488900/53
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Best Local Similarity
Matches 5; Conser
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
Homo sapiens
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                                   09-AUG-2001
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AAMS5013
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                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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                                                                                                                                               analyzing gene expression
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0;
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(MOLE-) MOLECULAR DYNAMICS INC
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                                               Chen W,
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
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specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver.

(I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                          st disease; breast cancer; development disorder; se; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #1654 encoded by probe for measuring breast gene
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                                                                                                                                                                                                                                                                                                                            protein; 55 AA.
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
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2000US-0236359P
2000GB-00024263
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                          human;
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammatory
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26-MAY-2000;
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative

Claim 27; SEQ ID NO 11712; 322pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes ; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung
                                                                                                                                                                                                                                                                                                                                                                                               Human peptide encoded by genome-derived single exon probe SEQ ID 26690.
                                                                                                                                                                                                                                                                                                                                                                                                                          Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary hastiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
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breast disease and non-carcinoma tumours. Note: The sequence this patent did not form part of the printed specification, k obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                  Indels
                                                                                                                   Length
                                                                                                 100.0%; Score 35; DB 4; I
100.0%; Pred. No. 2.1e+02;
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                               ABG37025 standard; peptide;
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                                                                                                Query Match
Best Local Similarity
5; Conserve
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                                                                                  Sequence 55 AA;
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array, identifying exons in a eukaryotic genome, comprising (a)
algorithmically predicting at least one exon from genomic sequences of
algorithmically predicting at least one exon from genomic sequences of
the eukaryote; and (b) detecting specific hybridisation of detectably
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
having a fragment identical to the predicted exon, the probe is included
in the above mentioned microarray; assigning exons to a single gene,
comprising (a) identifying exons from genomic sequence by the method
above mentioned microarray; assigning exons in several
comprising (a) identifying exons from genomic sequence by the method
above mentioned microarray; assigning exons in several
comprising (a) identifying exons in the exons in several
comprising (a) identifying exons in the tissues and/or cell types indicates that
compression of the exons in the tissues and/or cell types indicates that
compression of the exons in the tissues are used for gene expression
compression of the exons in the specification, or encoded by the
comprise, and for identifying exons in a gene, particularly using human
compression reading frames (ORP). The probes are used for gene expression
concer, chronic obstructive pulmonary fibrosis, neurofibromatosis,
concer, chronic obstructive pulmonary dysplasia, primary ciliary
concern sequence is a peptide/protein encoded by a single exon probe of
the invention. Note: The sequence data for this patent did not form part
concern for present sequence and protein encoded by a single exon probe of
concern free prime appetide/protein encoded protein encoded protein e
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   detectably bound to each probe of the
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, Jen S, Carter D;
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02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 55 AA;
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AAU54664
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and diagnostic agents for determining P. acnes presence. for example, by caryme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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Jones R, Carter
                             Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 57;
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Pred. No. 2.2e+02;
0; Mismatches 0;
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Benson DR,
                                                                                                      Example 1; SEQ ID NO 15859; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitcham JL, Skeiky YAW, Persing DH,
Zhang Y, Wang S, Jen S, Lodes MJ,
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABM51183 standard; protein; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-381789/36.
N-PSDB; ACF64495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
hes 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
N-PSDB; AAS59566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 57 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PPPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2003
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ABM51183
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The invention relates to an isolated polymucleotide (ACF64435-ACF64733)
encoding a Propionibacterium acnes protein. The invention also relates to
encoding a Propionibacterium acnes protein. The invention also relates to
compared to the polymucleotides (ABM35624-ABM64536) and to
immunogenic fragments of P. acnes polypeptides. The invention a
ddittonally encompasses expression vectors and host cells comprising a
comparisor of the invention; antibodies against polypeptides of the
invention; fusion proteins comprising a polypeptide of the invention; a
comparisor of the invention; antibodies against polypeptides of the
invention; fusion proteins comprising P. acnes polypeptides,
which this method; a vaccine composition comprising P. acnes polypeptides,
comparisor of determining the presence or absence of P. acnes in a
comparient. The P. acnes polypeptides, polymucleotides, antibodies, fusion
comparient. The P. acnes polypeptides, polymucleotides, antibodies, fusion
proteins, T cell populations or antigen-presenting cells that express the
composition and a method for inhibiting the development of P. acnes in a
comparient. The P. acnes polypeptides, polymucleotides, antibodies, fusion
proteins, T cell populations or antigen-presenting cells that express the
collypeptides are useful for adagnosing preventing or treating acne,
composition of an immune response specific for a P. acnes
conclete acid hybridisation. The vaccine composition is useful for the
conclete acid hybridisation. The vaccine composition as useful for the
contained of an immune response against P. acnes, or for treating acne,
cond the kit is useful for performing a diagnostic assay. The present
contained frame) contained within the P. acnes polymucleotides or acnes polymperion
contained within the P. acnes polymered for the
convenion. Note: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format directly
convenion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
   or treating acne vulga for a P. acnes protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 57;
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100.0%; Pred. No. 2.2e+02; wiematches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes immunogenic protein #4056.
   l for diagnosing, preventing
an immune response specific
                                                           NO 15859; 1481pp; English
useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 60 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-2001; 2001WO-US012865
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                   or for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 5; Conserv
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                                                             Example 1; SEQ ID
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 polypeptide,
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Best Local S
Matches 5
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carter D;
                                                                                                      polypeptides and nucleic acids useful for diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maisonneuve JL;
Jones R, Carte
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     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indela
     Bhatia
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Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 35; DB 4; I ilarity 100.0%; Pred. No. 2.3e+02; Conservative 0; Micmatherial
     SS,
     Wang
    Mitcham JL, Wang
, Jen S, Carter
                                                                                                                                                                        Example 1; SEQ ID NO 4355; 1069pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acne vulgaris; antiseborrhoeic; dermatolo; immunostimulant; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABM39679 standard; protein; 60 AA
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Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-OCT-2001; 2001US-00978825
Persing DH, M
s J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-OCT-2003 (first entry)
                                                                                                     Propionibacterium acnes vaccinating against and treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Propionibacterium acnes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
5; Conserve
                                                  WPI; 2001-616774/71.
N-PSDB; AAS59519.
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                     L'maisonneuve J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 PPPHG
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                  from human placenta. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanzel DK,
                                                                              Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-488900/53.
                                                                                                       WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                               PPPHG 22
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                                                                                                                                                                                                                                                                                          Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                                      1 PPPHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                18
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                                                                               Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                   Human
                                                                                                                                               gene
 ###X#X#X#X##X
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                                                                                                             The invention relates to an isolated polymucleotide (ACF64435-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to encoding a Propionibacterium acnes protein. The invention also relates to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a convention; fusion proteins comprising a polypeptide of the invention; antibodies against polypeptides of the invention; a vaccine composition (comprising P. acnes polypeptides, antibodies, a vaccine composition (comprising P. acnes polypeptides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the patient; and a method for inhibiting the development of P. acnes in a contigen-presenting cells that express the patient; and a method for inhibiting the development of P. acnes in a contigen. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the patient; or for stimulating an immune response specific for a P. acnes polypeptides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the sequence represents a polypeptide predicted to be encoded by an ORF (open creating frame) contained within the P. acnes yolymented in electronic format directly the printed specification, but was obtained in electronic format directly from WNPO at ftp. wipo.int/pub/published_pct_sequences
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                                    ium acnes polypeptides and polynucleotides encoding the
l for diagnosing, preventing or treating acne vulgaris,
an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            measuring placental gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 6; Length 60; 100.0%; Pred. No. 2.3e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; placenta; antenatal diagnosis;
                                                                                          VO 4355; 1481pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #11925 encoded by probe for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 61 AA.
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rative
                                   New Propionibacterium polypeptide, useful fo or for stimulating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
 WPI; 2003-381789/36
N-PSDB; ACF64448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe; microarray; genetic disorder.
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                                                                                           Example 1; SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60 AA;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Best Local S:
Matches 5
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                                                                                                                                                               for analyzing
                                                                                                                                                                                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed probe encoded protein SEQ ID NO: 37988.
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                                                                                                                                                               exon nucleic acid probes useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 4; I Pred. No. 2.3e+02; Mismatches 0;
                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 38157; 654pp; English.
                                                     R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rank
                                                     Rank
                                                                                                                                                                 n genome-derived single exon n expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM77682 standard; protein; 61 AA.
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(MOLE-) MOLECULAR DYNAMICS INC
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                   Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001WO-US000668
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PPPHG 22

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of
                                                                                                                                                                                                                                                                                                                                                                  Human brain expressed single exon probe encoded protein SEQ ID NO: 37058
                                                                                                                                                                                                                                                                                                                                                                                              ed exon; gene expression analysis; probe; microarray multiple sclerosis; schizophrenia; epilepsy; cancer
                                                                                                                                                                                                                                                                                                                                                                                                microarray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression in human
                                                                                                                                                       Gaps
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                                                                                                                            Length 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 35; DB 4; Length 61; 100.0%; Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analyzing gene
                                                                                                                          Score 35; DB 4; 1
Pred. No. 2.3e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                                           100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                         entry)
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Human; brain expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                           Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single exon nucleic brains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-483446/52
                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's diseas
                                                                                                                                                                                                                                                                                 AAM64953 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR
                                                                                                                                                                                                          18 PPPHG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the probes of the
                                                                                                                                                                                  1 PPPHG 5
                                                                                                 Sequence 61 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 61 AA;
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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AAM64953
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG59930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                      Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 4; I
100.0%; Pred. No. 2.3e+02;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 27; SEQ ID NO 37977; 658pp; English
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S
                                                                                                         Human liver peptide, SEQ ID No 37977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucl
gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU32380 standard; protein; 75 AA.
              Z
              61
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000664
              standard; peptide;
                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22
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                                                                                                                                                                                        Homo sapiens
                                                                           25-FEB-2003
                                                                                                                                                                                                                                                    09-AUG-2001
                                             ABG59329;
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              ABG59329
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AAU32380
ID AAU3
ABG59329
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Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel human secreted polypeptides. The polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AMU29510-AMU33304 represent the amino acid sequences of novel human contactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                               Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
                                                                         Human; vaccination; gene therapy; nutritional supplement;
stem cell proliferation; haematopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
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0
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                                                                                                                                                                                                                                                                                                                                                -598; 765pp; English.
                                                    Novel human secreted protein #2871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; 77 AA.
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26-JAN-2001; 2001US-00770160
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                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium a
                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 597
                                                                                                                                                                                                                                                                                          WPI; 2001-611725/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU41116 standard;
                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 PPPHG 5
                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 75 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPPHG
                                                                                                                                            WO200179449-A2
                                                                                                                       Homo sapiens.
                               18-DEC-2001
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                                                                                                                                                                  25-OCT-2001
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Best Local S
Matches 5
          AAU32380;
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by the treatment, prevention and diagnosis of medical conditions caused by a canes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The ploypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and diagnostic agents for determining P. acnes presence for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful treating acne vulgaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitcham JL, Wang SS,
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 2311; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU43934 standard; protein; 77 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                                                                                                                                                                                                                                                  20-APR-2001; 2001WO-US012865
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L'maisonneuve J, Zhang Y,
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                                                                                                                                                  Propionibacterium acnes
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N-PSDB; AAS59514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies and convergulate expression and activity of P. acnes polypeptides and convergence for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 acnes polypeptides and nucleic acids useful for
t and diagnosing infections, especially useful
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                                                                                                                                                                                                                                                                                                Bhatia A;
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100.0%; Pred. No. 2.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                               Mitcham JL, Wang SS, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO 5129; 1069pp; English.
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ftp.wipo.int/pub/published_pct_sequences
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Zhang Y,
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                                                                   acnes
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Best Local Similarity
Matches 5; Conser
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treating acne vulg
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| PPPHG 17
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                                                                 Propionibacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ
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                                                                                               WO200181581-A2
                                                                                                                                                               20-APR-2001;
                                                                                                                                                                                                                                                                                                YAW,
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The invention relates to an isolated polynucleotide (ACF64435-ACF64733)

cncoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polynucleotides (ABM35624-ABM64556) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polymetrion fusion proteins comprising a polypeptide of the invention; an immune response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polypeptides, or the invention; and a method is a vaccine composition (comprising P. acnes polypeptides). The P. acnes polypeptides, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide; a method and kit for detecting or determining the presence or absence of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes polypeptides are useful for diagnosing, preventing or treating acne and the kit is useful for performing a diagnostic assay. The present sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymetion, but was obtained in encoded by an ORF (open reading frame) contained within the P. acnes polymetic format directly the printed specification, but was obtained and electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                  New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                        Maisonneuve JL;
Jones R, Carter D;
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100.0%; Pred. No. 2.9e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                       Persing DH, Bhatia A, Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 5129; 1481pp; English
immunostimulant; immune response; vaccine
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ID ABM37635 standard; protein; 77 AA.
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Zhang Y, Wang S, Jen S, Lod
Barth B, Vallieve-Douglass J;
                                                                                                                                                               11-OCT-2002; 2002WO-US032727
                                                                                                                                                                                                         15-OCT-2001; 2001US-00978825
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                                          Propionibacterium acnes
                                                                                                                                                                                                                                              (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-381789/36.
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Best Local Similarity
Matches 5, Conserv
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                                                                               WO2003033515-A1
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The invention relates to an isolated polymucleotide (ACF64435-ACF6473) encoding a Propionibacterium acnes protein. The invention also relates to prolymetrides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a comprising a polypeptide of the invention; antibodies against polypeptides of the invention; unamnue response specific for a P. acnes polypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient. The P. acnes polypeptides, polymucleotides, antibodies, fusion proteins, T cell populations or antigen-presenting cells that express the polypeptides are useful for diagnosing, preventing or treating acne protein. The polymucleotides can also be used as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the expression of an immune response against P. acnes, or for treating acne, and the kit is useful for performing a diagnostic assay. The present cut sequence represents a polypeptide predicted to be encoded by an ORF (open reading frame) contained within the P. acnes polymetric act his patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pt_generales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
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                                                                                                                                                                                                                                                                                                                                                                                                 Maisonneuve JL;
Jones R, Carter D;
                    Propionibacterium acnes predicted ORF-encoded polypeptide #2311
                                                            Acne vulgaris; antiseborrhoeic; dermatological; antibacterial; immunostimulant; immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                 Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40 2311; 1481pp; English
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Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Douglass J;
                                                                                                                                                                                                                                                               11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                          15-OCT-2001; 2001US-00978825
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ng S, Jen S,
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Barth B, Vallieve
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                                                                                                                            Propionibacterium
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                                                                                                                                                                         WO2003033515-A1
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                        Gaps
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 Length 77;
                       Indels
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 100.0%; Score 35; DB 6; 100.0%; Pred. No. 2.9e+02;
                       Mismatches
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0
Query Match
Best Local Similarity
Matches 5; Conser
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protein; 79 AA. RESULT 28 AAY12827 ID AAY12827 standard; 31 PPPHG 5 \_ 27 qq ਨੇ

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AAX51459 to AAX51691 represent 5' expressed sequence tags (ESTs) for human secreted proteins, and encode the proteins given in AAY12681 to AAY12913, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopolesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
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                                                                                                                                      forensic, gene therapy, chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity, cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from testis, ovary, uterus and spleen tissue.
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                                                                                                                       secreted protein; EST; expressed sequence tag;
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100.0%; Pred. No. 2.9e+02;
Live 0; Mismatches 0;
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                                                                                   secreted protein SEQ ID NO:417.
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                                                                                                                                                                                                                                                                                                                                                  98WO-IB001231.
                                                                                                                                                                                                                                                                                                                                                                                     97US-00905279
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N-PSDB; AAX51605.
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                                                                                   EST
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1997;
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                                                 21-JUN-1999
                                                                                                                                                                                                                                                                                                                  11-FEB-1999.
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                AAY12827;
                                                                                   Human 5'
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                                                                                                                        Human;
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ABB61183
ID ABB61.
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WO200277183-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hyperproliferative disorder; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                      pmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Length 80;
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Drosophila melanogaster polypeptide SEQ ID NO 10341
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100.0%; Pred. No. 3e+02;
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                                                                                                                       23-MAR-2001; 2001WO-US009231
                                                                                                                                             23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
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Best Local Similarity 100
Matches 5; Conservative
                                                      Drosophila melanogaster
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                                                                                                                                                                                                                       WPI; 2001-656860/75.
N-PSDB; ABL05286.
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                     Drosophila; develo
pharmaceutical.
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                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID
                                                                                                                                                                                                   Venter JC, Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP11024 standard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 80 AA;
                                                                            WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 PPPHG
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                                                                                                  27-SEP-2001
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORFX in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP001010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated with an ORFX-associated with an ORFX-associated with orFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperprolificative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, infectious cateoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, autoimmune disorders such as multiple sclerosis, infectious diseases, autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune thyroiditis, myasthenia gravis, sortensus sortection or regenerative disorders, or periodontal disease, and for gut procection or regenerative disorders, or periodontal disease, and for gut perfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the printed specification, int/pub/published_pct_energe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by Prokaryotic essential gene #19844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 35; DB 5; I
100.0%; Pred. No. 3.3e+02;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 22030; 1037pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU34317 standard; protein; 89 AA
29-MAY-2001; 2001WO-US010836
                                                                       30-MAY-2000; 2000US-0206132P
29-AUG-2000; 2000US-0228716P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                          Shimkets RA, Leach MD;
                                                                                                                                                                                   (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                 WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium avium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 5, Conser
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                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ABN26776
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Wang Wall

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The invention relates to isolated polynucleotide (I) and polypeptide (II)

sequences. (I) is useful as hybridisation probes, polymerase chain

reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
cactivity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal

cactivity of (II) or to treat disease states involving (II). (II) as molecular weight markers and as a food
supplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving aberrant protein expression or biological activity. The
polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
capped to produce other types of data and products dependent on DNA and
amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
amino acid sequences of the invention. Note: The sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from WIPO at
capped to the capped of the sequences
capped to the capped of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 35; DB 4; Length 97; 100.0%; Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; SEQ ID NO 54853; 103pp; English.
                                                      Novel human diagnostic protein #24485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO63515 standard; protein; 98 AA
                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT,
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS88681.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 97 AA;
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                                                                                                                                                                                                                                                   WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
                                                                                                                                                                                                   Homo gapiens,
  18-FEB-2002
                                                                                                                                                                                                                                                                                                            11-OCT-2001
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ABO63515
ID ABO63:
XX
AC ABO63:
XX
DT 29-JUJ
XX
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  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense correction cell containing the vector; (3) an isolated correction cells acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (5) producing the polypeptide; (6) inhibiting cellular correction or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an compound sactivity; (11) a culture comprising strains in which the gene compound the strains in a culture or collection of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound the strains is present in a culture compound that inhibits the correction of an organism; or (13) identifying the target of a compound that inhibits the correction or an organism. Or he antipanse ancleic acids are useful for correction proliferation or for screening for homologous nucleic acids required for greening or for screening drug drug discovery programs or for screening drug drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening
                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screfor homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                       Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 35; DB 6; I
100.0%; Pred. No. 3.3e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 25; SEQ ID NO 62241; 1766pp; English
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                                                                                                                                                                                                                                                                                                                                     Malone C,
Carr GJ,
                                                      2002WO-US009107
                                                                                                         21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                  Zamudio C, N
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                        2003-029926/02
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ACA38187.
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                                                      21-MAR-2002;
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03-OCT-2002
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Best Local S
Matches 5
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(first entry)

29-JUL-2004

ABG24494

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RESULT 32 ABG24494

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           Mccrae
                                                                         cancer
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                                                                                                                                                                                                                                                  The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                     New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
preparing a vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiangiogenic receptor;
rich glycoprotein; HPRG; cytostatic; antidiabetic;
antiinflammatory; gynaecological; antiarthritic;
rmatological; cardiant; vasotropic; vulnerary;
e therapy; rabbit.
                  expression vector; transcription regulatory element; oneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                              100.0%; Score 35; DB 7; Length 98; 100.0%; Pred. No. 3.6e+02; ive 0; Mismatches 0; Indels
Klebsiella pneumoniae polypeptide segid 10032
                                                                                                                                                                                                                                  NO 10032; 932pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabbit HPRG protein H/P rich domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 101 AA
                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                     99US-0117747P.
                                                                                                  27-JAN-2000; 2000US-00489039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-2003; 2003WO-US008060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                            Klebsiella pneumoniae.
                                                                                                                                                         Breton GL, Osborne M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryctolagus cuniculus.
                                                                                                                                                                          WPI; 2003-895346/82.
N-PSDB; ACH97066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tpm; tropomyosin; an histidine-proline ri ophthalmological; an antipsoriatic; derma angiogenesis; gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                Recombinant expres
                                                                                                                                                                                                                                  Disclosure; SEQ ID
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADH10412 standard;
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                                                                                                                                                                                                                                                                                                                            Sequence 98 AA;
                                                                                                                    29-JAN-1999;
                                                              US6610836-B1
                                                                                26-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 34
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The invention relates to an isolated tropomyosin (Tpm)-related antianglogenic receptor polypeptide or peptide, which is a is a fragment of a full-length native Tpm protein expressed on the surface of endothelial cells, or a variant of the fragment. It has a molecular mass of about 17 kDa and corresponds in its sequence to, or is a variant of, an internal fragment of a native Tpm isoform which is a binding site for antianglogenic polypeptide agents; The isolated antianglogenic receptor polypeptide, peptide or variant has substantially the same biochemical activity of binding to the antianglogenic polypeptide agents, as does the isolated polypeptide or peptide is human histidine-proline crich glycoprotein (HRG), rabbit HRG, a Tpm-binding, antianglogenic human kininogen (HK), the D5 domain of fragment of human or rabbit HPRG, two chain human kininogen (HK), the D5 domain of fragment of the kW or its D5 domain. The Tpm-related antianglogenic receptor polypeptide or peptide, antianglogenic homologue, variant, domain of fragment of the kW or its D5 antianglogenic homologue, variant, domain or fragment of the kW or its D5 antianglogenic homologue, variant, domain or fragment of the kW or its D5 antianglogenic receptor polypeptide or peptide in andothelial cell apoptosis, or for treating tumours or cancer, diabetic endothelial cell apoptosis, or for treating tumours or cancer, diabetic retinopathy, neovascular glaucoma, uveitis, endometriosis, arthritis, psoriasis, or scleroderma. The antibody may be also used for detecting the presence of a Tpm polypeptide or peptide in a biological sample, for promoting wound healing, or for treating diseases or conditions in which increased anglogenesis is desired, e.g. coronary artery disease or peripheral artery disease. The present sequence represents a rabbit HPRG, protein His-Pro (H/P) rich domain.
                                                                                                                                                             New tropomyosin-related antiangiogenic receptor polypeptide, useful for inhibiting endothelial cell migration, invasion, proliferation or angiogenesis, inducing endothelial cell apoptosis, or treating tumors or
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100.0%; Pred. No. 3.7e+02;
ative 0; Mismatches 0;
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AP;
   Mazar
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 24; 117pp; English
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Juarez J,
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Donate F,
                                                                           WPI; 2004-090604/09
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AAG16968 standard; protein; 115 AA.
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Best Local Similarity
Matches 5; Conserv
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                                                               Sequence 111
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                                                                                                                                                                                                                                                                                                                                     Unidentified
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Best Local S:
Matches 5
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                                                                                                                            The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the human glycosylhydrolase 12 protein. Also described are: (1) polynucleotides encoding for the glycosylhydrolase 12 protein; (2) production of the protein using a DNA recombination process; and (3) an agonist resisting the protein and its
                                                                         coding a Klebsiella pneumoniae polypeptide, useful composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New glycosylhydrolase 12 polypeptide and the polynucleotide encoding useful in the treatment of various diseases, such as malignant tumor, hemopathy, HIV Infection, immunological diseases and various inflammations.
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; glycosylhydrolase 12; cytostatic; antiviral; anti-HIV; immunomodulatory; antiinflammatory; malignant tumour; haemopathy; HIV Infection; immunological disease; inflammation.
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                                                                                                                                                                                                                                        Length 103;
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100.0%; Pred. No. 3.8e+02;
ive 0; Mismatches 0;
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                                                                                                         English.
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RAPEUTICS CORP
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preparing a vaccine compos
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                     Osborne
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N-PSDB; ACH99730.
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(GENO-) GENOME THE
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                     Breton GL,
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AAG67890
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Glycosyl hydrolase; cytostatic; haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy; malignant tumour; haemopathy; HIV infection; immunological disease; inflammation.
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     antiviral, anti-
The
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treatment effect. Glycosylhydrolase 12 has cytostatic, antiviral, ant HIV, immunomodulatory and antiinflammatory activities. The glycosylhydrolase protein and polynucleotide sequence can be used for treating various diseases, such as malignant tumour, haemopathy, HIV Infection, immunological diseases and various inflammations
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                                                                                      pathway;
promoter;
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                                                                                       on; signal transduction
genetic mapping; gene e
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99US-0123180P.
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                                      17-0CT-2000
                                                                                                                                                                                           06-SEP-2000
              AAG16968
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                             99US - 0121825P - 99US - 0123180P - 99US - 0123548P - 99US - 0123548P - 99US - 0125788P - 99US - 0125788P - 99US - 0125788P - 99US - 0125788P - 99US - 0126264P - 99US - 0128234P - 99US - 0130449P - 99US - 0130449P - 99US - 0132484P - 99US - 0134256P - 99US - 0134256P - 99US - 0134455P - 99US - 0139455P - 99US - 0139453P - 99US - 0139899P - 99US - 0139899P
                                                                               2000EP-00301439
                                Arabidopsis thaliana
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99US-015066P.
99US-0151068P.
99US-0151066P.
99US-0151080P.
99US-015103P.
99US-015133P.
99US-01533P.
99US-01533P.
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99US-015438P.
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99US-015645BP.
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310-AUG-1999;

10-SEP-1999;

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113-SEP-1999;

12-SEP-1999;

13-SEP-1999;

14-OCT-1999;

14-OCT-1999;

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14-OCT-1999;

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AC AAG16
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DT 17-OC
XX
DE Arabi
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Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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99US-0151930P.
99US-0152363P.
99US-0153070P.
99US-0153070P.
99US-0154018P.
99US-0154039P.
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99US-0161360P.
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21-SEP-1999;
22-SEP-1999;
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AAO01973
ID AAO011
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DT 06-NO
XX
DD Human
XX
KW Vaccii
KW Vaccii
KW LESSU
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 Query Match
 100.0%;
 Score 35;
 DB 4;
 Length 118;

 Best Local Similarity 100.0%;
 Pred. No. 4.3e+02;

 Matches 5;
 Conservative 0;
 Mismatches 0;
 Indels

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 Db 18 PPPHG 22
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Search completed: June 15, 2005, 14:15:52 Job time : 92 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 15, 2005, 14:06:20 ; Search time 23.5 Seconds (without alignments) 15.883 Million cell updates/sec Run on:

US-10-074-225A-10 35 1 PPPHG 5

Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

513545 seqs, 74649064 residues Searched: Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Patents AA: \* Issued Database :

1: /cgn2 6/ptodata/1/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	Appl	Appl	32, 1	96, 1	32, 7	19, 1	App	Appl	5, Ap	Appl	38, 7	15, 7	04, 1	, Appl:		l, Ap	34, 7	App	App	Appl	App]	Appl	538602	5386025	Appl	Appl	Appl:
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Patent No.	Patent No.	Sequence	Sequence	Sequence
SOMMENTES ID	US-07-745-206A-28	US-08-311-363-28		-09	US-09-270-767-32232	US-09-270-767-47449	US-08-683-262B-47	US-09-361-707-47	US-09-640-211A-1165	PCT-US93-00227-4	US-09-270-767-43608	US-09-252-991A-32545	US-09-270-767-45004	US-08-894-139-4	US-09-949-016-11268	o	5	-08	-10	US-08-455-543A-42	US-08-223-305C-42	US-08-336-257A-6	5386025-4	5386025-4	US-08-895-590-9	-91	US-09-082-059-2
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Sequence 9, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 22, Appli Sequence 138, App Sequence 17, Appl Sequence 382, App Sequence 382, App Sequence 382, App Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 116, Appl Sequence 116, Appl Sequence 303, Appl Sequence 303, Appl Sequence 303, Appl Sequence 303, Appl Sequence 303, Appl
US-08-938-291A-9 US-09-589-619-9 US-09-697-898-3 US-09-697-898-2 US-09-460-384-22 US-08-556-597-138 US-10-118-575A-17 US-08-602-999A-382 US-09-500-124-382 US-09-500-124-382 US-09-500-124-382 US-09-500-124-382 US-09-500-124-382 US-09-136-218-16 US-08-0602-999A-416 US-08-602-999A-416 US-08-602-999A-416 US-08-602-999A-416 US-08-602-999A-303 US-08-602-999A-371
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1250 1250 1495 1512 4377 10 112 115 116 117 117 117 118
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## ALIGNMENTS

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Sequence 28, Application US/07745206A
Sequence 28, Application US/07745206A
Patent No. 542931
GENERAL INFORMATION:
APPLICANT: Bilis, Steven
APPLICANT: Williams, Mark
APPLICANT: Feldman, Daniel
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 1135 S. LaSalle
CITY: Chicago
CITY: Chicago
STREET: 1111nois
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER EPERENCE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER EDAPH PROMATION:
COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER FORM:
MEDIUM TYPE: 19910815
COMPUTER STORE PROMATION:
SOFTWARN: 19910815
COMPUTER FREENCE FORM:
MAME: Feder, Scott B
FILING DATE: 19910815
CASSIFFORMICATION INFORMATION:
NAME: Feder, Scott B
FERENCE CHARACTERISTICS:
LENGTH: 52 amino acids
FTPER TYPE: PROCEIN
NAME: FEDERAL TYPE: PROCEIN
NAME: FEDERAL TYPE: PROCEIN
TOPOLOGY: Linear
MING-745-206A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 35; DB 1; Length 52; 100.0%; Pred. No. 26; tive 0; Mismatches 0; Indels
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Matches 5; Conservative
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Query Match
Best Local Similarity 100.
Matches 5, Conservative
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US-09-489-039A-12696
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US-09-270-767-32232
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US-09-270-767-47449
TYPE: PRT
ORGANISM:
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!: Human Calcium Channel Compositions and
!: Methods
!S: 32
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                                                    Sequence 28, Application US/08311363

Sequence 28, Application US/08311363

Patent No. 587658

Sequence 28, Application US/08311363

Patent No. 587658

Sequence 28, Application

APPLICANT: Harpold, Michael

APPLICANT: Williams, Mark

APPLICANT: Williams, Mark

APPLICANT: McCue, Ann

APPLICANT: Brenner, Robert

TITLE OF INVENTION: Human Calcium Channel Compositi

TITLE OF INVENTION: Hearbook

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STREET: 1660 Union Street

CONFITY: USA

ZIP: 9101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Falopy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: TIOPPY disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Reachin Release #1.0, Version #1.25

COMPUTER PREDARIE PORM:

MEDIUM TYPE: Recentin Release #1.0,

SOFTWARE: Patentin Street

APPLICATION NUMBER: US/08/311,363

FILING APPLICATION Street

TELEPRONE COMPUTER: 33,779

REFERENCE/DOCKET NUMBER: 33,779

REPERENCE/DOCKET N
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; MOLECULE TYPE: protein
US-08-311-363-28
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US-09-489-039A-10032
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                                       RESULT 2
US-08-311-363-28
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Best Local S
Matches 5
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Sequence 12696, Application US/09489039A

Sequence 12696, Application US/09489039A

Batent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NOS: 14342

SEQ ID NOS: 14342
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Sequence 32232, Application US/09270767

Sequence 32232, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster.

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 32232

LENGTH: 135
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                                                       DB /
                                                                    ; Score 35; DB; Pred. No. 47; 0; Mismatches
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100.0%; Pred. No. 64;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 35; DB
100.0%; Pred. No. 50;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Drosophila melanogaster
US-09-270-767-32232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-12696
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10032
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GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 47449

LENGTH: 135
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BLE FORM:
Floppy disk
IBM PC compatible
STEM: PC-DOS/MS-DOS
PATENTIN Release #1.0, Version #1.30
CATION DATA:
NUMBER: US/08/683,262B
: 18-JUL-1996
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100.0%; Pred. No. 81;
ative 0; Mismatches 0
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Pred. No. 64;
0; Mismatches
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US-08-683-262B-47

i Sequence 47, Application US/08683262B

i Patent No. 5929220

GENERAL INFORMATION:

APPLICANT: Shuping Tong et al.

TITLE OF INVENTION: HEPADNAVIRUS RECEPTO!

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STRET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

CONNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER: IBM PC COMPATIAL

COMPUTER: Patent Nelease #1.0, Version

COMPUTER: Patent Nelease #1.0, Version

COMPUTER: Patent NUMBER: US/08/683,262B

FILING DATE: 18-JUL-1996

CLASSIFICATION NUMBER: US/08/683,262B

FILING DATE: 18-JUL-1996

CLASSIFICATION NUMBER: 00786/287002

FELERPHONE: (617) 542-5070

TELECPHONE: (617) 542-5070

TELEPHONE: (17) 542-5070

TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g Tong et al.
: HEPADNAVIRUS RECEPTOR
S: 75
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Best Local Similarity 100.0%;
Matches 5; Conservative 0
                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Drosophila
US-09-270-767-47449
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Best Local Similarity
Matches 5; Conser
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PPPHG 72
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Sequence 1165, Application US/09640211A

Patent No. 6833446

GENERAL INFORMATION:

APPLICANT: Wood, Marion

APPLICANT: Shenk, Michael A.

APPLICANT: Glenn, Matthew

TITLE OF INVENTION: Compositions and Methods for the

TITLE OF INVENTION: Composition of Gene Transcription

FILE REFERENCE: 11000.1021CUU

CURRENT APPLICATION NUMBER: US/09/640,211A

CURRENT FILING DATE: 2000-08-16

NUMBER OF SEQ ID NOS: 2368

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 02110-2804
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/361,707
FILING DATE: 27-Jul-1999
PRIOR APPLICATION NUMBER: 08/683,262
FILING DATE: 18-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Sequence 47, Application US/09361707
Patent No. 6258937
GENERAL INFORMATION:
APPLICANT: Tong, Shuping
Li, Jisu
Wands, Jack R.
TITLE OF INVENTION: HEPA DNA VIRUS RECEPTOR
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Creason, Gary L.
REGISTRATION NUMBER: 34,310
REFERENCE/DOCKET NUMBER: 00786/287003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB
Pred. No. 81;
; Mismatches
                                                                                                                                                                                           ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street CITY: Boston STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
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TELEFAX: (617) 542-8906
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US-09-640-211A-1165
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Best Local Similarity
Matches 5; Conserv
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, Jerome B.
: ANTIGEN RECOGNIZED BY PATIENTS WITH
: ANTIBODY ASSOCIATED LAMBERT-EATON MYASTHENIC SYNDROME
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  100.0%; Score 35; DB 4; Length 202; 100.0%; Pred. No. 93;
                                                           0; Indels
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TITLE OF INVENTION: ANTIGEN RECOGNIZED BY PATIENTS WI
TITLE OF INVENTION:
NUMBER OF SCOURNCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
COUNTY: New York
COUNTY: U.S.A.
ZIP: 1012
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100.0%; Pred. No. 1.1e+02;
ive 0; Mismatches 0;
                                                           Mismatches
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GENERAL INFORMATION:
APPLICANT: Furneaux,, Henry M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                internal
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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Query Match
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196 PPPHG 200
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222 PPPHG 226
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US-09-270-767-43608
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; LOCATION:
PCT-US93-00227-4
                                                                                                                                                                                                                                               RESULT 10
PCT-US93-00227-4
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Sequence 32545, Application US/09252991A
Sequence 32545, Application US/09252991A
Sequence 32545, Application US/09252991A
Sequence 32545, Application US/09252991A
Setent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32545
LENGTH: 321
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Sequence 43608, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43608
LENGTH: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45004, Application US/09270767
; Sequence 45004, Application US/09270767
; Fatent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45004
; LENGTH: 332
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Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Xaa means any amino acid US-09-270-767-43608
                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Drosophila melanogaster
FEATURE:
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US-09-252-991A-32545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudol US-09-252-991A-32545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-09-270-767-45004
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Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                       ORGANISM: Human
US-09-949-016-11268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Huma
US-09-949-016-6701
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POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                       Gaps
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                                                        Query Match 100.0%; Score 35; DB 4; Length 332; Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                       Sequence 4, Application US/08894139
; Sequence 6 448376
; General INFORMATION:
APPLICANT: LA THANGUE, NICHOLAS B.
APPLICANT: BERNARDS, RENE
APPLICANT: HIJMANS, ELEANORE M.
TITLE OF INVENTION: TRANSCRIPTION FACTOR E2F-5
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,139
FILING DATE: 13-AUG-1997
CLASSIFICATION: AND ATA:
ANDER ATTORNEY/AGENT INFORMATION:
ANDER ATTORNEY/AGENT INFORMATION:
ANDER ATTORNEY/AGENT INFORMATION:
ANDER ATTORNEY/AGENT INFORMATION:
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2000-04-14
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US-09-949-016-11268
; Sequence 11268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOW
; TITLE OF INVENTION: WITH HUMAN DISEASE,
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 620-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
; ORGANISM: Drosophila melanogaster
US-09-270-767-45004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ID NO: 4:
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INFORMATION FOR SEQ
SEQUENCE CHARACTER
                                                                                                                                          1 PPPHG 5
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20 PPPHG
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; MOLECULE TYPE:
US-08-894-139-4
                                                                                                                                                                                                                                          RESULT 14
US-08-894-139-4
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Best Local S
Matches 5
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Sequence 1848. Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6701, Application US/09949016

Sequence 6701, Application US/09949016

Sequence 6701, Application US/09949016

Setent No. 681233

Setent No. 681233

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

FRIOR PELLOR DATE: 2000-10-20

FRIOR PELLOR DATE: 2000-10-03

FRIOR PELLING DATE: 2000-10-03

FRIOR PELLING DATE: 2000-10-03

FRIOR PELLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6701
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Pred. No. 1.6e+02;
; Mismatches 0;
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100.0%; Pred. No. 1.9e+02;
ative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 11268
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RESULT 20
US-08-455-543A-42
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N: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
V: METHODS
3S: 40
                                                                                                                                                                                                                              Length 439
                                                                                                                                                                                                                           100.0%; Score 35; DB 4; Length 43
100.0%; Pred. No. 1.9e+02;
iive 0; Mismatches 0; Indels
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oppy disk
C compatible
I: PC-DOS/MS-DOS
III Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n, Martin, Haller & McClain
ion Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Son Union Street
CITY: Son Diego
STREET: California
COUNTRY: USA
ZIP: 92101-2926
COMPUTER: READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,097D
FILING DATE: 11-AUG-1993
RIOR APPLICATION NUMBER: WO PCT/US92/06903
FILING DATE: 11-AUG-1992
RRIOR APPLICATION NUMBER: US 07/914,231
RPIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,231
FILING DATE: 13-JUL-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 10-APR-1992
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 10-APR-1990
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,350
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 20-FEB-1990
RRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
FRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
FRIOR APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
FRIOR APPLICATION NUMBER: WO PCT/US89/01408
FRIOR APPLICATION NUMBER: WO PCT/US89/01408
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US-08-149-097D-38
; Sequence 38, Application US/08145;
; Patent No. 5874236
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael
; APPLICANT: Williams, Mark
; APPLICANT: Williams, Mark
; APPLICANT: Williams, Mark
; APPLICANT: Feldman, Daniel
; APPLICANT: Feldman, Daniel
; TITLE OF INVENTION: HUMAN CAL
; TITLE OF INVENTION: HUMAN CAL
; TITLE OF INVENTION: METHODS
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Brown, Marti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ld, Michael
Steven
; SEQ ID NO 18484
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18484
                                                                                                                                                                                                                                                                                                           vative
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Best Local Similarity
Matches 5, Conser
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PRIOR APPLICATION
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US-10-029-180-106

is Sequence 106, Application US/10029180

is APPLICANT: Cali, Brian M.

is APPLICANT: Madden, Kevin T.

APPLICANT: Malna, G. Todd

APPLICANT: Madden, Kevin T.

APPLICANT: Malna, G. Todd

APPLICANT: Silva, Jeffry C.

APPLICANT: Sanay, Lixin

ITLE OF INVENTION: No. 6806082el Regulators of Fungal Gene Expression

FILE REFERENCE: MIC-004

CURRENT FILING DATE: 2001-12-22

RUMBER OF SEQ ID NOS: 138

SOFTWARE: FRASEEQ for Windows Version 4.0

SEQ ID NO 106

LENGTH: 491

TYPE: PRT

CREANISM: Artificial Sequence

FEATURE:

PRANTER:

FEATURE:

PRANTER:

FEATURE:

PRANTER:

FEATURE:

PRANTER:

PRANT
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100.0%; Pred. No. 2.1e+02;
vative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
CIHER INFORMATION: /standard_name= "Betal-1"
US-08-149-097D-38
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-55038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 238-0959
TELEFAX: (619) 238-0959
TELEFAX: (619) 238-062
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 479 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
HYPOTHETICAL: NO
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: fungal gene US-10-029-180-106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 5; Conserv
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APPLICANT: Brenner, Robert
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Brown, Martin, Haller & McClain STREET: 1660 Union Street CITY: San Diego STATE: California COUNTRY: USA ZIP: 92101-2926 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM COMPUTED COMPUTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: DISKECLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/223,305C
FILING DATE: April 4, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/868,354
FILING DATE: April 10, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/745,206
FILING DATE: 30-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/620,250
FILING DATE: 20-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US89/01408
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/603,751
FILING DATE: 04-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/176,899
FILING DATE: 04-APR-1988
ATTORNEY/AGENT INFORMATION:
ANDER APPLICATION NUMBER: US 07/176,899
                                                                                                                                                                                                                                                            Sequence 42, Application US/08223305C Patent No. 5851824 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52516
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REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 5251
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)238-0999
TELEFAX: (619)238-0062
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      Harpold, Michael
Ellis, Steven
Williams, Mark
Feldman, Daniel
McCue, Ann
                                |||||
249 PPPHG 253
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Sequence 42, Application US/0845543A

Patent No. 572846

GENERAL INFORMATION:
APPLICANT: Barpold, Michael
APPLICANT: Bills Steven
APPLICANT: Bills Steven
APPLICANT: Bills Steven
APPLICANT: Fellams, Mark
APPLICANT: Bills Steven
APPLICANT: Brown, Martin, Haller & McClain
ITILE OF INVENTION: MARTHON
MATTHE COUNTRY: DAY
COUNTRY: LOA
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TI NUMBER: 6362-52517
1 INFORMATION:
9)238-0999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
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5; Conservative
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FRAGMENT TYPE:
US-08-455-543A-42
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Best Local S
Matches 5
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Length 523;

Score 35; DB 2; Pred. No. 2.3e+02;

> Query Match Best Local Similarity

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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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                          Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                                                                                                                249 PPPHG 253
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5386025-4
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 Gaps
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                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Elis, Scott D
APPLICANT: Elis, Steven B.
APPLICANT: Harpold, Michael M.
APPLICANT: Harpold, Michael M.
APPLICANT: Campbell, Kevin P.
TITLE OF INVENTION: CALCIUM CHANNEL COMPOSITIONS AND METHODS NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain STREET: 1660 Union Street CITY: San Diego STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESQ Version 1.5
CURRENT APPLICATION DATE: 07-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33 773
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 Indels
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ches 0;
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 Mismatches
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5386025-4
; Patent No. 5386025
; APPLICANT: JAY, SCOTT D.; ELLIS, STEVEN
; TITLE OF INVENTION: CALCIUM CHANNEL CO!
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,384
; FILING DATE: 20-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08336257A Patent No. 5726035 GENERAL INFORMATION:
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5; Conservative
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PPPHG 253
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5; Conserv
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INFORMATION FOR SEQ
SEQUENCE CHARACTER
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TYPE: amino aci
STRANDEDNESS: s
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                            PPPHG
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US-08-336-257A-6
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Best Local S
Matches 5
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APPLICANT: Lev, Sima
Plowman, Gregory D.
Schlessinger, Joseph
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.1e+02;
                                                                   RESULT 28
US-08-938-291A-9
; Sequence 9, Application US/08938291A
; Patent No. 6117673
; GENERAL INFORMATION:
; APPLICANT: Lev, Sima
APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: RDGB PROTEINS AND RELAT
TITLE OF INVENTION: PRODUCTS AND METHODS
; TITLE OF INVENTION: PRODUCTS AND METHODS
; ORRESPONDENCES: 11
CORRESPONDENCE ADDRESS:
; ADDRESSE: Lyon & Lyon
STREET: Suite 4700
; STATE: California
COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: BOARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWALES FISHER: TEM F.C. DOS 3.0
SOFTWARE: FASESCY
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,291A
FILING DATE: September 26, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard 1.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 228/172
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1250 amino acids
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Patent No. 6576442
GENERAL INFORMATION:
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Best Local Similarity 100
Matches 5; Conservative
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                 627 PPPHG 631
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US-09-589-619-9
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US-09-082-059-2
i Sequence 2, Application US/09082059A
j Sequence 2, Application US/09082059A
j Patent No. 6225086
j GENERAL INFORMATION:
APPLICANT: Morrow, 5.25086el Ankyrin Proteins and a Method for Their Identificat
TITLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identificat
FILE REFERENCE: 44574-5002-US
CURRENT APPLICATION NUMBER: 60/047356
j CURRENT FILING DATE: 1998-05-21
j EARLIER PILING DATE: 1997-05-21
software: Patentin Ver. 2.0
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Sequence 94, Application US/09917254;
Patent No. 6703204;
GENERAL INFORMATION:
APPLICANT: Mutter, George;
APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer;
FILE REFERENCE: B0801/7224(JRV);
CURRENT APPLICATION NUMBER: US/09/917,254;
CURRENT FILING DATE: 2001-07-27;
PRIOR FILING DATE: 2000-07-28;
NUMBER OF SEQ ID NOS: 102;
SOFTWARE: Patentin version 3.0;
SEQ ID NO 94;
LENGTH: 702
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                                                                                                                                                           Length 554;
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                                                                                                                                                                              .4e+02;
                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Pred. No. 2.4
Matches 5; Conservative 0; Mismatches
TYPE: amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-895-590-9
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Best Local Similarity 100
Matches 5; Conservative
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5; Conservative
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; ORGANISM: Homo Sapiens
US-09-917-254-94
                                                                                                                                                                                                                                                                              250 PPPHG 254
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US-09-917-254-94
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Best Local S
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Conservative
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Best Local Similarity
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Best Local Similarity
Matches 5; Conserv
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            92 PPPHG 96
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US-09-697-898-2
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ORGANISM: Human
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                                                                     US-09-697-898-2
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100.0%; Pred. No. 5.1e+02;
ative 0; Mismatches 0; Indels
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US-09-697-898-3
; Sequence 3, Application US/09697898
; Patent No. 6818427
; GENERAL INFORMATION:
; APPLICANT: Palombella, Vito J.
; APPLICANT: Liao, Sha-Mei
; TITLE OF INVENTION: MEKKI Molecules and Uses Thereof
; FILE REFERENCE: 103576.144
; CURRENT FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1495
; TYPE: PRT
        STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                               ICATION DATA:
ICATION DATA:
ICON NUMBER: US/09/589,619
DATE: 07-Jun-2000
ICATION: <Unknown>
ATION DATA:
IION NUMBER: US/08/938,291
DATE: September 26, 1997
IION NUMBER: 60/027,337
DATE: October 11, 1996
NT INFORMATION:
                                                                                                                                      IBM Compatible
SYSTEM: IBM P.C. DOS 5.0
FastSeq
                                                                                                                                                                                                                                                                                                                          arburg, Richard J.
ATION NUMBER: 32,327
EL/DOCKET NUMBER: 228/172
ATION INFORMATION:
IE: (213) 489-1600
(213) 955-0440
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IPTION: SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                 7-3510
Q ID NO: 9:
ACTERISTICS:
1250 amino acids
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESS: single
linear
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MOLECULE TYPE: p

SEQUENCE DESCRIP
US-09-589-619-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                    CURRENT APPLICATION SOFTWARE:
SOFTWARE:
SOFTWARE:
APPLICATION ELLING DATH
FILING DATH
ATTORNEY/AGENT
NAME: WARD
REGISTRATION
                                                                                                                                                                                                                                                                                                                                                        REFERENCE/
TELECOMMUNICATION TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 67-:
INFORMATION FOR SEQ
SEQUENCE CHARAC'
LENGTH: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amin
STRANDEDNE
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Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 5; Conserv
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PPPHG 5

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US-09-949-016-6978

US-09-949-016-6978

Sequence 6978, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHIGNS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237, 768

PRIOR APPLICATION NUMBER: 60/231, 498

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6978

LENGTH, 4377
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Sequence 2, Application US/09697898
; Sequence 2, Application US/09697898
; Patent No. 6818427
; GENERAL INFORMATION:
; APPLICANT: Palombella, Vito J.
; APPLICANT: Liao, Sha-Mei
; TITLE OF INVENTION: MEKKI Molecules and Uses Thereof
; FILE REFERENCE: 103576.144
; CURRENT APPLICATION NUMBER: US/09/697,898
; CURRENT FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 1512
; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 4; I larity 100.0%; Pred. No. 6.1e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 4; I 100.0%; Pred. No. 1.6e+03; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 33
US-09-460-384-22
; Sequence 22, Application US/09460384
; Patent No. 6337316
; GENERAL INFORMATION:
; APPLICANT: EL TAYAR, Nabil
BLECHNER, Steven
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Сарв
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APPLICANT: ZHANG, Hui
APPLICANT: YANG, Bin
TITLE OF INVENTION: Multimerization of HIV-1 VIF Protein as
TITLE OF INVENTION: a Therapeutic Target
TITLE OF INVENTION: a Therapeutic Target
FILE REFERENCE: 8321-82 PC
CURRENT APPLICATION NUMBER: US/10/118,575A
CURRENT FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/282,270
PRIOR FILING DATE: 2001-04-06
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic peptide containing PXP motif US-10-118-575A-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/556,597 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.9%; Score 29; DB 4;
100.0%; Pred. No. 63;
ive 0; Mismatches 0
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63;
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Pred. No. 63;
1; Mismatches
                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEFHONE: (716) 263-1636
TELEFAX: (716) 263-1630
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE: CHARACTERISTICS:
LENGTH: 12 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 382, Application US/08602999A; Patent No. 6184205; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 17, Application US/10118575A; Patent No. 6653443; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 82.9%;
Best Local Similarity 80.0%;
Matches 4; Conservative
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-138
                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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Best Local Similarity
Matches 4; Conserv
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6 PPPYG 10
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US-08-602-999A-382
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US-10-118-575A-17
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                     JAMESON, Brad
TEPPER, Mark
INVENTION: CD28/CTLA-4 INHIBITING PEPTIDOMIMETICS,
PHARMACEUTICAL COMPOSITIONS THEREOF, AND METHOD OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                              NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 624 Ninth Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/460,384
FILING DATE: 13-Dec-1999
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/12312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.9%; Score 29; DB 3; Length 10;
80.0%; Pred. No. 53;
vative 1; Mismatches 0; Indels
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1: MIMOTOPES AND ANTI-MIMOTOPES OF
1: HUMAN PLATELET GLYCOPROTEIN ID/IX
5S: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1, Hargrave, Devans & Doyle LLP
Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENI INFORMATION

NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: EL TAYAR=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US98/12312
FILING DATE: 11-JUN-1998
APPLICATION NUMBER: US 60/049,470
FILING DATE: 12-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide
IPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 34
US-08-556-597-138
IS-08-556-597-138
Sequence 138, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: MIMOTOPES AND AN TITLE OF INVENTION: HUMAN PLATELET G NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEB: Nixon, Hargrave, Devans STRET: Clinton Square, P.O. Box 1 CITY: Rochester
COUNTRY: USA
ZIP: 14603
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESS: single
                                                                                                   SAME
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MOLECULE TYPE:

SEQUENCE DESCR
US-09-460-384-22
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PPPYG
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F
                                                             TITLE
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Best Local S
Matches 4
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RESULT 38
5378805-5
; Patent No. 5378805
; APPLICANT: Lai, Renu B.
; TITLE OF INVENTION: IMMUNOREACTIVE HTLV-I/II ENV AND POL PEPTIDES
; TUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/574,352
; FILING DATE: 29-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5378805

Herent No. 5378805

APPLICANT: Lai, Renu B.

TITLE OF INVENTION: IMMUNOREACTIVE HTLV-I/II ENV AND POL PEPTIDES

NUMBER OF SEQUENCES: 5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/574,352

FILING DATE: 29-AUG-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 1101-202
FELECOMMUNICATION NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
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83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 78
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.9%; Score 29;
100.0%; Pred. No.
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100.0%; Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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5378805-5
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    APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: POWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: ISOLATING AND USING SAME
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SPARKS, Andrew B.
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: DER, Channing J.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF TITLE OF INVENTION: ISOLATING AND USING SAME NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29; DB 3; Length 15;
Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tion US/09500124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 382:
SEQUENCE CHARACTERISTICS:
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100.0%;
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GY: unknown
TYPE: peptide
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US-09-500-124-382
; Sequence 382, Applicati
; Patent No. 6432920
; GENERAL INFORMATION:
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Best Local S
Matches 4
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Gaps

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                               0; Indels
                                                                                                                                                                                                         RESULT 40

US-08-982-597A-16

Sequence 16, Application US/08982597A

Patent No. 5932693

GENERAL INFORMATION:

APPLICANT: Staatz, William D.

TITLE OF INVENTION: Antithrombotic Peptides

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADRESSE: Scott J. Meyer

STREET: 800 No. 5932693th Lindbergh Blvd.

CITY: St. Louis

STREET: 800 No. 5932693th Lindbergh Blvd.

CITY: St. Louis

STREET: WO.

COUNTRY: USA

COMPUTER: IBM PC Compatible

OPERATION TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATION SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/982,597A

FILING DATE: 10-DEC-1996

CLASSIFICATION: 530

PRIOR APPLICATION: 530

PRIOR APPLICATION: 530

PRIOR APPLICATION: 530

PRIOR APPLICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Meyer SCOCTE J.

REGISTRATION NUMBER: 25,275

REFERENCE/DOCKET NUMBER: WU-3002

TELECOMMUNICATION INFORMATION:

NAME: Meyer SCOCTE J.

REFERENCE/DOCKET NUMBER: WU-3002

TELECOMMUNICATION INFORMATION:

NAME: Meyer SCOCTE J.

REFERENCE/DOCKET NUMBER: WI-307

TELECOMMUNICATION INFORMATION:

NAME: Meyer SCOCTE J.

REFERENCE/DOCKET NUMBER: WI-307

TELECOMMUNICATION INFORMATION:

NAME: Meyer SCOCTE J.

REGISTRATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:

LENGTH: TOPOLOGY: Inner and CIGHS

TOPOLOGY: Inner and CICHS

MOTECTIFE TYDE: DEATING
Best Local Similarity 100.0%; Pred. No. 83; Matches 4; Conservative 0; Mismatches
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; MOLECULE TYPE: peptide
US-08-982-597A-16
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12 PPPH 15
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15, 2005, 14:24:21

Search completed: June Job time: 24.5 secs

|||:| 12 PPPYG 16

1 PPPHG 5

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Sequence 10, Appl
Sequence 307567,
Sequence 139202,
Sequence 340254,
Sequence 199641,
Sequence 242501,
Sequence 19953, A
Sequence 199579,
Sequence 199279,
Sequence 152655,
Sequence 152655,
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                                                                                                                                        2005, 14:21:52 ; Search time 79.75 Seconds (without alignments) 24.034 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*

| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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6 US-10-425-115-307567
6 US-10-425-115-30202
6 US-10-425-115-340254
6 US-10-425-115-199641
6 US-10-425-115-242501
US-09-864-761-34953
5 US-10-424-599-170955
6 US-10-425-115-199279
6 US-10-425-115-199279
6 US-10-425-115-199279
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Maximum Match 100%
Listing first 45 summaries
                                                                                             protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match
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Perfect score:
Sequence:
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0-425-115-2	1-425-115-35277	-864-761-46134	8-10-425-115-2393	)-425-115-3445	-424-599-2(	-425-115-3166	1-437-963-	-437-963-15	1-424-599-	-425-115-1	4-599-1873	-10-767-701-512	10-425-115-30	10-425-115-	10-437-963-15	10-437-963-13291	10-424-599-22	5-115-2	10-425-115-32357	10-437-963-10958	10-425-115-2	10-425-115-27168	10-424-599-163	10-424-599-27	437-963-133	-10-425-115-20432	-10-424-599-143	4-599-26073	-10-282-122A-6224	-10-425-115-23281	-10-437-963-12	-10-424-599-15123	4-599-25289
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12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Sequence 10, Application US/10074225A

Fublication No. US2033082740A1

GENERAL INFORMATION:
APPLICANT: DONATE, Fernando
APPLICANT: HARRIS, Scott
APPLICANT: MAZAR, Andrew P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC P
TITLE OF INVENTION: HISTIDINE PROLINE RICH GLYCOPROTEIN (HPRG) AS AN ANTI-ANGIOGENIC P
TITLE OF INVENTION: ANTI-TUMOR AGENT
FILE REFERENCE: 38342-178463
CURRENT APPLICATION NUMBER: US/10/074,225A
CURRENT APPLICATION NUMBER: US 60/268,370
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 35; DB 14;
100.0%; Pred. No. 1.5e+06;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 5; Conserv
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TYPE: PRT
ORGANISM: Zea mays
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RESULT 2
US-10-425-115-307567

US-10-425-115-307567, Application US/10425115

Sequence 307567, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 307567

LENGTH: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 35; DB 16; Length 4
100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: MRT4577_43570C.1.pep
US-10-425-115-307567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-10-437-963-139202
; Sequence 139202, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; TITLE OF INVENTION: Plants and Uses There
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 139202
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; OTHER INFORMATION: ur
; FEATURE:
; OTHER INFORMATION: Cl
US-10-437-963-139202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Oryza sativ
FEATURE:
NAME/KEY: unsure
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Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 5; Conser
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FEATURE:
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US-10-12-199641

| Sequence 199641, Application US/10425115 |
| Sequence 199641, Application US/10425115 |
| Publication No. US20040214272A1 |
| GENERAL INFORMATION: |
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Plants |
| TITLE OF INVENTION: Plants |
| FILE REFERENCE: 38-21 (5322) B |
| CURRENT APPLICATION NUMBER: US/10/425,115 |
| CURRENT FILING DATE: 2003-04-28 |
| NUMBER OF SEQ ID NOS: 369326 |
| SEQ ID NO 199641 |
| LENGTH: 51 |
| LENGTH: 51 |
| LENGTH: 51 |
| LENGTH: 51 |
| CONTRACT |
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Sequence 340254, Application US/10425115
; Sequence 340254, Application US/10425115
; Sequence 340254, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 340254
; LENGTH: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 35; DB 16; Best Local Similarity 100.0%; Pred. No. 2.3e+02; Matches 5; Conservative 0; Mismatches 0;
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US-10-425-115-340254
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; Sequence 242501, Application US/10425115
; Publication No. US2004021427241
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
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APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 170955
LENGTH: 55
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US-10-425-115-199279
; Sequence 199279, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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N: EXPRESSED IN BT474, SIGNAL = 4.1

N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.4

N: EXPRESSED IN FLACENTA, SIGNAL = 7.1

N: EXPRESSED IN HELLOO, SIGNAL = 3.1

N: EXPRESSED IN HELA, SIGNAL = 5.9

N: EXPRESSED IN HEART, SIGNAL = 4.4

N: EXPRESSED IN BRAIN, SIGNAL = 4.4

N: EXPRESSED IN BRAIN, SIGNAL = 3.1

N: EXPRESSED IN LUNG, SIGNAL = 2.5

N: EXPRESSED IN LUNG, SIGNAL = 2.5
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US-10-424-599-170955
                                                : Annomax Sequence Listing Engine vers. 1.1
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100.0%; Pred. No. 2.6e+02;
ive 0; Mismatches 0;
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Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
          NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence
SEQ ID NO 34953
LENGTH: 55
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Best Local Similarity 100.
Matches 5, Conservative
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                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: BY
OTHER INFORMATION: EX
OTHER INFORMA
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Best Local Similarity
Matches 5; Conser
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US-10-424-599-170955
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            Nucleic Acid Molecules and Other Molecules Associated With
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N: HUMAN GENOME-DERIVED SINGLE EXON NUCLEI
N: GENE EXPRESSION ANALYSIS BY MICROARRAY
eomica-X-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 16;
100.0%; Pred. No. 2.5e+02;
Mismatches 0;
; TITLE OF INVENTION: Nucleic Acid Molecules a
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 242501
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Zea mays
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OR APPLICATION NUMBER: PCT/US01/00668

OR APPLICATION NUMBER: PCT/US01/00668

OR APPLICATION NUMBER: PCT/US01/00663

OR APPLICATION NUMBER: PCT/US01/00662

OR APPLICATION NUMBER: PCT/US01/00662

OR APPLICATION NUMBER: PCT/US01/00661

OR APPLICATION NUMBER: PCT/US01/00661

OR APPLICATION NUMBER: PCT/US01/00670

OR APPLICATION NUMBER: PCT/US01/00670

OR APPLICATION NUMBER: US01-01-30

OR APPLICATION NUMBER: US 60/234,687
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US-09-664-761-34953

US-09-664-761-34953

Sequence 34953, Application US/09664761

Patent No. USCO20048763A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENE EXPRESSION ANALY
FILE OF INVENTION: HUMAN GENE EXPRESSION ANALY
FILE OF INVENTION: HUMBER: US/09/64,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2000-09-27

PRIOR PILING DATE: 2001-01-00

PRIOR PILING DATE: 2001-01-00

PRIOR PILING DATE: 2001-01-00

PRIOR PILING DATE: 2001-01-30

PRIOR PILING DATE: 2000-01-31

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TUMBER: US 60/207,456

2000-05-26

TUMBER: US 09/632,366

2000-08-03

TUMBER: GB 24263.6

2000-10-04

TUMBER: US 60/236,359

2000-09-27
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001-01-30
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001-01-30
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MBER: US 60/180,312
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0000-09-21
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MBER: US 09/774,203
001-01-29
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, OTHER INFORMATION:
US-10-425-115-242501
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Best Local S:
Matches 5
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Gaps

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Sequence 261805, Application US/10425115
; Sequence 261805, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 261805
: LENGTH: 59
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US-10-425-115-352770
; Sequence 352770, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 352770
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US-10-425-115-261805
                                                                                                                                                                       100.0%; Score 35; DB 16; 100.0%; Pred. No. 2.7e+02;

; OTHER INFORMATION: Clone ID: MRT4577_84894C.1.pep
US-10-425-115-352770

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100.0%; Pred. No. 2.7e+02;
ative 0; Mismatches 0;
                                                                                  FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_5835C.1.pep
US-10-425-115-323782
                                                                                                                                                                                                               0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 5; Conserv
    SEQ ID NO 323782
LENGTH: 58
TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                              11 PPPHG 15
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ORGANISM: Zea mays
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US-10-425-115-261805
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Boukharcov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Brack
APPLICANT: Di, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILES OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILES TAPPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 152655
LENGTH: 58
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US-10-425-115-323782
; Sequence 323782, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21 (53222) B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                             Clone ID: MRT4577_113318C.1.pep
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100.0%; Pred. No. 2.7e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      100.0%; Score 35; DB 16; ilarity 100.0%; Pred. No. 2.6e+02; Conservative 0; Mismatches 0;
; TITLE OF INVENTION: Plants; FILE REFERENCE: 38-21(53222)B; CURRENT APPLICATION NUMBER: US/10/425,115; CURRENT FILING DATE: 2003-04-28; NUMBER OF SEQ ID NOS: 369326; SEQ ID NO 199279; LENGTH: 56; TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-437-963-152655
; Sequence 152655, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 5; Conser
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CTHER INFORMATION:
US-10-425-115-199279
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ORGANISM: Oryza
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US-10-425-115-239349

US-10-425-115-239349

Sequence 239349, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: 10/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 239349

LENGTH: 61
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Pred. No. 2.8e+02;
: Mismatches 0;
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100.0%; Pred. No. 2.8e+02;
ative 0; Mismatches 0;
     100.08;
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Best Local Similarity 100.
 Best Local Similarity 100 Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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                             Gaps
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GARRAL INFORMATION:
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Rank, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC AC
TITLE OF INVENTION: HUMAN GENOMES: US 60/180,312
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/207,466
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-05-27
PRIOR PELING DATE: 2000-01-30
PRIOR PELING DATE: 2000-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-20
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1.6
                              Indels
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EXPRESSED IN BRAIN, SIGNAL = 1.3
EXPRESSED IN ADULT LIVER, SIGNAL = 1
EXPRESSED IN BONE MARROW, SIGNAL = 1
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   Pred. No.
                                                                                                                                                                                               RESULT 14
US-09-864-761-46134
; Sequence 46134, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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Best Local Similarity 100 Matches 5; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-09-864-761-46134
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SOFTWARE: Annomax
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SEQ ID NO 46134
LENGTH: 61
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US-10-425-115-344565

US-10-425-115-344565

Sequence 344565, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 344565

LENGTH: 62
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.larity 100.0%; Pred. No. 2.9e+02;
Conservative 0; Mismatches 0;
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US-10-425-115-344565
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us-10-074-225a-10.rapb

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 150972
LENGTH: 70
              APPLICANT: Barbazuk, Brad Applicant: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NOS: 204966 SEQ ID NO 130521 LENGTH: 68 TYPE: PRT ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 181807, Application US/10424599;
Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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US-10-437-963-130521
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US-10-437-963-150972
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100.0%; Pred. No. 3.2e+02;
Ative 0; Mismatches 0;
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US-10-437-963-150972
; Sequence 150972, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Boukharov, Andrey A.
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Best Local Similarity 100.
Matches 5; Conservative
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TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
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Best Local Similarity
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48 PPPHG 52
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US-10-424-599-181807
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US-10-425-115-316672

Sequence 316672, Application US/10425115

Sequence 316672, Application US/10425115

Sequence 316672, Application US/10425115

Sequence 316672, Application US/0040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 316672

LENGTH: 65
      Sequence 206662, Application US/10424599
Sequence 206662, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 206662
LENGTH: 65
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; APPLICANT: La Rosa, Thomas J.; APPLICANT: Kovalic, David K.; APPLICANT: Zhou, Yihua; APPLICANT: Cao, Yongwei; APPLICANT: Wu, Wei
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5; Conserv
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Best Local Similarity
Matches 5; Conser
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION:
US-10-424-599-206662
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US-10-425-115-316672
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Glycine
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPHG 29
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US-10-437-963-130521
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Best Local S
Matches 5
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Sequence 307219, Application US/10425115

Sequence 307219, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Acou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 307219
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                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_140183C.1.pep
US-10-424-599-187344
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US-10-767-701-51220
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CORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(75)
CTHER INFORMATION: unsure at all Xaa locations
FEATURE:
CTHER INFORMATION: Clone ID: MRT4577_43257C.1.pep
US-10-425-115-307219
                                                                                                                                              Query Match 100.0%; Score 35; DB 15; Best Local Similarity 100.0%; Pred. No. 3.3e+02; Matches 5; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                               RESULT 24
US-10-767-701-51220
; Sequence 51220, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yongwei; TITLE OF INVENTION: Plants and Uses Thereof For; FILE OF INVENTION: Plants and Uses Thereof For; FILE REFERENCE: 38-21(53535) B
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 51220
; LENGTH: 75
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Best Local Similarity 100.v.
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ORGANISM: Sorghum bicolor
FEATURE:
 LENGTH: 73
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                          69 PPPHG 73
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US-10-424-599-187344, Application US/10424599
; Sequence 187344, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rovalic David K
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 187344
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                                                                                                                                                                                                                                                 100.0%; Score 35; DB 15; Similarity 100.0%; Pred. No. 3.2e+02; 5; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 3.2e+02;
ative 0; Mismatches 0;
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US-10-425-115-185365
; Sequence 185365, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules a:
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 185365
; LENGTH: 72
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 181807
LENGTH: 72
                                                                                                                        ; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clon
US-10-424-599-181807
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; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: ur
; FEATURE:
; OTHER INFORMATION: Cl
US-10-425-115-185365
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Best Local Similarity
Matches 5; Conser
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Best Local S
Matches 5
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Sequence 132911, Application US/10437963
; Sequence 132911, Application US/10437963
; Publication No. US2004012334341
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Weil
; APPLICANT: Weil
; APPLICANT: Weil
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 132911
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Sequence 220866, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 220866

LENGTH: 80
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US-10-437-963-132911
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US-10-424-599-220866
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100.0%; Pred. No. 3.5e+02;
ative 0; Mismatches 0;
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Glycine max FEATURE:
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APPLICANT: La Rosa. Thomas J.
APPLICANT: La Rosa. Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
APPLICANT: NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
                                                                                                                                                                                                                                                      RESULT 26
US-10-425-115-258243
; Sequence 258243, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 258243
; SEQ ID NO 258243
; LENGTH: 76
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100.0%; Score 35; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
                      Score 35; DB 16; Length 7 Pred. No. 3.4e+02; Mismatches 0; Indels
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100.0%; Pred. No. 3.4e+02;
iive 0; Mismatches 0;
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S-10-437-963-158099
Sequence 158099, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
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                      100.08;
                    Query Match 100.
Best Local Similarity 100.
Matches 5; Conservative
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5; Conservative
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; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clon
US-10-437-963-158099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION:
US-10-425-115-258243
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Best Local S
Matches 5
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NOWBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
SEQ ID NOS: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 33
US-10-425-115-213659
Sequence 233659, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 233659
LENGTH: B1
LENGTH: B1
LENGTH: B1
LENGTH: B1
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US-10-425-115-271683
; Sequence 271683, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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US-10-437-963-109589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: MRT4577_144690C.1.pep
US-10-425-115-233659
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 16;
Pred. No. 3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
 La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
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Best Local Similarity 100.
Matches 5, Conservative
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FEATURE:
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| PPPHG 60
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                                                                                     Sequence 249543

US-10-425-115-249543

Sequence 249543, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322) B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 249543

LENGTH: 80
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 323576
LENGTH: 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 35; DB 16;
100.0%; Pred. No. 3.5e+02;
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100.0%; Pred. No. 3.5e+02;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone ID: MRT4577_58171C.1.pep
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US-10-425-115-323576
; Sequence 323576, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 32
US-10-437-963-109589
; Sequence 109589, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
| | | | | | 44 PPPHG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||
PPPHG 16
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US-10-425-115-323576
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Sequence 133341, Application US/10437963
; Sequence 133341, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Rovalic, David K.
; APPLICANT: Rovalic, David K.
; APPLICANT: Buckharcv, Andrey A.
; APPLICANT: Bing and Uses Thereof for Plant Improvement
; APPLICANT: Barbazuk, Bing
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Dayles
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT BAT
; CORGANISM: OFYZE SETION
; FEATURE:
; NAME/KEY: unsure
; COATION: (1). (84)
; COATION: (1). (84)
; COATION: (1). (84)
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US-10-425-115-204320
; Sequence 204320, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei;
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 204320
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_35220C.1.pep
US-10-437-963-133341
                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_90677C.1.pep
US-10-424-599-275367
                                                                                                                                                                                   100.0%; Score 35; DB 15;
llarity 100.0%; Pred. No. 3.7e+02;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 35; DB 16;
100.0%; Pred. No. 3.7e+02;
:ive 0; Mismatches 0;
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OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
                         LENGTH: 84
TYPE: PRT
ORGANISM: Glycine "FEATURE:
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7 PPPHG 11
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     SEQ ID NO 275367
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US-10-424-599-163493
; Sequence 163493, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Abou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION NUMBER: US/10/424,599
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 163493
; LENGTH: 84
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US-10-424-599-275367
; Sequence 275367, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Rosa Thomas J
; APPLICANT: Zhou Yihua
; APPLICANT: Zhou Yihua
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
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100.0%; Pred. No. 3.6e+02;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 35; DB 15; Best Local Similarity 100.0%; Pred. No. 3.7e+02; Matches 5; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 271683
LENGTH: 82
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 5; Conservative
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ORGANISM: Glycine max
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NAME/KEY: unsure
LOCATION: (1)..(84)
OTHER INFORMATION: un
                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: C
US-10-425-115-271683
                                                                                                                                                                                                                                                                                                                                                                                                                                              44 PPPHG 48
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US-10-424-599-163493
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PPPHG
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Matches
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US-10-424-599-260730
is Sequence 260730, Application US/10424599
is Publication No. US20040031072A1
is GENERAL INFORMATION:
is APPLICANT: La Rosa Thomas J
is APPLICANT: La Royalic David K
is APPLICANT: Cao Yongwei
is APPLICANT: Cao Yongwei
is APPLICANT: Cao Yongwei
is APPLICANT: Cao Yongwei
is TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
is TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
is TITLE OF INVENTION: 104.28
is CURRENT APPLICATION NUMBER: US/10/424,599
is CURRENT FILING DATE: 2003-04-28
is NUMBER OF SEQ ID NOS: 285684
is SEQ ID NOS: 285684
is SEQ ID NOS: 260730
is LENGTH: 88
is ORGANISM: Glycine max
is FEATURE:
is OTHER INFORMATION: Clone: ID: PAT_MRT3847_77461C.1.pep
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                                                                                                                                    Indels
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                                                                                                         Length
                                                            Clone ID: MRT4577_117932C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 35; DB 15;
100.0%; Pred. No. 3.8e+02;
Live 0; Mismatches 0;
                                                                                                     Query Match 100.0%; Score 35; DB 16; Best Local Similarity 100.0%; Pred. No. 3.8e+02; Matches 5; Conservative 0; Mismatches 0;
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Pred. No. 3.8e+02;
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Best Local Similarity 100.
Matches 5; Conservative
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: C
US-10-425-115-204320
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Best Local Similarity
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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OM protein - protein search, using sw model

Run on:

2005, 14:04:57; Search time 17.5 Seconds (without alignments)
27.491 Million cell updates/sec June 15,

Title: US-10-074-225A-10 Perfect score: 35 Sequence: 1 PPPHG 5 Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

segs, 96216763 residues 283416 Searched:

283416 Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## CITAMADIES

SUMMARIES	Η	2 C72714 hypothetical prot	S37485 gene msql pro	conserved	D70906 hypothetic	A48013 proline-rich	T51469 glycine/proli	T19341	T46665 hypothetical	A86441 hypothetical	PIRT3 acidic prolin	F72641	B87440 transcription	T10586 small nuclear		T35805	A55852	S16681	I48338 E2F-5 - n	T26449	G84769	G87723	T07967	T32632	S19010 homeotic prot	F81046 hypothet	B69458	G02738 FREAC-4	
	Length DB	111	147		169													316						6		4	6	2	
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score			35																									
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Gaps

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Query Match 100.0%; Score 35; DB 2; Length 147; Best Local Similarity 100.0%; Pred. No. 38; Matches 5; Conservative 0; Mismatches 0; Indels

SPB binding protei	RAD57 related prot	B-alpha pheromone-	L-type voltage-gat	calcium channel pr	hypothetical prote	probable CCCH-type	hypothetical prote	hypothetical prote	probable ABC trans	Na+ channel protei	probable integral	chitin synthase (E	probable mmpL2 pro	hypothetical prote	C-terminal domain-
JC6203	T49422	S61920	165767	A41347	T00677	G84825	E86194	S48424	C87048	A49585	T36683	A41638	F70746	T00353	T31425
~	~	~	0	~	7	~	~	N	~	N	~	0	~	~	0
509	516	518	522	524	529	597	614	627	629	699	830	960	968	896	1048
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
35	35	35	35	35	35	35	32	35	35	35	35	35	35	35	35
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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Cypecies: Aeropyrum pernix
Cypecies: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
CyAccession: C72714
Rykawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takaha awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K. DNA Res. 6, 83-101, 1999
AyTitle: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Accession: C72714
AyReference number: A72450; MUID:99310339; PMID:10382966
AyAccession: C72714
AyAccession: C72714
AyAccession: C72714
AyReference: Traiminary
AyMolecule type: DNA
AyCossures: UNIPROT: Q9YCY2; DDBJ:AP000060; NID:g5104188; PIDN:BAA80115.1; PID:d1(CyGenetics:
AyExperimental source: strain Kl
CyGenetics:
AyGene: APE1130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generally protein - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C; Accession: 148669; S37485
R; Tronik-Le Roux, D.; Senorale-Pose, M.; Rougeon, F.
Gene 142, 175-182, 1994
A; Title: Three novel SMR1-related cDNAs characterized in the submaxillary gland of mice the A; Reference number: 148669; MUID:94252564; PMID:8194749
A; Accession: 148669
A; Accession: 148669
A; Accession: 148669
A; Accession: 148669
A; Cansidues: 1-147 < RES>
A; Cross-references: UNIPROT:Q61900; EMBL:X71629; NID:9406256; PIDN:CAA50636.1; PID:940625; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
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0
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Best Local Similarity
Matches 5; Conserv
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C;Accession: A48013
R;Castle, A.M.; Castle, J.D.
J. Biol. Chem. 268, 20490-20496, 1993
A;Title: Novel secretory proline-rich proteoglycans from rat parotid. Cloning and charact A;Reference number: A48013; MUID:93388626; PMID:8376404
A;Reference number: A48013
A;Residues: 1-170 <CAS>
A;Residues: 1-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  glycine/proline-rich protein - Arabidopsis thaliana
N;Alternate names: protein K10A8 130
C;Species: Arabidopsis thaliana [mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Aato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; Mewe submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Reference number: Z25394
A;Reference number: Z25394
A;Reference number: Z25394
A;Residues: 1-173 <SAT>
A;Residues: 1-173 <SAT
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-173 <WIL>
A; Residues: 1-173 <WIL>
A; Experimental source: clone C16D6
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Map position: X
A; Introns: 42/1
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T19341
hypothetical protein C16D6.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19341
R;Gardner, A.
submitted to the EMBL Data Library, November 1996
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44;
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; Pred. No. 44;
0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                           RESULT 3
C87235
C0nserved hypothetical protein ML2605 [imported] - Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Sate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: C87235
R; Coles. S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hc
R; Davies, R.M.; Devlin, K.;
Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A; Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A; Fitle: Massive gene decay in the leprosy bacillus.
A; Reference number: A86909; MUID:21128732; PMID:11234002
A; Reference number: A86909; MUID:21128732; PMID:11234002
A; Residues: 1-168 «STO»
A; Residues: 1-168 «STO»
A; Residues: 1-168 «STO»
A; Croses-references: UNIPROT:006065; GB:AL450380; NID:g13093836; PIDN:CAC32137.1; GSPDB:CC; Genetics:
A; Genetics:
A;
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D70906

hypothetical protein Rv0185 - Mycobacterium tuberculosis (atrain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Species: D70906
R; Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A; Authorers Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MuID:98295987; PMID:9634230
A; Residues: 1-169 cCOL>
A; Accession: D70906
A; Accession: D70906
A; Residues: 1-169 cCOL>
A; Residues: 1-169 cCOL>
A; Residues: 1-169 cCOL>
A; Residues: 1-169 cCOL>
A; Coss-references: UNIPROT:007429; GB:Z97050; GB:AL123456; NID:93256008; PIDN:CAB09736.
A; Contention: Rv0185
C; Superfamily: Mycobacterium tuberculosis hypothetical protein Rv0185
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A48013
proline-rich proteoglycan 1 precursor, parotid - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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100.0%; Pred. No. 43;
ive 0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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PPPHG 135
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Best Local Similarity
Matches 5; Conser
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C; Species: Rattus norvegicus (Norway rat)
C; Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C; Accession: A03296
R; Ziemer, M.A.; Swain, W.F.; Rutter, W.J.; Clements, S.; Ann, D.K.; Carlson, D.M.
J. Biol. Chem. 259, 10475-10480, 1984
A; Title: Nucleotide sequence analysis of a proline-rich protein cDNA and peptide homologi A; Reference number: A03296; MUID:84289443; PMID:6547951
A; Accession: A03296
A; Molecule type: mRNA
A; Cossion: A03296
C; Comment: This protein contains six 18- to 19-residue repeats.
C; Comment: This protein may protect teeth by binding to tannins.
C; Comment: This protein may protein
C; Comment: This protein may protect teeth by binding to tannins.
C; Superfamily: proline-rich protein
C; Keywords: duplication; parotid gland; saliva; tandem repeat
F; 1-13/Domain: signal sequence #status predicted <MAT>
F; 14-206/Product: acidic proline-rich protein #status predicted <MAT>
F; 80-189/Region: 18-residue repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
F72641
hypothetical protein APE0566 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F72641
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Tamaka, T.; Kudoh, Y.; Jin-no, K.; Takahi awa, H.; Tanaka, T.; Kudoh, Y.; Jin-no, K.; Takahi BNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Catuus: proliminary
A;Molecule type: DNA
A;Residues: 1-215 <KAW>A;Residues: 1-215 <KAW>A;Catus: Proliminary
A;Catus: Proliminary
A;Catus: Proliminary
A;Catus: A;Generical source: strain K1
C;Genetics:
A;Gene: APE0566
C;Superfamily: proline-rich protein
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transcription regulator, TetR family [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C; Accession: B87440
C; Accession: B87440
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.F.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolone
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Reference number: B87440
A; Status: preliminary
A; Molecule type: DNA
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local S
Matches 5
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                                                                                                                                                                                                                                         RESULT 8
T46665
hypothetical protein [imported] - Rhodococcus corallinus (fragment)
C;Species: Rhodococcus corallinus
C;Species: Rhodococcus corallinus
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46665
R;Shao, Z.Q.; Seffens, W.; Mulbry, W.; Behki, R.M.
J. Bacteriol. 177, 5748-5755, 1995
A;Title: Cloning and expression of the s-triazine hydrolase gene (trzA) from Rhodococcus erbicide atrazine.
A;Reference number: Z23125; MUID:96011356; PMID:7592318
A;Accession: Tf6665
A;Etatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-175 <SHA>
A;Residues: 1-175 <SHA>
A;Residues: 1-175 <SHA>
A;Cross-references: UNIPROT:052724; EMBL:L16534; NID:g294669; PIDN:AAA90930.1; PID:g2946
A;Experimental source: tissue lib NRRL 154448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
A86441
hypothetical protein FSM6.24 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: A86441
C; Accession: A86441
E; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.C., J.J.; Li, J.H.; Li, Y.; Lin, S.; Lin, S.; Khaykin, E.; Kim, C.C., J.J.; Li, J.H.; Li, Y.; Lin, J.J.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: A86441; MUD:21016719; PMID:11130712
A; Residues: 1-176 <STO>
A; Cross-references: UNIPROT:09C428; GB:AE005172; NID:g11136740; PIDN:AAG31321.1; GSPDB:GCGGenetics:
A; Map position: 1
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                                        Indels
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100.0%; Pred. No. 45;
ive 0; Mismatches
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    Pred. No. 44;
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       100.08;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
  Best Local Similarity 100 Matches 5; Conservative
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72 PPPHG 76
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PIRT3
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Gaps

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Indels

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RESULT 16
A55852
membrane-associated protein A - Synechococcus sp.
C;Species: Synechococcus sp.
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: A55852
R;Accession: A55852
R;Accession: Troyan, T.; Sherman, D.; Sherman, L.A.
J. Bacteriol. 176, 4906-4913, 1994
A;Title: MapA, an iron-regulated, cytoplasmic membrane protein in the cyanobacterium Syné
A;Reference number: A55852; MUID:94327456; PMID:8051004
A;Reference number: A55852
A;Accession: A55852
A;Accession: A55852
A;Accession: A55852
A;Cross-references: UNIPROT:Q55277; GB:L01621; NID:g484231; PIDN:AAA59057.1; PID:g484232
C;Genetics:
A;Gene: mapA
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S16681
homeotic protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C;Accession: S16681
R;Deguchi, Y.; Kehrl, J.H.
Nucleic Acids Res. 19, 3742, 1991
A;Title: Nucleotide sequence of a novel diverged human homeobox gene encodes a DNA bindir A;Reference number: S16681; MUID: 91305125; PMID: 1677181
A;Recession: S16681
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-316 < DEG>
A;Cross-references: EMBL:X56537
A;Cross-references: EMBL:X56537
A;Cross-references: EMBL:X56537
A;Cross-references: EMBL:X56537
A;Cross-references: EMBL:X56537
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;73-127/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                                                                          EMBL: AL035569; PIDN: CAB37565.1; GSPDB: GN00070; SCOEDI
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 12-Jul-2004
C;Accession: T35805
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, February 1999
A;Reference number: Z21589
A;Reference number: Z21889
A;Reference number: Z21
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Pred. No. 77;
); Mismatches
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Pred. No. 78;
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|larity 100.0%;
| Conservative 0;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thalian (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10586
R;Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16991
A;Reference number: Z16991
A;Accession: T10586
A;Molecule type: DNA
A;Residues: 1-257 <BEV>
A;Cross-references: UNIPROT:Q9SUNS; EMBL:AL080253; GSPDB:GN00062; ATSP:F9F13.90
A;Experimental source: cultivar Columbia; BAC clone F9F13
C;Genetics:
A;Gene: ATSP:F9F13.90
A;Map position: 4
C;Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immediate-early protein IE68 - human herpesvirus 3
C;Species: human herpesvirus 3, varicella-zoster virus
C;Species: human herpesvirus 3, varicella-zoster virus
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C;Accession: B27345; I27345
R;Davison, A.J.; Scott, J.E.
J. Gen. Virol. 67, 1759-1816, 1986
A;Title: The complete DNA sequence of varicella-zoster virus.
A;Reference number: A27345; MUID:86306657; PMID:3018124
A;Reference number: A27345
A;Molecule type: DNA
A;Residues: 1-278 < DNA
A;Residues: 1-278 < DNA
A;Residues: 1-278 < DNA
A;Cross-references: UNIPROT:P09255; EMBL:X04370; NID:g59989; PIDN:CAA27946.1; PID:g60052
C;Genetics:
A;Gene: 63; 70
C;Superfamily: herpesvirus immediate-early protein IE68
C;Keywords: early protein
       A;Residues: 1-224 <STO>
A;Cross-references: UNIPROT:Q9A825; GB:AE005673; NID:g13422922; PIDN:AAK23518.1; GSPDB:G
C;Genetics:
A;Gene: CC1539
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Pred. No. 57;
0; Mismatches
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Pred. No. 66;
0; Mismatches
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100.0%; Pred. No. 71;
iive 0; Mismatches
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5, Conservative
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PPPHG 223
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221 PPPHG 225
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T10586
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T35805
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GSPDB: GNC

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protein R06A10.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G87723
R; anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G87723
A;Accession: G87723
A;Residues: 1-391 <STO>
A;Conecule type: DNA
A;Residues: 1-391 <STO>
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 1
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Mandelonitrile lyase (EC 4.1.2.10) - flax

Mandelonitrile lyase (Soboriation of May 1999 #text_change 09-Jul-2004

C, Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004

C, Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004

C, Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004

C, Accession: T07967

R, Pereithaupt, H.M.; Boenigk, W.; Pohl, M.; Kula, M.R.

A, Description: Cloning and overexpression of (R)-hydroxynitrile lyase from Linum usitatis

A, Description: Cloning and overexpression of (R)-hydroxynitrile lyase from Linum usitatis

A, Accession: T07967

A, Status: preliminary; translated from GB/EMBL/DDBJ

A, Status: preliminary; translated from GB/EMBL/DDBJ

A, Status: Dreliminary; translated from GB/EMBL/DDBJ

A, Generics: A, Generics: A, Generics: UNIPROT:022574; EMBL:AF024588; NID:g2565287; PIDN:AAB81956.1; PID:g2: C, Genetics: A, Generics: A, Gen
                                                                                                                                                                                                                                                                                                                                                                                                                                        domain homology
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84769
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-368 <STO>
A;Cross-references: UNIPROT:082288; GB:AE002093; NID:g3608135; PIDN:AAC36168.1; GC;Genetics:
A;Genetics:
A;Genetics:
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Pred. No. 1e+02;
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Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 5; Conserv
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T26449
hypothetical protein Y113G7B.23 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T26449
R; Lennard, N.
submitted to the EMBL Data Library, September 1999
R; Lennard, N.
submitted to the EMBL Data Library, September 1999
A; Reference number: Z20215
A; Accession: T26449
A; Reterence number: Z20215
A; Accession: T26449
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-366 <WIL>
A; Molecule type: DNA
A; Residues: 1-366 <WIL>
A; Conserveferences: UNIPROT: Q9UZW6; EMBL: ALI10477; NID:e1542121; PIDN: CAB54337.1; CESP: X A; Experimental source: clone Y113G7B
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Hitrons: 318/1
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148338
E2F-5 - mouse
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 11995 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C; Accession: 1483338
R; Buck, V.; Allen, K.E.; Sorensen, T.; Bybee, A.; Hijmans, E.M.; Voorhoeve, P.M.; Bernar Oncogene 11, 31-38, 1995
A; Title: Molecular and functional characterisation of E2F-5, a new member of the E2F famt A; Reference number: 148338
A; Reference number: 148338
A; Accession: 148338
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Accession: type: mRNA
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-335 < RES>
A; Cross-references: UNIPROT:Q61502; EMBL:X86925; NID:g806571; PIDN:CAA60508.1; PID:g8065C; Genetics:
A; Genetics:
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G84769
hypothetical protein At2g35530 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84769
C;Accession: G84769
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
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                                                 Mismatches
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      Best Local Similarity 100.
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Best Local Similarity
Matches 5; Conser
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10 PPPHG 14
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S19010
Noneotic protein PBX3a - human
N.Alternate names: homeobox protein; pre-B-cell leukemia transcription factor 3
C;Species: Home sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
C;Accession: S19010
R;Monica, K.; Galili, N.; Nourse, J.; Saltman, D.; Cleary, M.L.
Nol. Cell. Biol. 11, 6149-6157, 1991
A;Teference number: S19010
A;Teference number: S19010
A;Teference number: S19010
A;Teterence numbe
                                                                                                                                                                                                                                                                                                                            RESULT 23
T32632
hypothetical protein F15E6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32632
R;Miller, N.; Stellyes, L.; Bradshaw, H.; Keppler, D.
R;Miller, N.; Stellyes, L.; Bradshaw, H.; Keppler, D.
R;Miller, N.; Stellyes, L.; Bradshaw, H.; Keppler, D.
A;Description: The EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F15E6.
A;Reference number: Z21202
A;Reference number: Z21202
A;Accession: T32632
A;Accession: T32632
A;Molecule type: DNA
A;Residues: 1-429 <MIL>A;Molecule type: DNA
A;Residues: 1-429 <MIL>A;Coss-references: UNIPROT:044497; EMBL:AF038614; PIDN:AAB92062.1; GSPDB:GN00022; CESP:A;Experimental source: strain Bristol N2; clone F15E6
C;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 4
A;Introns: 196/3; 241/3; 338/1
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                                Length 422;
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100.0%; Score 35; DB 2; I illarity 100.0%; Pred. No. 1.1e+02; Conservative 0: Micmatch.
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conser
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Best Local Similarity
Matches 5; Conser
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Figure 1 protein NWB1759 - Neisseria meningitidis (strain MC58 serogroup B) C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004 C;Accession: P81046 B;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; It, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Neference number: A81000; MUID:20175755; PMID:10710307 A;Reference number: A81000; MUID:20175755; PMID:10710307 A;Accession: F81046 A;Actatus: preliminary A;Molecule type: DNA A;Residues: 1-454 <TET> A;Accession: F81046 A;Cross-references: UNIPROT:Q9JY39; GB:AE002525; GB:AE002098; NID:g7227004; PIDN:AAF42100 A;Accession: RB1759 C;Genetics: A;Genetics: A;Genetics
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B69458
sulfate adenylyltransferase (sat) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Dischamor, R.D.; Dec-1997 #text_change 21-Jul-2000
C;Accession: B69458
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, .; Fleischmann, R.D.; Quackenbueh, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69458
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-459 <KLE>
A;Cross-references: GB:AE000988; GB:AE000782; NID:g2689311; PIDN:AAB89581.1; PID:g2648886
C;Superfamily: sulfate adenylyltransferase met3-1; sulfate adenylyltransferase homology
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G02738
FREAC-4 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 16-Aug-2004
C;Accession: G02738
R;Enerback, S.
submitted to the EMBL Data Library, June 1996
A;Reference number: H01646
A;Reference number: H01646
A;Accession: G02738
A;Accession: G02738
A;Status: preliminary; translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
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RESULT 30
JC6203
SP8 binding protein homolog - cucumber
C; Species: Cucumis sativus (cucumber)
C; Species: Cucumis sativus (cucumber)
C; Species: Cucumis sativus (cucumber)
C; Accession: JC6203
R; Kim, D.J.; Smith, S.M.; Leaver, C.J.
Gene 185, 265-269, 1997
A; Title: A cDNA encoding a putative SPFI-type DNA-binding protein from cucumber.
A; Reference number: JC6203; MUID:97208883; PMID:9055825
A; Accession: JC6203
A; Molecule type: mRNA
A; Residues: 1-509 < KIM>
A; Residues: 1-509 < KIM>
A; Residues: 1-509 < KIM>
A; Residues: 1-509 commercial is a DNA-binding protein consisting of a monomer. It is involved C; Genetics:
A; Genetics:
A; Genetics:
A; Genes sz71
C; Keywords: DNA binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAD57 related protein [imported] - Neurospora crassa
N;Alternate names: protein B17C10.30
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49422
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49422
A;Accession: T49422
A;Status: preliminary
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A;Residues: 1-516 <SCH>
A;Cross-references: UNIPROT:09P6E6; EMBL:AL355926; GSPDB:GN00116; NCSP:B17C10.30
A;Experimental source: BAC clone B17C10; strain OR74A
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S61920
B-alpha pheromone-receptor 2 - bracket fungus (Schizophyllum commune) (fragment)
      A,Map position: 4
A;Introns: 36/3; 73/2; 114/2; 154/1; 190/3; 211/3; 287/1; 364/3; 398/3; 449/2
                                                               100.0%; Score 35; DB 2; Length 486; 100.0%; Pred. No. 1.2e+02; ive 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
                                                                 Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                     283 PPPHG 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: NCSP:B17C10.30
A;Map position: 6
A;Introns: 31/3
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                                                                                                                                                      1 PPPHG 5
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T20482
hypothetical protein F01G10.10 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T20482
R; Hembry, C.
submitted to the EMBL Data Library, October 1996
A; Reference number: Z19280
A; Reference number: Z19280
A; Accession: T20482
A; Accession: T20482
A; Accession: T486
A; Residues: 1-486
A; Residues: 1-486
A; Residues: 1-486
A; Experimental source: clone F01G10
C; Genetics:
A; Genetics:
A; Genetics:
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A; Molecule type: mRNA
A; Residues: 1-465 <ENE>
A; Cross-references: UNIPROT:Q16676; EMBL:U59832; NID:g1399238; PID:g1399239
C; Genetics:
A; Gene: FREAC-4
C; Superfamily: fork head DNA-binding domain homology
C; Superfamily: fork head DNA-binding domain homology
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A44461
voltage-dependent calcium channel beta-1 chain, M isoform - human
                                                                                                                                                                      100.0%; Score 35; DB 2; Length 465; 100.0%; Pred. No. 1.2e+02; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 35; DB 2; Length 475; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 5; Conservative
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Query Match
Best Local Similarity 100.
Matches 5; Conservative
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G84825
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165767
L-type voltage-gated calcium channel B subunit - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 18-Aug-2000
C;Accession: 165767
Circ. Res. 72, 1337-1344, 1993
Circ. Res. 72, 1337-1344, 1993
A;Title: Molecular: 152859; MUID:93265672; PMID:7916667
A;Reference number: 152859; MUID:93265672; PMID:7916667
A;Ratus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-522 <RES>
A;Cross-references: GB:L06112; NID:g187018; PIDN:AAA36169.1; PID:g187019
C;Superfamily: human voltage-dependent calcium channel beta chain
C;Species: Schizophyllum commune
C;Date: 23-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S61920
R;Wendland, J.; Vaillancourt, L.J.; Hegner, J.; Lengeler, K.B.; Laddison, K.J.; Specht, EMBO J. 14, 5271-5278, 1995
A;Title: The mating-type locus Balphal of Schizophyllum commune contains a pheromone rec A;Reference number: S61919; MUID:96080162; PMID:7489716
A;Reference number: S61919; MUID:96080162; PMID:91143553; PIDN:CAA62595.1; PID:9114
A;Residues: 1-518 <WEN>
A;Re
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A41347
calcium channel protein beta chain, dihydropyridine-sensitive, skeletal muscle - rabbit
calcium channel protein beta chain, dihydropyridine-sensitive, skeletal muscle - rabbit
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: O3-Apr-1992 #sequence_revision O3-Apr-1992 #text_change O9-Jul-2004
C; Accession: A41341
R; Muth, P: Nochrkasten, A.; Biel, M.; Bosse, E.; Regulla, S.; Meyer, H.E.; Flockerzi, V
Science 245, 1115-1118, 1989
A; Title: Primary structure of the beta subunit of the DHP-sensitive calcium channel from
A; Reference number: A41347; MUID:89368946; PMID:2549640
A; Accession: A41347
A; Molecule type: mRNA
A; Residues: 1-524 < RUT>
A; Molecule type: mRNA
A; Residues: 1-524 < RUT>
C; Superfamily: human voltage-dependent calcium channel beta chain
C; Keywords: skeletal muscle
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Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels
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hypothetical protein At2943970 [imported] - Arabidopsis thaliana
NyAlternate names: hypothetical protein F6E13.10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00677; G84872
E;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A;Reference number: Z14180
A;Reference number: Z14180
A;Reference number: Z14180
A;Residues: 1-529 <ROUS
A;Residues: 1-529 <ROUS
A;Cross-references: UNIPROT: O80567; EMBL: AC0044005; NID: G33212846; PID: G3212854
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
B;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. W.; Ko, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frasser, C.M.; Venter, J. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C; Accession: G84825

R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A; Reference number: A84420; MUID:20083487; PMID:10617197

A; Accession: G84825

A; Accession: G84825

A; Accession: G84825

A; Molecule type: DNA

A; Residues: 1-597 <STO>
A; Cooss-references: UNIPROT:Q9XEE6; GB:AE002093; NID:g6598933; PIDN:AAF18728.1; GSPDB:GNC
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <STO>
A;Cross-references: GB:AE002093; NID:g3212854; PIDN:AAC23405.1; GSPDB:GN00139
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A;Gene: F6E13.10; At2g43970
A;Map position: 2
A;Introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3
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100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0;
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Length 629;

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eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq.
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: C87048
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-629 <STO>
A;Residues: 1-629 <STO>
A;Cross-references: UNIPROT:Q9CC89; GB:AL450380; NID:g13093097; PIDN:CAC31494.1; GSPDB:GPCGenetics:
A;Genetics:
A;Genet
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-669 <RES>
A;Cross-references: UNIPROT:P37088; EMBL:X76180; NID:g452649; PIDN:CAA53773.1; PID:g45265
A;Cross-references: UNIPROT:P37088; EMBL:X76180; NID:g452649; PIDN:CAA53773.1; PID:g45265
R;McDonald, F.J.; Snyder, P.M.; McCray, P.B.
Am. J. Physiol. 266, L728-L734, 1994
A;Title: Cloning, expression, and tissue distribution of a human amiloride-sensitive Na+A;Reference number: I51911; MUID:94295729; PMID:8023962
A;Reference number: I51911
A;Racession: I51911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A49585
Na+ channel protein, amiloride-sensitive - human
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
C;Accession: A49585; I51911
R;Voilley, N.; Lingueglia, E.; Champigny, G.; Mattei, M.G.; Waldmann, R.; Lazdunski, M.;
Proc. Natl. Acad. Sci. U.S.A. 91, 247-251, 1994
A;Title: The lung amiloride-sensitive Na+ channel: biophysical properties, pharmacology, A;Reference number: A49585; MUID:94105144; PMID:8278374
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A;Residues: 1-669 <RE2>
A;Cross-references: GB:L29007; NID:g493125; PIDN:AAA21813.1; PID:g493605
C;Genetics:
A;Map position: 12p13
C;Superfamily: human amiloride-sensitive sodium channel protein; fibrone
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100.0%; Pred. No. 1.6e+02;
tive 0; Mismatches 0;
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                                                                                                                                                       RESULT 37

E86194

hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear crees)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86194

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; M., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Residues: 1-614 <STO>
A;Cross-references: UNIPROT:09LNF0; GB:AE005172; NID:g8810458; PIDN:AAF80119.1; GSPDB:GN C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 39
C87048
probable ABC transporter, ATP-binding component ML1113 [imported] - Mycobacterium leprae probable ABC transporter, ATP-binding component ML1113 [imported] - Mycobacterium leprae C;Species: Mycobacterium leprae C;Species: Mycobacterium leprae C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004 C;Accession: C87048
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Holroyd, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
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S48424
hypothetical protein YIL055c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
C;Accession: S48424
R;Smith, V.
submitted to the EMBL Data Library, September 1994
A;Reference number: S48407
A;Recession: S48424
A;Molecule type: DNA
A;Residues: 1-627 <SMI>A;Residues: 1-627 <SMI>A;Cross-references: UNIPROT:P40523; GB:Z47047; EMBL:Z38060; NID:g603997; PID:g76
C;Genetics:
A;Gene: MIPS:YIL055c
A;Cross-references: SGD:S0001317
A;Map position: 9L
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Pred. No. 1.6e+02;
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100.0%; Pred. No. 1.6e+02;
Mismatches 0;
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                                           456 PPPHG 460
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Best Local Similarity
Matches 5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 PPPHG 50
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us-10-074-225a-10.rup

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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2005, 13:53:11; Search time 83.5 Seconds (without alignments) 30.663 Million cell updates/sec OM protein - protein search, using sw model June 15, Run on:

US-10-074-225A-10 35 1 PPPHG 5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

segs, 512079187 residues 1612378 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: Maximum DB seq length:

2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	02832	Q9v8yl drosophila	Q6ub47 hyaloperono	_	_	_	Q62cg2 burkholderi	Q63k18 burkholderi	Q655p3 oryza sativ						Q7wmt3 bordetella	Q61900 mus musculu		Q8abu0 bacteroides	Q8grk5 oryza sativ		_		Q63rt2 burkholderi		O06065 mycobacteri	007429 mycobacteri	Q7u2m4 mycobacteri	Q07610 rattus norv	'n		Q8llm4 triticum ae
SUMMARIES		ai	002832	Q9V8Y1	Q6UB47	PN2D_LITSE	Q9VP <u>2</u> 1	Q94J14	Q62CG2	Q63KL8	Q655P3	Q9YCY2	Q67867	Q7 YWR5	Q7VVE3	Q7WBB4	Q7WMT3	SMR1_MOUSE	QBN1P8	Q8ABU0	QBGRK5	Qegsl3	Q657L2	Q62HZ3	Q63RT2	Q62W55	006065	007429	Q7U2M4	Q07610	062063	062789	Q8LLM4
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		Match Length	ı	23	62	72	80	93	94	94	108	111	119	134	135	135	135	147	151	152	164	164	164	164	164	165	168	169	169	170	173	173	173
J	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	Ю				35			35	38			32		32	35	32	32	32	32	35	32	32	32	32	32	32	35	35		32	35
	Result	No.	H	7	m	4	S	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29	30	31

Q91f59 arabidopsis	Q52724 rhodococcus	Q8lep5 arabidopsis		Q28261 canis famil	Q8zy20 pyrobaculum	Q67u43 oryza sativ				Q9yel2 aeropyrum p	Q9fyn6 oryza sativ	oryza	Q9a825 caulobacter
Q9LF59	052724	Q8LEP5	Q9C4Z8	Q28261	Q8ZY20	Q67U43	QBND66	Q67IV2	PRP3_RAT	Q9YEL2	Q9FYN6	Q8RYZ6	Q9A825
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173	175	176	176	181	185	192	201	203	206	215	216	221	224
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
35	35	35	35	35	35	32	32	32	32	32	32	32	35
32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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MEDLINE=96326790; PubMed=8766138;
Pecheux C., Gall A.L., Kaplan J.C., Dode C.;
"Sequence analysis of the CAG triplet repeats region in the Huntington disease gene (IT15) in several mammalian species.";
Ann. Genet. 39:81-86(1996).
EMBL; S93377; AAB50771.1; -.
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MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                               Ol-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 19, Last annotation update)
Huntingtin protein (Fragment).
Name=IT15;
Gorilla gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
NCBI_TaxID=9593;
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0
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 35; DB 2; Length 33; 100.0%; Pred. No. 46; 0; Indels ative 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
CG15126-PA.
ORFNames=CG15126;
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                                                                    33
                                                                    PRT;
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5; Conservative
                                                                    PRELIMINARY;
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Q9V8Y1
ID Q9V8
AC Q9V8
DT 01-M
DT 01-M
DT 01-J
DE CG15
GN ORFN
GN ORFN
OC BPh
RESULT 1
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Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

Ballew R.M., Basu A., An H.J., Andrews Pfannkoch C., Baldwin D.,

Ballew R.M., Basu A., Baradale J., Bayrakaraglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolbakov S.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Chornel J. Bornellan A.E., Gars M. D., Edel Davies P., Hourk J.,

RA Durbin K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Bortin D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Harris N.L., Harvey D., Heiman T.J., Wei M.H., Inbeyam C.,

Alali M., Kodira C.D., Kraft C., Kraft C., Krail Son J.A., Kelly B., Lai Z.,

Lasko P., Lei Y., Levitsky A.A., Lil J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,

Mount S.M., Moy M., Murphy B., Murryy B., Murryy D.M., Nelson D.L.,

RA Balazolo M., Pittman G.S., Pan S., Pollard J., Mosleon D.L.,

RA Spier E., Spandling A.C., Stapleton M., Skupski M.P., Smith T.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Shue B.C., Saden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Shue B.C., Saden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

Rang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

Weiber S., Tector C., Turner R., Vanter B., Wang A.H., Wang A.,

Wang S.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

The genome sequence of Drosophila melanogaster.";

Science 287:2185-2195 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N [2]

SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

A Reliner S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

Conome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., S.
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster"
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"Use of suppression subtractive hybridization to identify downy mildew genes expressed during infection of Arabidopsis thaliana.";
Mol. Plant Pathol. 0:0-0(2003).

EMBL; AY373968; AAQ83520.1; -.
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Immunogenetics 54:442-445(2002).
-!- FUNCTION: Antibacterial and antifungal activity. Presents chitin-
binding activity (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic granules of hemocytes and to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hyaloperonospora parasitica.
Eukaryota; stramenopiles; Oomycetes; Peronosporales; Peronosporaceae;
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 44, Last annotation update)
55-JUL-2004 (Rel. 44, Last annotation update)
Penaeidin-2d precursor (Pen-2d).
Litopenaeus setiferus (Atlantic white shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
Penaeidae; Litopenaeus.
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MEDLINE=22226701; PubMed=12242595; DOI=10.1007/800251-002-0487-z;
Cuthbertson B.J., Shepard E.F., Chapman R.W., Gross P.S.;
"Diversity of the penaeidin antimicrobial peptides in two shrimp
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                          FlyBase;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003795; AAF57523.1; -.
IntAct; Q9V8Y1; -.
FlyBase; FBgn0040729; CG15126.
SEQUENCE 53 AA; 5388 MW; 68828750C9C82142 CRC64;
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53 AA; 5388 MW; 68828750C9C82142 CRC64;
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62 AA; 6729 MW; D883FC9E4E838A58 CRC64;
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iive 0; Mismatches
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Best Local Similarity
Matches 5; Conserv
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NCBI_TaxID=123356;
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Anaton R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Aspayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Abrils K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Ade Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Burbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W., Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                         group)
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Lysine amide (G-72 provides amide
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI TaxID=7227;
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By similarity.
By similarity.
Pyrrolidone carboxylic acid (By similarity).
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Last annotation update)
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HSSP; P81058; 1UEO.
InterPro; IPR009226; Penaeidin.
Pfam; PF05927; Penaeidin; 1.
Amidation; Antibiotic; Chitin-binding; Fungicide;
Pyrrolidone carboxylic acid; Signal.
SIGNAL 1 21 Potential.
lesser extent in small granules of hemocytes-1- SIMILARITY: Belongs to the penaeidin family.
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Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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IntAct; Q9VPZ1; -.
FlyBase; FBgn0040723; CG5011.
SEQUENCE 80 AA; 8699 MW; D57F2D6B3443B4BF CRC64;
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100.0%; Pred. No. 1.1e+02;
tive 0; Mismatches 0;
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Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Query Match
Best Local Similarity 100.
Matches 5; Conservative
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                                  EMBL; CP000011; AJ
DNA-binding.
SEQUENCE 94 AA;
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75 PPPHG 79
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Q655P3;
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Q63KL8;
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Q63KL8
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Q655P3
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Bubbed=124474343 DOI=10.1038/nature01184;

Bubbed=124474343 DOI=10.1038/nature01184;

Bubbed=124474343 DOI=10.1038/nature01184;

Bubbed=124474343 DOI=10.1038/nature01184;

Bubbed=12474343 DOI=10.1038/nature01184;

Bubbed=12011184;

Bubbed=1244311;

Bubbed=1244314 DOI=10.1038/nature01184;

Bubbed=1244311;

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Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.
Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
P0481E12.34 protein.
Name=P0481E12.34;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=243160;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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DNA-binding protein.
ORFNames=BMAA0931;
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  12 PPPHG 16
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X PubMed=1537794;

A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
Reith K.E., Maddison M., Moule S., Frice C., Quail M.A.,
Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
A Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
A Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
A Rabbinowitsch E., Rutherford K., Tumapa S., Vesaratchavest M.,
Mhitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
Burkholderia pseudomallei.";
Broc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
BEMBL; BX571966; CAH38814.1; -.
DNA-binding.
A RADINEWER W. BODAS022E10EE8FF CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein B1011A07.27.
Name=B1011A07.27;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Shrhartoideae; Oryzeae; Oryza.
NCBI TaxID=39947;
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Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
NCBI_TaxID=272560;
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                                                                                                                                              Length 94;
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Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004)
EMBL; CP000011; AAU46112.1; -.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative DNA-binding protein.
                                                                                                                                       100.0%; Score 35; DB 2; 1
100.0%; Pred. No. 1.3e+02;
ative 0; Mismatches 0;
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                                                                                      9817 MW;
                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 5; Conservative
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=adr;
MEDLINE=89183619; PubMed=2928116;
Rho H.M., Kim K., Hyun S.W., Kim Y.S.;
"The nucleotide sequence and reading frames of a mutant hepatitis
                                                                                                                                                                                                                                  Viruses, Retroid viruses, Hepadnaviridae, Orthohepadnavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Harris B.R.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL034392; CAE17989.1; -.
WormBase; WBGene00012736; Y40B1A.5.
WormPep; Y40B1A.5; CE35082.
Hypothetical protein.
SEQUENCE 134 AA; 14532 MW; E1CFF526E97C297D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 AA; 12553 MW; 8EE9E93CD66F1E6D CRC64;
                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Pre-S1 region (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y40BlA.5.
ORFNames=Y40BlA.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 35; DB 2; I
100.0%; Pred. No. 1.7e+02;
ative 0; Mismatches 0;
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Nucleic Acids Res. 17:2124-2124(1989),
EMBL; X14193; CAA32406.1; -.
GO, GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000349; Hepvir_surfAg.
Pfam; PF00695; vMSA; 1.
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          NCBI_TaxID=10407;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||
88 PPPHG 92
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NON TER
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PubMed=12447438;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikeno M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi T., Mukai Y.,
Nakasawa W., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Nagasaki H., Nakashima M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
Yano M., Jiang J., Gojobori T.;
"The genome sequence and structure of rice chromosome 1.";
"The genome sequence and structure of rice chromosome 1.";
"Hypothetical protein.
"W SEQUENCE 108 AA; 11886 MW; 6B93CD836E85C0A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 2; Length 1(
100.0%; Pred. No. 1.5e+02;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aeropyrum pernix.
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
12537 MW; 3CE2AE76F92522BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein APE1130.
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EMBL; AP000060; BAA80115.1; -. PIR; C72714; C72714.

Complete proteome; Hypothetica SEQUENCE 111 AA; 12537 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APE1130;
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01-MAR-2004 (TrEMBL)
Hypothetical proteir
OrderedLocusNames=AR
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Best Local S
Matches 5
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Q61900;
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Q7WMT3
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SEQUENCE FROM N.A.

XTRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

REDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

RATAIN=10 J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,

Ratharia D.E., Holden M.TG., Churcher C.M., Bentley S.D., Mungall K.L.,

Ratharia D.E., Holden M.TG., Churcher C.M., Bentley S.D., Mungall K.L.,

RACHMAN M., Atkin R., Baker S., Bakam D., Bason N., Cherevach I.,

RACHMAN M., Atkin R., Callins M., Cronin A., Davis P., Doggett J.,

Reltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

Rabbinowitsch S., Barrell B.G., Maskell D.J.;

Nordetella parapertussis and Bordetella bronchiseptica.";

Rochetella parapertussis and Bordetella bronchiseptica.";

Roch Go:0016021; C:integral to membrane; IEA.

InterPro; IPR05171; COX4_pro.

Remplete proteome.

Complete proteome.

SEQUENCE 135 AA; 14848 MW; EF2B611E6F958A5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22827954; PubMed=12910271; DOI=10.1038/ng1227;
Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
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Alcaligenaceae, Bordetella.
NCBI_TaxID=519;
                                                                                                                                                                                                                                                                    cteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 35; DB 2; Length 135; 100.0%; Pred. No. 1.9e+02; vative 0; Mismatches 0; Indels
                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome ubiquinol oxidase subunit IV.
OrderedLocusNames=BP2728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome ubiquinol oxidase subunit IV.
OrderedLocusNames=BPP1091;
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STRAIN=12822 / ATCC BAA-587;
MEDLINE=22827954; PubMed=129
                                                                                                                                                                                                                                       Bordetella pertussis.
Bacteria, Proteobacteria, B
Alcaligenaceae, Bordetella.
NCBI_TaxID=520;
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                                                                    PRELIMINARY;
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Best Local Similarity
Matches 5, Conser
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Q7WBB4;
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Q7WBB4
ID Q7WBB
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Q7VVE3
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SEQUENCE FROM N.A.

STRAIN=RBSO / ATCC BAA-588;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

A Cerdeno-Tarraga A.—M., Temple L., James K.D., Harris B., Quail M.A.,

A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Atkin R., Baker S., Davis P., Doggett J.,

A Achtman M., Atkin R., Baker S., Norberczak H., O'Neil S., Ormond D., Price C.,

A Rabbinowitsch E., Rutter S., Sanders M., Squares S., Stevens K.,

A Sharp S., Simmonds M., Skelton J., Squares S., Stevens K.,

A Comparative analysis of the genome sequences of Bordetella pertussis,

I Comparative analysis of the genome sequences of Bordetella pertussis,

R Bordetella parapertussis and Bordetella bronchiseptica.";

Nat. Genet. 35:32-40(2003).

Nat. Genet. 35:32-40(2003).

R PABL; BX640441; CAB21805.1; -

R GO; GO:00060118; P:electron transport; IEA.

R InterPro; IPR065171; COX4_pro.

R PABL; BX640441; CAS1805.1; -

R PABL; PARLS PR03626; COX4_pro.

R PABL; PARLS PR03626; COX4_pro.
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     Stevens K.,
                                                                 pertussis,
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Cytochrome ubiquinol oxidase subunit IV.
OrderedLocusNames=BB1307;
Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella.
NCBI_TaxID=518;
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Sharp S., Simmonds M., Skelton J., Squares R., Squares S., S
Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella
Bordetella parapertussis and Bordetella bronchiseptica.";
Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 135;
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                                                                                                                            Nat. Genet. 35:32-40 (2003).

EMBL, BX640426; CAE36392.1; -.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0006118; P:electron transport; IEA.

InterPro; IPR005171; COX4 pro.

Pfam; PF03626; COX4 pro; 1.

Complete proteome.

SEQUENCE 135 AA; 14848 MW; BF2B611E6F958A5D CRC64;
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; Pred. No. 1.9e+02;
0; Mismatches 0;
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100.0%; Pred. No. 1.9e+02;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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ID Q8ABU
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RTSUSE-Salivary gland;

RC TSUSUS-Salivary gland;

RC TSUSUS-Salivary gland;

RE TISSUS-Salivary gland;

RA Straubberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. B. Buerow K.H., Schemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. B. Buerow K.H., Schemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B. B. Buerow K.H., Scheefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., Usdin T.B., Schers G.J., Abramson R.D., Mullahy S.J.,

RA Brownstein M.J., WcEwran K.J., Malek J.A., Gunaratne P.H.,

RA Brownstein M.J., Worder M.J., Madan A., Rodrigues S., Sanchez A.,

RA Blakeley R.W., Touchman J.W., Scherzer B.D., Dickson M.C.,

RA Blakeley R.W., Touchman J.W., Schmutz J., Myers R.W.,

RA Blakeled Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

ROBERELULAR LOCATION: May play a role in protection or detoxification.

C. I- FUNCTION: May play a role in protection or detoxification.

C. I- SUBCELLULAR LOCATION: Secreted

C. I- SUB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  itry is copyright. It is produced through a collaboration institute of Bioinformatics and the EMBL outstation - formatics Institute. There are no restrictions on its t institutions as long as its content is in no way
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                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Submaxillary gland;
STRAIN=94252564; PubMed=8194749; DOI=10.1016/0378-1119(94)90258-5;
Tronik-Le Roux D., Senorale-Pose M., Rougeon F.;
Tronik-Le Roux D., Senorale-Pose M., Rougeon F.;
"Three novel SMR1-related cDNAs characterized in the submaxillary "Three novel show extensive evolutionary divergence in the protein
       41, Created)
41, Last sequence update)
44, Last annotation update)
1 androgen regulated protein 1 precursor (Salivary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential.
Submaxillary gland androgen regulated
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Submaxillary gland androgen regulated protein 1 precursor (Salivar protein MSG1).
Name=Smr1; Synonyms=MSG1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 1.
3 X 12 AA tandem repeats of
P-[HP]-P-P-P-[PF].
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AH31806.1; -.
AH31921.1; -.
AH34553.1; -.
AH55857.1; -.
                                                                                                                                                                                                                                                             "Three novel SMR1-relate
gland of mice show exter
coding region.";
Gene 142:175-182(1994).
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EMBL, BC031806; AAH31806
EMBL, BC031921; AAH31921
EMBL, BC034553; AAH34553
EMBL, BC055857; AAH55857
PIR, 148669; S37485.
MGD; MGI:102763; Smrl.
Repeat; Signal.
SIGNAL
1 22
CHAIN 23 147
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RA OLDENCE FROM N.A.

RA CT TISSUB—TONGUE;

RA CT TISSUB—TONGUE;

RA CT TISSUB—TONGUE;

RA CT TISSUB—TONGUE;

RA Makamateu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishiis H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Mamamoto J., Saitor K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Murakami K., Yasuda T., Iwayanagi T., Nakamura Y., Nagahari K.,

RA Murakami M., Kanda K., Yokoi T., Furuya T., Kikkawa B., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

Abe K., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Ishidas S.,

Annomiya K., Ishibashi T., Yamashita H., Murakawa M., Yamazaki M.,

RA Anai H., Kimata M., Matanabe M., Hiraoka S., Chiba Y., Ishida S.,

Annomiya S., Komai F., Hara R., Takeuchi K., Arita W., Imose N.,

Musashino K., Yuuki H., Oshima A., Sasaki M., Imose N.,

Noshikawa Y., Matsunaba H., Ishihara T., Shiohata N., Sano S.,

Noshikawa Y., Matsunaba H., Satoh N., Takemi S., Terashima Y., Sazuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

Ramazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

Rujimorii Y., Komiyama H., Tashiro H., Tanao M., Chimata T.,

Rujimorii Y., Komiyama H., Tashiro M., Chumura Y., Okamoto S.,

Rawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

Atsubihama Y., Makajima Y., Milayami T., Matsumura K., Seaba T.,

Matumura K., Nakajima Y., Milayami Y., Matsumura K., Nakajima Y., Milayami Y., Matsumura K., Nakajima Y., Makamura N., Matanabe M., Komatsu T.,

Matumura K., Nakajima Y., Matanabe M., Komatsu T.,

Matumura K., Nakajima Y., Matanabe M., Komatsu T.,

Matumura K., Nakajima Y., Milayama Y., Matanabe M., Komatsu T.,

Matumura K., Nakajima Y., Matanabe M., Komatsu T.,

Mataumura K., Nakajima Y., Matanabe M., Komatsu T.,

Mataumura K., Nagase T., Nomura N., Kikuchi H., Masuho S.,

Makai K., Yada T., Nakailari N., Okamoto S.,

Makai K., Yada T., Nagase T., Nomura O., Isagai T., Sagahi M.,

Makai K., Yada A., Nakai M
                                                                                                                                Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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07D64E22F1BF58C2 CRC64;
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EMBL; AK095331; BAC04532.1; -.
SEQUENCE 151 AA; 16189 MW; 091EADD64FECEE89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-OCT-2002 (TrEMBLrel. 22, Last annotation update) Hypothetical protein FLJ38012.
                                                                 Score 35; DB 1; 1
Pred. No. 2.1e+02;
Mismatches 0;
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Pred. No. 2.1e+02;
0; Mismatches 0;
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147 AA;
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Pred. No. 2.3e+02;

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                                                                                                                                                                                                                                                                                                                                    ATCC 29148;
PubMed=12663928; DOI=10.1126/science.1080029;
K., Himrod J., Deng S., Carmichael L.K.,
ir L.V., Gordon J.I.;
the human-Bacteroides thetaiotaomicron symbiosis.";
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                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein.
OrderedLocusNames=BT0020;
Bacteroides thetaiotaomicron.
Bacteroides thetaiotaomicron.
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales; NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 152
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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome clone:OJ1112_E08.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17665 MW; 1991F9218509F8D9 CRC64;
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100.0%; Pred. No. 2.1e+02;
iive 0; Mismatches 0;
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Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, ch.
clone:OJ1720 F04.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ
EMBL; AP003705; BAC15806.1; -.
EMBL; AP003705; BAC15809.1; -.
EMBL; AP005296; BAD31277.1; -.
EMBL; AP005296; BAD31277.1; -.
Gramene; Q8GRK5; -.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR008994; Nucleic_acid_OB.
Hypothetical protein.
SEQUENCE 164 AA; 17805 MW; E6F13AF5FA7E4E
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STRAIN=VPI-5482 / AT
MEDLINE=22550858; Pt
Xu J., Bjursell M.K.
Chiang H.C., Hooper
"A genomic view of t
Science 299:2074-207
EMBL; AE016926; AAO7
Complete proteome.
SEQUENCE 152 AA;
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5; Conserv
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Submitted (MAY-200:
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Pubmed=12447438;
Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Sasaki T., Matsumoto T., Yamamoto K., Antonio B.A., Kanamori H.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 28, Last annotation update)
15-OCT-2004 (TrEMBLrel. 28, Last annotation update)
15-OCT-2004 (TrEMBLrel. 28, Last annotation update)
15-OCT-2004 (TrEMBLrel. 28, Last annotation update)
001720 F04-123).
Name=001112 E08.110; Synonyms=001720 F04.123;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                Indels
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"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, clone:0J1720 F04.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 164 AA; 17708 MW; 02369EB26D9ADBIC CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein P0468H06.16.
Name=P0468H06.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 35; DB 2; I llarity 100.0%; Pred. No. 2.3e+02; Conservative 0; Mismatches 0;
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EMBL; AP005296; BAD31279.1; -...
Gramene; Q8GSL3; -...
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR008994; Nucleic_acid_OB.
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                                         Mismatches
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100.08;
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Q657L2
ID Q657L
AC Q657L
DT 25-OC
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O06065;
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SEQUENCE 1
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Q6ZW55
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Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,

Ikeno M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,

Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,

Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,

Magasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,

Mamiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,

Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,

Maki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,

Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,

Yano M., Jiang J., Gojobori T.;

"The genome sequence and structure of rice chromosome 1.";

Nature 420:312-316(2002).

EMBL; AP003075; BAD45005.1; -.

Mypothetical protein.

SEQUENCE 164 AA; 18134 MW, 6CF81BD88C3C30C7 CRC64;
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STRAIN-ATCC 23344;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
Bavidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
Zhou L., Fraser C.M.;
"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
EMBL; CP000010; AAU50017.1; -.
SEQUENCE 164 AA; 17543 MW; 3B29EF2562073ABB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative lipoprotein.
ORFNames=BPSL2589;
Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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Burkholderiaceae; Burkholderia.
NCBI_TaxID=243160;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
TonB domain protein.
ORFNames=BMA2105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 AA
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5; Conservative
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Matches 5
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                                                                                                                                                            PubMed=1537794;

PubMed=1537794;

Atkins T., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R., Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I., Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D., Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K., Keith K.E., Maddison M., Moule S., Price C., Quail M.A., Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M., Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M., Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.; Genomic plasticity of the causative agent of melioidosis, I. Burkholderia pseudomallei.";

Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
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Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Sugiyama T.
IISSUE-Tongue;
Ota T., Nakagawa S., Senoh H., Wakamatsu A., Ishii S., Yamamoto J.,
Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda B.,
Wagatsuma M., Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima Bugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK123582; BAC85651.1; -.
SEQUENCE 165 AA; 17648 MW; 9CADD2C8FDFCB90F CRC64;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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(TrEMBLrel. 04, Last sequence update)
Burkholderiaceae; Burkholderia.
NCBI_TaxID=272560;
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                                                                                                                                                                                                                                                                                    MEDLINE=21128732; PubMed=11234002; DOI=10.1038/35059006; Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C.M., Harris D.E., Mungall K.L., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L.D., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M., Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
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                                                                                                       MEDLINE=93188700; PubMed=8446027; Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.; "Use of an ordered cosmid library to deduce the genomic organization
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           in MLCCL622.02 (Hypothetical protein ML2605) OrderedLocusNames=ML2605;
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R., Parkhill J., Garnier T., Churcher C.M.,
                         Mycobacterium leprae.
Bacteria, Actinobacteria, Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                            SEQUENCE FROM N.A.
Hamlin N., Churcher C.M.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                       B.G., Rajandream M.A.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR006025; Pept M Zn BS.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
Complete proteome; Hypothetical protein.
SEQUENCE 168 AA; 18602 MW; 6A6ED74C046359B1 CRC64;
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
OrderedLocusNames=MT0194, Rv0185;
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
EMBL, Z95398; CAB08794.1; -.
EMBL, ALS83926; CAC32137.1; -.
PIR; C87235; C87235.
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            Hypothetical protein MLCCL622.02
Name=MLCCL622.02; OrderedLocusNar
                                                                                                                                           eprae.";
197-206(1993)
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Submitted (MAY-1997)
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=TN;
MEDLINE=21128732;
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Mol. Microbiol. 7:
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MEDLINE=98295987;
Cole S.T., Brosch
                                                                                            SEQUENCE FROM N. MEDLINE=93188700
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MEDLINE-22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;
Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
Pryor M., Duthoy S., Grondin S., Lacroix C., Monsempe C., Simon S.,
Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
"The complete genome sequence of Mycobacterium bovis.";
Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
EMBL; BX248334; CAD93055.1; -.
InterPro; IPR006025; Pept M. Zn. BS.
PROSITE; PS00142; ZINC PROTEASE; UNKNOWN I.
Complete proteome; Hypothetical protein.
SEQUENCE 169 AA; 18397 MW; BE7677B0190054F3 CRC64;
Harris D.E., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Feltwell T., Gentles S., Hamlin Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.D., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares S. Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; Nature 393:537-544(1998).
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TIGR; MT0194; -.

TubercuList; Rv0185; -.

InterPro; IPR006025; Pept M Zn BS.

InterPro; IPR006025; Pept M Zn BS.

PROSITE; PS00142; ZINC_PRÖTEASE; UNKNOWN 1.

PROSITE; PS00142; ZINC_PRÖTEASE; UNKNOWN 1.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Mb0191.
OrderedLocusNames=Mb0191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 35; DB 2; 1 Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 5; Conservative 0; Mismatches 0;
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Pred. No. 2.4e+02;
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J. Bacteriol. 184:5479-5490(2002)
EMBL; BX842572; CAB09736.1; -.
EMBL; AE000516; AAK44414.1; -.
PIR; D70906; D70906.
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Q8LLM4
ID Q8LLMA
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RP SEQUE
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RL SUDMI
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MEDLINE=93388626; PubMed=8376404;
Castle A.M., Castle J.D.;
"Novel secretory proline-rich proteoglycans from rat parotid. Cloning and characterization by expression in AtT-20 cells.";
J. Biol. Chem. 268:20490-20496(1993).
EMBL; L17317; AAA03073.1; -..
PIR; A48013; A48013.
 Gaps
                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 24, Last annotation update)
4) Ol-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein C16D6.1.
ORFNames=C16D6.1;
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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 Indels
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3889.1; -.
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                                                                                                                                                                 007610 PRELIMINARY; PRT; 170 AA. 007610; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Proline-rich proteoglycan.
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Mismatches
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CE08230.
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Conservative
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                                                                      132 PPPHG 136
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5; Conser
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investigating biolo
Science 282:2012-2
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80 PPPHG
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Thaumatin-like protein 1.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Triticeae; Triticum.
NCBI TaxID=4565;
                                                                                                                                                                                                                                                                               062789;
01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AUG-1998 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Collagen VIII (Fragment).
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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       100.0%; Score 35; DB 2; Length 173; 100.0%; Pred. No. 2.4e+02;
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TISSUE=ACTION MUSCLE;
Reichenberg S., Plenz G., Robenek H.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054891; AAC08999.1; -.
HSSP; Q00780; 1091.
InterPro; IPR001073; Clq.
InterPro; IPR008983; TNF_like.
Pfam; PF00386; Clq; 1.
PRINTS; PR00007; COMPLEMNTCLQ.
SMART; SM00110; ClQ; 1.
                                                    Indels
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Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF389883; AAM69454.1; -.
HSSP; P33679; 1DU5.
InterPro; IPR001938; Thaumatin.
Pfam; PF00314; Thaumatin; 1.
PRINTS; PR00347; THAUMATIN.
ProDom; PD001321; Thaumatin; 1.
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173 173
173 AA; 18973 MW; 03489B6FBAAB6CAD CRC64;
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                                                    Mismatches
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Query Match
Best Local Similarity 100.
Matches 5; Conservative
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PPPHG 11
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strains capable of dealkylating and dechlorinating the herbicide
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NCBI_TaxID=3702;
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SEQUENCE
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Q9C4Z8
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Q8LEP5
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Q52724,
Q52724;
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Rhodococcus corallinus (NRRL 15444B) N-ethylammeline chlorohydrolase (trzA) (Fragment).
Rhodococcus corallinus.
Rhodococcus corallinus.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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MEDLINE=96011356; PubMed=7592318;
Shao Z.Q., Seffens W., Mulbry W., Behki R.M.;
"Cloning and expression of the s-triazine hydrolase gene (trzA) from Rhodococcus corallinus and development of Rhodococcus recombinant
                                                                               Gaps
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Glycine/proline-rich protein (At5g17650).
Name=K10A8 130;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                       Length 173;
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0) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
 17646 MW; EC172D12ACD944D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18536 MW; E3510947AA98BC0A CRC64;
                      100.0%; Score 35; DB 2; I 100.0%; Pred. No. 2.4e+02;
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AS76258.1;
                                                                                rative
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Submitted (MAR-2004)
EMBL; AL391151; CACO1
EMBL; BT012163; AAS76
PIR; T51469.
                                                         Similarity 5; Conserv
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Ishida J., Kamiya A
Seki M., Shinozaki
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145 PPPHG 149
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   173 AA;
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Matches 5
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Best Local S
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SEQUENCE
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Q9LF59;
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Q52724
ID Q5272
AC Q5272
DT 01-NO
DT 01-OC
DE Rhodo
DE (trzA
OC Bacte
OC COLY
OX NCBL
RP SEQUE
RX MEDLI
RA Shao
RT "Clon
RT Rhodo
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Gaps
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein F27M3 5 (Hypothetical protein F5M6.24).
Name=F27M3 5; Synonyms=F5M6.24;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22088475; PubMed=12093376;
Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; "Full-length messenger RNA sequences greatly improve genome annotation.";
Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002).
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InterPro; IPR006031; XYPPX.
Pfam; PF02162; XYPPX; 8.
SEQUENCE 176 AA; 18434 MW; E84E78E58D435547 CRC64;
                                                                                                                                                                                                                                                                 175 AA; 19406 MW; 881A0E9059A62528 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 2; L
100.0%; Pred. No. 2.5e+02;
iive 0; Mismatches 0;
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atrazine.";
J. Bacteriol. 177:5748-5755(1995).
EMBL; L16534; AAA90930.1; -.
PIR; T46665; T46665.
HSSP; Q12178; 1P6O.
GO; GO:0016787; F:hydrolase activity; IE
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Best Local Similarity 100.
Matches 5; Conservative
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28 PPPHG 32
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QBND66
ID QBND6
AC QBND6
DT 01-OC
DT 01-MA
DE HYPOT
GN NAME=
OS HOMO
OC EUKAT
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Proc. Natl. Acad. Sci. U.S.A. 93:1993-1996(1996).
EMBL; U33628; AAC48538.1; -.
InterPro; IPR001589; Actbind_actnin.
PROSITE; PS00019; ACTININ_1; UNKNOWN 1.
SEQUENCE 181 AA; 20062 MW; 3214CI85A69418FB CRC64;
                                                                                            Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AC074360; AAG60137.1; -. EMBL; AC079041; AAG50730.1; -. EMBL; A86441; A86441. InterPro; IPR006031; XYPPX. InterPro; IPR016031; XYPPX. Pfam; PF02162; XYPPX; B. Hypothetical protein. SEQUENCE 176 AA; 18395 MW; FAEB3F158D5C777A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=8700873; DOI=10.1073/pnas.93.5.1993; Almenoff J.S., Rudner X.L., Kearney D.M.,
                                                                                                                                                                                                                                                                                                                                                 ; Score 35; DB 2; Length 176; Pred. No. 2.5e+02; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 35; DB 2; Length 181; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Sphingolipid Ca2+ release mediating protein of endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eota; Thermoprotei; Thermoproteales;
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Q8ZY20;
Q8ZY20;
O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-JUN-2003 (TrEMBLrel. 24, Last annotation update)
P. aerophilum family 70 protein.
OrderedLocusNames=PAE0984;
Pyrobaculum aerophilum.
Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum.
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI _TaxID=3702;
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MEDLINE=96312527; I
Mao C., Kim S.H., I
Kindman L.A.;
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5; Conserv
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|PPPHG 181
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                                                                           SEQUENCE FROM N.A
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Q28261
ID Q2826
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082Y20
ID 082Y2
AC 082Y2
DT 01-MA
DT 01-JU
DE P. ae
GN Order
OS Pyrob
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
4 yPothetical protein OJ1123 B08.33.
Name=OJ1123 B08.33;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                        "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum aerophilum.";
Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009797; AAL63176.1; -.
Complete proteome.
SEQUENCE 185 AA; 20778 MW; D9FDF694FAD2D2D6 CRC64;
SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
Miller J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sasaki T., Matsumoto T., Hattori M., Sakaki Y., Katayose Y.;
Cryza sativa nipponbare (GA3) genomic DNA, chromosome 9, BAC clone:OJ1123 B08.";
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
C.!- SIMILARITY: Contains 1 RING-type zinc finger.
R EMBL; AP005720; BAD38328.1; -.
R InterPro; IPR001841; Znf_ring.
R Pfam; PF00097; zf-C3HC4; 1.
R PKANT; SM00184; RING; 1.
R PROSITE; PS50089; ZF_RING_2; 1.
R Hypothetical protein; Metal-binding; Zinc; Zinc-finger.
O SEQUENCE 192 AA; 20843 MW; E9A7D6F14B6C3DD9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                      Length 185;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp434G2126 (Fragment).
Name=DKFZp434G2126;
                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 35; DB 2; I
100.0%; Pred. No. 2.6e+02;
vative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 5; Conservative
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Best Local Similarity 100.
Matches 5; Conservative
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                         P SEQUENCE FROM N.A.

TISSUE=Testis;
Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
Ansorge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;
Bubmitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; ALB34172; CAD38870.1; -.

R HSSP; P42771; 2A5E.

R InterPro; IPR002110; ANK.

R Ffam; PF00023; Ank; 2.

R PRINTS; PR01415; ANK REPEAT; 1.

R SMART; SM00248; ANK REPEAT; 1.

R PROSITE; PS50297; ANK REPEAT; 1.

R PROSITE; PS50297; ANK REP REGION; 1.

ANK repeat; Hypothetical protein.

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SEQUENCE 201 AA; 21709 MW; 1E26E07B168873E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0048L03.37.
Name=OSJNBa0048L03.37;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki T., Matsumoto T., Fujisawa M.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC clone:OSJNBa0048L03.";
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AP007205; BAD38589.1; -.
Hypothetical protein.
SEQUENCE 203 AA; 21805 MW; 204D6EED4120FD35 CRC64;
                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 35; DB 2; Length 201; Best Local Similarity 100.0%; Pred. No. 2.8e+02; Matches 5; Conservative 0; Mismatches 0; Indels
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188 PPPHG 192
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9 PPPHG 13
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NCBI_TaxID=9606;
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Search completed: June 15, 2005, 14:21:29 Job time : 85.5 secs